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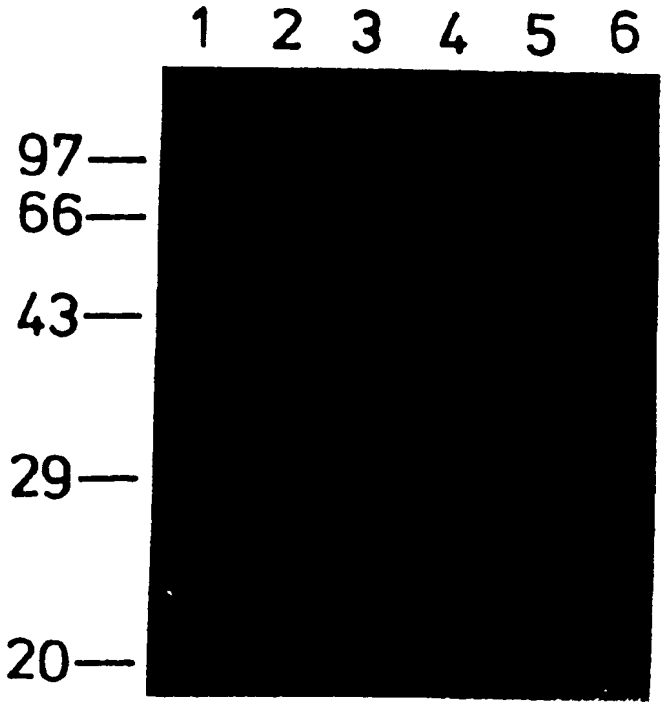
(54) Title: PROTEIN PHOSPHATASE-1 CATALYTIC SUBUNIT INTERACTIONS

(57) Abstract

A method of identifying a compound which modulates the interaction between a PP1c and a regulatory subunit thereof, the method comprising determining whether a compound enhances or disrupts the interaction between (a) a PP1c or a fragment, variant, derivative or fusion thereof or a fusion of a fragment, variant or derivative and (b) a regulatory subunit which is able to bind to PP1c or a PP1c-binding fragment, variant, derivative or fusion of said subunit or a fusion of said fragment, variant or derivative. A method of affecting cellular metabolism or function, the method comprising administering to a cell (a) a compound which modulates the interaction between a PP1c and a regulatory subunit thereof or (b) a compound which mimics the effect of a regulatory subunit of PP1c or (c) a peptide capable of binding a PP1c and which affects the ability of PP1c to bind to a particular target and/or affects the regulation of PP1c activity, or a functional equivalent thereof.



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# PROTEIN PHOSPHATASE-1 CATALYTIC SUBUNIT INTERACTIONS

The present invention relates to peptides and protein-protein interactions and to the use of peptides, peptide analogues and compounds which modulate protein-protein interactions in the control of cellular metabolism and function.

Cellular metabolism or function is controlled by a number of regulatory agents, which are affected by extracellular factors, for example the physical condition of the cell or the binding of a messenger molecule to a receptor located on the cell surface. The extracellular factor may then initiate a cascade of secondary messenger reactions within the cell itself, leading ultimately to changes in some aspects(s) of metabolism or cell function.

It is well recognised by those skilled in the art that phosphorylation or dephosphorylation reactions often play a key role in regulating the activity of the proteins affected. Dephosphorylation reactions are catalysed by phosphatase enzymes, the activity of which may themselves be controlled by phosphorylation and/or dephosphorylation events. Whilst a substantial amount of knowledge has been accumulated regarding protein phosphatases as a group, the number and variety of these enzymes is such that detailed information concerning the mode of action of a specific phosphatase is not always available. There remains a need to further elucidate and characterise particular key enzymes.

The reversible phosphorylation of proteins regulates most aspects of cell life. About a third of all mammalian proteins are now thought to contain covalently bound phosphate and, since protein kinases and phosphatases probably account for approximately 2-3% of all human gene products (Hunter, 1995), many of these enzymes must typically phosphorylate/dephosphorylate numerous proteins *in vivo*. However, it is becoming increasingly clear that some protein kinases

and phosphatases do not find their physiological substrates by simple diffusion within cells and that they are frequently directed to particular loci in the vicinity of their substrates by interaction with targeting subunits. In this way, the actions of protein kinases and phosphatases with inherently broad specificities are restricted and their properties tailored to the needs of a particular subcellular location, organelle or process (reviewed in Hubbard and Cohen, 1993; Faux and Scott, 1996).

Protein phosphatase-1 (PP1), one of the major protein serine/threonine phosphatases of eukaryotic cells, participates in the control of a variety of cellular functions that include glycogen metabolism, muscle contraction, the exit from mitosis (reviewed in [1,2]) and the splicing of mRNA [3]. However, evidence has been accumulating that different processes are regulated by distinct forms of PP1 in which the phosphatase catalytic subunit (PP1c) is complexed to specific "targeting subunits". These proteins not only direct PP1c to particular subcellular locations, but modify its specificity in unique ways and confer regulation by extracellular agonists (reviewed in [2,3]).

Several targeting subunits have been isolated and characterised, including the $G_M$-subunit that targets PP1c to both the glycogen particles and sarcoplasmic reticulum of striated muscles [4,5], the $G_L$ subunit that targets PP1c to liver glycogen [6,7], the M-complexes responsible for the association of PP1c with the myofibrils of skeletal muscle [8,9] and smooth muscle [9-12], the p53 binding protein p53BP2 [13] and nuclear proteins such as sds22 [14] and NIPP1 [15,16]. PP1c is also reported to interact with other mammalian proteins such as the retinoblastoma gene product [17], ribosomal protein L5 [18], a 110 kDa nuclear protein that has yet to be identified [15] and two cytosolic proteins, termed inhibitor-1 and inhibitor-2. Inhibitor-1, and its homologue termed dopamine and cyclic AMP-regulated phosphoprotein (DARPP), become potent PP1 inhibitors after phosphorylation by cyclic AMP-dependent protein kinase

(PKA). Inhibitor-1 is thought to inactivate PP1c released from glycogen particles when $G_M$ is phosphorylated by PKA [19]. Inhibitor-2 is present as a complex with PP1 in the cytosol, and there is evidence that one of its roles is to act like a molecular chaperone to ensure that the PP1 catalytic centre is folded correctly prior to its delivery to a specific targeting subunit [20]. It seems likely that many other PP1-targeting subunits will be identified over the next few years as a result of the introduction of powerful new techniques such as microcystin Sepharose affinity chromatography [8] and the yeast "two hybrid system" [13].

The forms of PP1c isolated so far each contain a single PP1c-binding subunit, implying that the interaction of different targeting subunits with PP1c may be mutually exclusive. This, in turn, suggests that the binding sites for targeting subunits may overlap, and that the proportion of PP1 directed to any particular location may be determined by the amounts of each targeting subunit synthesised and their relative affinities for PP1. However, the different targeting subunits show surprisingly little similarity to one another. $G_M$ and $G_L$ are structurally related, yet display only 23% amino acid sequence identity over the first 286 residues of $G_M$, while $G_L$ lacks the C-terminal 750 residues of $G_M$ [7]. p53BP2 [13] and the $M_{110}$ subunits from smooth muscle [10,11] and skeletal muscle [8] contain ankyrin repeats, but no other similarities have so far been detected between other PP1 targeting subunits.

The paradigm for the targeting subunit concept is protein phosphatase-1 (PP1), one of the major serine/threonine specific protein phosphatases of eukaryotic cells (Stralfors *et al.*, 1985). This enzyme is involved in controlling diverse cellular functions including glycogen metabolism, muscle contraction, the exit from mitosis and the splicing of RNA (Cohen, 1989; Shenolikar, 1994; Wera and Hemmings, 1995). These different processes appear to be regulated by distinct PP1 holo-enzymes in which the same catalytic subunit (PP1c) is

complexed to different targeting or regulatory subunits. The latter class of subunits act to confer *in vivo* substrate specificity not only by directing PP1c to the subcellular loci of its substrates, but also by enhancing or suppressing its activity towards different substrates. In addition, the regulatory subunits allow the activity of PP1 to be modulated by reversible protein phosphorylation and second messengers in response to extracellular stimuli.

Many regulatory subunits modulate the activity of PP1 towards its substrates. In the instance of the regulatory $M_{110}$ subunit that targets PP1c to myosin, the region on the $M_{110}$ subunit that enhances the dephosphorylation of myosin by PP1 has now been shown to be distinct from the region involved in targetting the PP1-M holoenzyme to myosin. These observations indicate that alterations in the substrate specificity of PP1c are likely to result from conformational changes induced by interactions with the targetting subunit and not simply as a direct result of targetting PP1c to its substrate. However, in the case of the glycogen binding subunit $G_M$, the dephosphorylation of glycogen phosphorylase and glycogen synthase was enhanced only under conditions when both the PP1-$G_M$ complex and its substrates were bound to glycogen (Hubbard and Cohen, 1989) suggesting that targetting alone may be sufficient to enhance specificity.

Whilst the identity of the PP1-binding site(s) on any targeting subunit is unknown, it has now been realised that the control of the substrate specificity and activity of this key regulatory enzyme and its interactions are of therapeutic importance. Disruption of PP1-targeting subunit interactions provide a way of altering selectively the state of phosphorylation, and hence the activities, of particular PP1 substrates. We have now identified relatively small peptides from the $G_M$ and $M_{110}$-subunits that interact with PP1, and which either disrupt or mimic the distinctive properties of myofibrillar and glycogen-associated forms of PP1. The binding of the G-subunit and the M-subunit of PP1 has also

been found to be mutually exclusive.

A first aspect of the invention provides a method of identifying a compound which modulates the interaction between a PP1c and a regulatory subunit thereof, the method comprising determining whether a compound enhances or disrupts the interaction between (a) a PP1c or a fragment, variant, derivative or fusion thereof or a fusion of a fragment, variant or derivative and (b) a regulatory subunit which is able to bind to PP1c or a PP1c-binding fragment, variant, derivative or fusion of said subunit or a fusion of said fragment, variant or derivative.

Conveniently, the PP1c or a fragment, variant or derivative or fusion thereof or a fusion of a fragment, variant or derivative is one that is produced using recombinant DNA technology. By "fragment, variant, derivative or fusion of PP1c" we mean any such fragment, variant, derivative or fusion that retains the ability to interact with a regulatory subunit or a suitable PP1c-binding fragment, variant, derivative or fusion of said subunit or a fusion of said fragment, variant or derivative.

By "regulatory subunit" we mean any such regulatory subunit. Further subunits are being identified all of the time. It is preferred if the regulatory subunit contains the consensus peptide sequence Arg/Lys-Val/Ile-Xaa-Phe as described below.

By "PP1c-binding fragment, variant, derivative or fusion of said subunit or a fusion of said fragment, variant or derivative" we include any such fragments, variants, derivatives and fusions which are able to bind to PP1c. Conveniently, the fragments, variants, derivatives are made using recombinant DNA technology or, in the case of peptides and peptide derivatives and analogues they may be made using peptide synthetic methods.

The enhancement or disruption of the interaction between the said PP1c or a fragment, variant, derivative or fusion thereof or a fusion of a fragment, variant or derivative and the said regulatory subunit or a fragment, variant, derivative or fusion thereof or a fusion of a fragment, variant or derivative can be measured *in vitro* using methods well known in the art of biochemistry and including any methods which can be used to assess protein-protein, protein-peptide and protein-ligand interactions.

The said interaction can also be measured within a cell, for example using the yeast two-hybrid system as is well known in the art.

It should be appreciated that before the present invention the dissociation of a PP1c-regulatory subunit has not been achieved using a small molecule such as a peptide or a peptide analogue or derivative. Thus, it is preferred if the compounds screened in the method of the first aspect of the invention are small molecules and in particular that they are not intact regulatory subunits of PP1c.

By "small molecule" we include any compounds which have a molecular weight of less than 5000, preferably less than 2000 and more preferably less than 1000. Conveniently, the compounds screened are compounds which are able to enter a cell either passively *via* the cell membrane or *via* an active uptake system.

A second aspect of the invention provides a method of identifying a compound which mimics the effect of a regulatory subunit of PP1c, the method comprising contacting said compound with PP1c and determining whether, in the presence of the compound, PP1c adopts the function of properties of a PP1c in the presence of a given regulatory subunit.

By "mimics the effect of a regulatory subunit of PP1c" we include the meaning

that the compound modifies a property of PP1c in such a way that PP1c acts, in at least one respect, like PP1c that is interacting with a regulatory subunit.

Examples of the properties of PP1c that may be modified, and examples of compounds which modify the properties of PP1c which are therefore identifiable in this method are given below.

Preferably, in the methods of the first and second aspects the said regulatory subunit of PP1c is any one of $M_{110}$, $G_L$, $G_M$, M-complexes, p53 BP2, sds22, NIPPI, L5, Inhibitor-1, Inhibitor-2, or DARPP.

More preferably, the regulatory subunit of PP1c is any one of $M_{110}$, $G_L$, $G_M$, M-complexes or p53BP2, and still more preferably the regulatory subunit of PP1c is $M_{110}$ or $G_M$.

In relation to the method of the first aspect of the invention the fragment of a regulatory subunit which is able to bind to PP1c is any of the peptides [G63-T93], [G63-N75], [E2-R575], [E2-P243], [E2-D118], [H100-P350] and peptide 63-80 of $G_M$ or functional equivalents thereof or peptides comprising said peptide sequences provided that they are not the complete $G_M$ regulatory subunit. Preferably the peptides are not [E2-R575] or [H100-P350].

As is described in more detail in the Examples, these peptides have been shown to bind to PP1c and it is convenient, in some circumstances, for the method to be carried out such that one of these peptide is displaced from, or the binding is enhanced to, PP1c. Suitably, the peptide may be labelled in a detectable manner to facilitate the detection of the interaction with PP1c. Conveniently, the peptide is labelled radioactively or fluorescently using methods well known in the art.

Also in relation to the method of the first aspect of the invention the fragment of a regulatory subunit which is able to bind to PP1c is any of the peptides [M1-E309], [M1-F38], [M1-A150] or [L24-Y496] of $M_{110}$ or functional equivalents thereof or peptides comprising said peptide sequences provided that they are not the complete $M_{110}$ regulatory subunit.

As is shown in more detail in the Examples these peptides have been shown to bind to PP1c.

Also in relation to the first aspect of the invention the PP1c-binding fragment, variant or derivative of said regulatory subunit or a fusion of said fragment, variant or derivative comprises the consensus peptide sequence Arg/Lys-Val/Ile-Xaa-Phe wherein Xaa is any amino acid.

We have found that, surprisingly, many regulatory subunits that bind to PP1c contain the consensus peptide sequence Arg/Lys-Val/Ile-Xaa-Phe wherein Xaa is any amino acid, preferably a naturally occurring amino acid. Typically, the PP1c-binding fragment, variant or derivative of said regulatory subunit or a fusion of said fragment, variant or derivative is a peptide (typically 8-400 amino acid residues, preferably 8-200, more preferably 8-10 and still more preferably 8-20 amino acid residues in length which comprises the given consensus peptide sequence).

It is preferred if the PP1c-binding fragment, variant or derivative comprises, in addition to the said consensus peptide sequence, at least one basic residue in the four residues N-terminal of the consensus peptide sequence. Preferably, there are at least two basic residues in this position, more preferably at least three such residues.

It is also preferred wherein in the consensus peptide sequence Xaa is not Asp

or Glu because the negative charge is believed to interfere with binding to PP1c. Similarly, it is preferred if Xaa is not a large hydrophobic residue such as Phe, Tyr, Trp, Ile or Leu.

It is particularly preferred if the PP1c-binding fragment is a fragment of a regulatory subunit comprising the said consensus peptide sequence and therefore the peptide sequences which flank the consensus peptide sequence are the same as in the native regulatory subunit.

Preferably the PP1c-binding fragment is a fragment of any of the $M_{110}$, $G_L$, $G_M$, M-complexes, p53BP2, sds22, NIPPI, L5, Inhibitor-1, Inhibitor-2 or DARPP regulatory subunits comprising said consensus sequence.

Although the methods of the first and second aspects of the invention do not rely on any particular mechanism whereby the modulation or mimicking occurs, it is preferred if the compound binds to a PP1c. Alternatively, but still preferably, the compound binds to a regulatory subunit of PP1c.

A further aspect of the invention provides a compound identifiable by the method of the first or second aspects of the invention.

A further aspect of the invention provides a compound which modulates the interaction between a PP1c and a regulatory subunit thereof said compound comprising any of the peptides [G63-T93], [G63-N75], [E2-R575], [E2-P243], [E2-D118], [H100-P350] and peptide 63 to 80 of $G_M$ or functional equivalents or said compound comprising any of the peptides [M1-E309], [M1-F38], [M1-A150] or [L24-Y496] of $M_{110}$ or functional equivalents thereof or said compound comprising the consensus peptide sequence Arg/Lys-Val/Ile-Xaa-Phe wherein Xaa is any naturally occurring amino acid or functional equivalents thereof, provided that the said compound is not a complete regulatory subunit

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method comprising selecting a compound which is capable of adopting the same or substantially the same conformation as a peptide bound to the regulatory subunit-binding site of PP1c or the same or substantially the same conformation as the portion of PP1c which binds to said peptide. Suitably, the peptide comprises the consensus peptide sequence Arg/Lys-Val/Ile-Xaa-Phe wherein Xaa is any amino acid, preferably a naturally occurring amino acid. Conveniently, the said peptide consists of residues 63 to 75 of $G_M$.

It is particularly preferred if the conformation of the said peptide and the conformation of the said portion of PP1c is as defined by reference to the atomic coordinates given in Table A (see also Example 2). Example 2 provides further details of the peptide - PP1c interactions.

Table A provides the atomic coordinates for the given PP1c-peptide crystal structure.

A further aspect of the invention provides a compound identifiable by the aforementioned method of the invention.

It will be appreciated that the aforementioned compounds and peptides will be useful in medicine and, accordingly, the invention includes pharmaceutical compositions of the said compounds in combination with a pharmaceutically acceptable carrier.

The formulations may conveniently be presented in unit dosage form and may be prepared by any of the methods well known in the art of pharmacy. Such methods include the step of bringing into association the active ingredient (compound of the invention) with the carrier which constitutes one or more accessory ingredients. In general the formulations are prepared by uniformly and intimately bringing into association the active ingredient with liquid carriers

or finely divided solid carriers or both, and then, if necessary, shaping the product.

Formulations in accordance with the present invention suitable for oral administration may be presented as discrete units such as capsules, cachets or tablets, each containing a predetermined amount of the active ingredient; as a powder or granules; as a solution or a suspension in an aqueous liquid or a non-aqueous liquid; or as an oil-in-water liquid emulsion or a water-in-oil liquid emulsion. The active ingredient may also be presented as a bolus, electuary or paste.

A tablet may be made by compression or moulding, optionally with one or more accessory ingredients. Compressed tablets may be prepared by compressing in a suitable machine the active ingredient in a free-flowing form such as a powder or granules, optionally mixed with a binder (eg povidone, gelatin, hydroxypropylmethyl cellulose), lubricant, inert diluent, preservative, disintegrant (eg sodium starch glycolate, cross-linked povidone, cross-linked sodium carboxymethyl cellulose), surface-active or dispersing agent. Moulded tablets may be made by moulding in a suitable machine a mixture of the powdered compound moistened with an inert liquid diluent. The tablets may optionally be coated or scored and may be formulated so as to provide slow or controlled release of the active ingredient therein using, for example, hydroxypropylmethylcellulose in varying proportions to provide desired release profile.

Formulations suitable for topical administration in the mouth include lozenges comprising the active ingredient in a flavoured basis, usually sucrose and acacia or tragacanth; pastilles comprising the active ingredient in an inert basis such as gelatin and glycerin, or sucrose and acacia; and mouth-washes comprising the active ingredient in a suitable liquid carrier.

Formulations suitable for parenteral administration include aqueous and non-aqueous sterile injection solutions which may contain anti-oxidants, buffers, bacteriostats and solutes which render the formulation isotonic with the blood of the intended recipient; and aqueous and non-aqueous sterile suspensions which may include suspending agents and thickening agents. The formulations may be presented in unit-dose or multi-dose containers, for example sealed ampoules and vials, and may be stored in a freeze-dried (lyophilised) condition requiring only the addition of the sterile liquid carrier, for example water for injections, immediately prior to use. Extemporaneous injection solutions and suspensions may be prepared from sterile powders, granules and tablets of the kind previously described.

Preferred unit dosage formulations are those containing a daily dose or unit, daily sub-dose or an appropriate fraction thereof, of an active ingredient.

It should be understood that in addition to the ingredients particularly mentioned above the formulations of this invention may include other agents conventional in the art having regard to the type of formulation in question, for example those suitable for oral administration may include flavouring agents.

A further aspect of the invention provides a method of affecting cellular metabolism or function, the method comprising administering to a cell (a) a compound which modulates the interaction between a PP1c and a regulatory subunit thereof or (b) a compound which mimics the effect of a regulatory subunit of PP1c or (c) a peptide capable of binding a PP1c and which affects the ability of PP1c to bind to a particular target and/or affects the regulation of PP1c activity, or a functional equivalent thereof.

It will be appreciated that the said compounds are disclosed above with respect to specific compounds or with respect to methods of obtaining such compounds.

In particular, it is preferred if the compound administered to the cell is any one or more of the peptides [G63-T93], [G63-N75], [E2-R575], [E2-P243], [E2-D118], [H100-P350] and peptide 63-80 of $G_M$ or functional equivalents thereof or peptides comprising said peptide sequences or any one or more of the peptides [M1-E309], [M1-F38], [M1-A150] or [L24-Y496] of $M_{110}$ or functional equivalents thereof or peptides comprising said peptide sequences. Preferably, the peptide is not [E2-R575] or [H100-P350].

In this embodiment it will be appreciated that functional equivalents include those compounds defined above as being functional equivalents, in particular, derivatives of peptides which are more readily able to enter a cell.

The compound may be administered to the cell in any suitable way, in particular in such a way that the compound will enter the cell in a suitable form to have its desired effect. Method of facilitating the entry of a compound into the cell are known in the art, for example, in relation to peptides the importins and penetrations may be used, or the peptides may be micro-injected or they may enter the cell in a suitable vehicle such as in a liposome.

Preferably, the cell is a cell in a mammalian body.

The aforementioned compounds of the invention or a formulation thereof may be administered by any conventional method including oral and parenteral (eg subcutaneous or intramuscular) injection. The treatment may consist of a single dose or a plurality of doses over a period of time.

Whilst it is possible for a compound of the invention to be administered alone, it is preferable to present it as a pharmaceutical formulation, together with one or more acceptable carriers. The carrier(s) must be "acceptable" in the sense of being compatible with the compound of the invention and not deleterious to

the recipients thereof. Typically, the carriers will be water or saline which will be sterile and pyrogen free.

A further aspect of the invention provides a method of treating a patient in need of modulation of PP1c activity or function the method comprising administering to the patient an effective amount of a compound which modulates the interaction between a PP1c and a regulatory subunit thereof or (b) a compound which mimics the effect of a regulatory subunit of PP1c or (c) a peptide capable of binding a PP1c and which affects the ability of PP1c to bind to a particular target and/or affects the regulation of PP1c activity, or a functional equivalent thereof.

As will be apparent from what is described herein, protein phosphatase-1 (PP1) is one of the principal serine/threonine-specific protein phosphatases in human cells where it plays key roles in regulating a variety of physiological roles, including the metabolism of glycogen, the splicing of mRNA, the exit from mitosis and the contraction of smooth muscle. The different functions of PP1 are carried out by distinct species of this enzyme in which the same catalytic unit is complexed to different "targeting" subunits. The latter class of proteins direct PP1 to specific subcellular loci, tailor its properties to the needs of a particular locus and confer the ability to be regulated by extracellular signals (hormones, growth factors, neurotransmitters). Compounds as herein described that disrupt specific PP1-"targeting" subunits interactions or mimic the effect of a targeting subunit are likely to have a number of therapeutic uses as outlined below.

PP1 interacts with the M110-subunit which targets it to myosin in smooth muscle and enhances the rate at which PP1 dephosphorylates myosin. The dephosphorylation of myosin underlies the relaxation of smooth muscle. Thus compounds such as those disclosed herein which disrupt the interaction of PP1

with M110 in arterial muscle are expected to increase the phosphorylation of arterial myosin and elevate blood pressure.

The interaction of PP1 with M110 enhances the rate at which PP1 dephosphorylates myosin, but suppresses the rate at which it dephosphorylates glycogen phosphorylase. The disruption of the PP1-M110 interaction is therefore measured in a screen by looking for compounds which enhance the dephosphorylation of phosphorylase and/or suppress the dephosphorylation of the myosin P-light chain (see the Examples).

Compounds, such as those disclosed herein, that mimic the effect of the M110 subunit in stimulating myosin dephosphorylation are expected to be useful in lowering blood pressure. Such compounds are identified by their ability to stimulate the dephosphorylation of the myosin P-light chain by the catalytic subunit of PP1. An example of such an assay, which shows that the N-terminal 38 residues of the M110 subunit stimulate the dephosphorylation of the myosin P-light chain by PP1, is shown in the Examples.

The interaction of PP1 with $G_L$ targets the phosphatase to liver glycogen. This interaction enhances the dephosphorylation glycogen synthase which stimulates the conversion of glucose to glycogen. A compounds, such as those disclosed herein, disrupts the interaction between PP1 and $G_L$ is expected to be useful in treating hypoglycaemia. The interaction of $G_L$ with PP1 strongly suppresses the rate at which PP1 dephosphorylates glycogen phosphorylase. A compound, such as those disclosed herein, which disrupts the interaction of PP1 with $G_L$ can be screened for very simply by its ability to increase the phosphorylase phosphatase activity of PP1 $G_L$. This can be carried out, for example, using rat liver glycogen pellet as described in the Examples. There is no need to use the purified enzyme.

PP1 interacts with p53 BP2 (Helps *et al*, 1995) a protein which is known to interact with the tumour suppressor p53. The phosphorylation of p53 is known to enhance its ability to bind to DNA and hence its ability to function as a tumour suppressor. p53BP2 may be a protein which targets PP1 to p53 stimulating the dephosphorylation and inactivation of p53. A compound, such as those disclosed herein, which disrupts the interaction of PP1 with p53BP2 may enhance the phosphorylation of p53 and its ability to function as a tumour suppressor. Since p53BP2 suppresses the dephosphorylation of glycogen phosphorylase (Helps *et al*, 1995), compounds that disrupt the p53BP2-PP1 complex can be screened by measuring the increase in rate of dephosphorylation of glycogen phosphorylase.

The present invention provides peptides able to bind to the catalytic sub-unit of protein phosphatase-1 (hereinafter referred to as PP1c). Generally the peptides affect the ability of PP1c to bind to particular target(s) and/or the regulation of PP1c activity.

Peptides can be designed based on the sequences of regulatory subunits, especially in relation to the peptide consensus sequence found therein and its flanking sequences. Peptides can be synthesised by methods well known in the art. For example, peptides may be synthesised by the Fmoc-polyamide mode of solid-phase peptide synthesis as disclosed by Lu *et al* (1981) *J. Org. Chem.* **46**, 3433 and references therein. Temporary N-amino group protection is afforded by the 9-fluorenylmethyloxycarbonyl (Fmoc) group. Repetitive cleavage of this highly base-labile protecting group is effected using 20% piperidine in N,N-dimethylformamide. Side-chain functionalities may be protected as their butyl ethers (in the case of serine threonine and tyrosine), butyl esters (in the case of glutamic acid and aspartic acid), butyloxycarbonyl derivative (in the case of lysine and histidine), trityl derivative (in the case of cysteine) and 4-methoxy-2,3,6-trimethylbenzenesulphonyl derivative (in the case

of arginine). Where glutamine or asparagine are C-terminal residues, use is made of the 4,4'-dimethoxybenzhydryl group for protection of the side chain amido functionalities. The solid-phase support is based on a polydimethyl-acrylamide polymer constituted from the three monomers dimethylacrylamide (backbone-monomer), bisacryloylethylene diamine (cross linker) and acryloylsarcosine methyl ester (functionalising agent). The peptide-to-resin cleavable linked agent used is the acid-labile 4-hydroxymethyl-phenoxyacetic acid derivative. All amino acid derivatives are added as their preformed symmetrical anhydride derivatives with the exception of asparagine and glutamine, which are added using a reversed N,N-dicyclohexyl-carbodiimide/1-hydroxybenzotriazole mediated coupling procedure. All coupling and deprotection reactions are monitored using ninhydrin, trinitrobenzene sulphonic acid or isotin test procedures. Upon completion of synthesis, peptides are cleaved from the resin support with concomitant removal of side-chain protecting groups by treatment with 95% trifluoroacetic acid containing a 50% scavenger mix. Scavengers commonly used are ethanedithiol, phenol, anisole and water, the exact choice depending on the constituent amino acids of the peptide being synthesised. Trifluoroacetic acid is removed by evaporation *in vacuo*, with subsequent trituration with diethyl ether affording the crude peptide. Any scavengers present are removed by a simple extraction procedure which on lyophilisation of the aqueous phase affords the crude peptide free of scavengers. Reagents for peptide synthesis are generally available from Calbiochem-Novabiochem (UK) Ltd, Nottingham NG7 2QJ, UK. Purification may be effected by any one, or a combination of, techniques such as size exclusion chromatography, ion-exchange chromatography and (principally) reverse-phase high performance liquid chromatography. Analysis of peptides may be carried out using thin layer chromatography, reverse-phase high performance liquid chromatography, amino-acid analysis after acid hydrolysis and by fast atom bombardment (FAB) mass spectrometric analysis.

The peptides may be derived from the targeting subunit(s) of PP1c, in particular from the subunits $G_L$, $G_M$, $M_{110}$ and/or $M_{21}$. Additionally the peptides may be derived from other subunits such as different M-complexes, p53BP2, sds22, NIPP1, L5, Inhibitor-1, Inhibitor-2, DARPP or the like. Functional equivalents or portions of these peptides may also be used.

In a further aspect the present invention provides the use of peptides derived from targeting subunit(s) of PP1c, functional equivalents or portions thereof to affect cellular metabolism or function.

In a further aspect the present invention provides a method of treatment of the human or non-human (preferably mammalian) animal body, said method comprising altering the levels of peptides derived from targeting subunit(s) of PP1c, functional equivalents or portions thereof to an extent that cellular metabolism or function is affected.

Aspects of cellular metabolism that may be affected include (but are not limited to) glycogen metabolism, muscle metabolism, physiology and function.

Generally the levels of peptides or their activity will be enhanced in cells and this control may be achieved by causing higher levels of expression of nucleotides sequences encoding for such peptides (optionally linked to molecules which allow them to cross a cell membrane) or through the administration of such peptides or precursors thereof. Alternatively, in some circumstances, it may be more desirable to depress the levels of certain peptides or at least to depress the level of peptides in active form.

Preferred peptides according to the present invention are derivatives of $G_M$, especially [G63-T93], [G63-N75], [E2-R575], [E2-P243], [E2-D118], [H100-P350] and peptide 63 to 80, and derivatives of $M_{110}$, especially

[M1-E309], [M1-F38], [M1-A150], [L24-Y496]. Preferably, the peptide is not [E2-R575] or [H100-P350].

Particularly preferred peptides are those derived from amino acid nos. 63 to 93 (including 63-80 and 63-75) of $G_M$; or from amino acids 1 to 309 (including from 1-150 and 1-38) of $M_{110}$.

The sequence of $G_M$ is given in Chen *et al* (1994) *Diabetes* **43**, 1234-1241.

In yet further aspect the present invention provides chimeric proteins containing portions of other proteins or peptides or containing additional amino acids.

Additionally the present invention provides nucleotide sequences (optionally in the form of plasmids) encoding the peptides or chimeric proteins of interest. DNA which encodes the polypeptides or peptides of the invention or chimeric proteins can be made based on a knowledge of the peptide sequences disclosed herein. The DNA is then expressed in a suitable host to produce a polypeptide comprising the compound of the invention. Thus, the DNA encoding the polypeptide constituting the compound of the invention may be used in accordance with known techniques, appropriately modified in view of the teachings contained herein, to construct an expression vector, which is then used to transform an appropriate host cell for the expression and production of the polypeptide of the invention. Such techniques include those disclosed in US Patent Nos. 4,440,859 issued 3 April 1984 to Rutter *et al*, 4,530,901 issued 23 July 1985 to Weissman, 4,582,800 issued 15 April 1986 to Crowl, 4,677,063 issued 30 June 1987 to Mark *et al*, 4,678,751 issued 7 July 1987 to Goeddel, 4,704,362 issued 3 November 1987 to Itakura *et al*, 4,710,463 issued 1 December 1987 to Murray, 4,757,006 issued 12 July 1988 to Toole, Jr. *et al*, 4,766,075 issued 23 August 1988 to Goeddel *et al* and 4,810,648 issued 7 March 1989 to Stalker, all of which are incorporated herein by reference.

The DNA encoding the polypeptide constituting the compound of the invention may be joined to a wide variety of other DNA sequences for introduction into an appropriate host. The companion DNA will depend upon the nature of the host, the manner of the introduction of the DNA into the host, and whether episomal maintenance or integration is desired.

Generally, the DNA is inserted into an expression vector, such as a plasmid, in proper orientation and correct reading frame for expression. If necessary, the DNA may be linked to the appropriate transcriptional and translational regulatory control nucleotide sequences recognised by the desired host, although such controls are generally available in the expression vector. The vector is then introduced into the host through standard techniques. Generally, not all of the hosts will be transformed by the vector. Therefore, it will be necessary to select for transformed host cells. One selection technique involves incorporating into the expression vector a DNA sequence, with any necessary control elements, that codes for a selectable trait in the transformed cell, such as antibiotic resistance. Alternatively, the gene for such selectable trait can be on another vector, which is used to co-transform the desired host cell.

Host cells that have been transformed by the recombinant DNA of the invention are then cultured for a sufficient time and under appropriate conditions known to those skilled in the art in view of the teachings disclosed herein to permit the expression of the polypeptide, which can then be recovered.

Many expression systems are known, including bacteria (for example *E. coli* and *Bacillus subtilis*), yeasts (for example *Saccharomyces cerevisiae*), filamentous fungi (for example *Aspergillus*), plant cells, animal cells and insect cells.

The vectors include a prokaryotic replicon, such as the ColE1 *ori*, for

propagation in a prokaryote, even if the vector is to be used for expression in other, non-prokaryotic, cell types. The vectors can also include an appropriate promoter such as a prokaryotic promoter capable of directing the expression (transcription and translation) of the genes in a bacterial host cell, such as *E. coli*, transformed therewith.

A promoter is an expression control element formed by a DNA sequence that permits binding of RNA polymerase and transcription to occur. Promoter sequences compatible with exemplary bacterial hosts are typically provided in plasmid vectors containing convenient restriction sites for insertion of a DNA segment of the present invention.

Typical prokaryotic vector plasmids are pUC18, pUC19, pBR322 and pBR329 available from Biorad Laboratories, (Richmond, CA, USA) and p*Trc*99A and pKK223-3 available from Pharmacia, Piscataway, NJ, USA.

A typical mammalian cell vector plasmid is pSVL available from Pharmacia, Piscataway, NJ, USA. This vector uses the SV40 late promoter to drive expression of cloned genes, the highest level of expression being found in T antigen-producing cells, such as COS-1 cells.

An example of an inducible mammalian expression vector is pMSG, also available from Pharmacia. This vector uses the glucocorticoid-inducible promoter of the mouse mammary tumour virus long terminal repeat to drive expression of the cloned gene.

Useful yeast plasmid vectors are pRS403-406 and pRS413-416 and are generally available from Stratagene Cloning Systems, La Jolla, CA 92037, USA. Plasmids pRS403, pRS404, pRS405 and pRS406 are Yeast Integrating plasmids (YIps) and incorporate the yeast selectable markers *HIS3, TRP1,*

*LEU2* and *URA3*. Plasmids pRS413-416 are Yeast Centromere plasmids (YCps)

A variety of methods have been developed to operably link DNA to vectors via complementary cohesive termini. For instance, complementary homopolymer tracts can be added to the DNA segment to be inserted to the vector DNA. The vector and DNA segment are then joined by hydrogen bonding between the complementary homopolymeric tails to form recombinant DNA molecules.

Synthetic linkers containing one or more restriction sites provide an alternative method of joining the DNA segment to vectors. The DNA segment, generated by endonuclease restriction digestion as described earlier, is treated with bacteriophage T4 DNA polymerase or *E. coli* DNA polymerase I, enzymes that remove protruding, 3'-single-stranded termini with their 3'-5'-exonucleolytic activities, and fill in recessed 3'-ends with their polymerizing activities.

The combination of these activities therefore generates blunt-ended DNA segments. The blunt-ended segments are then incubated with a large molar excess of linker molecules in the presence of an enzyme that is able to catalyze the ligation of blunt-ended DNA molecules, such as bacteriophage T4 DNA ligase. Thus, the products of the reaction are DNA segments carrying polymeric linker sequences at their ends. These DNA segments are then cleaved with the appropriate restriction enzyme and ligated to an expression vector that has been cleaved with an enzyme that produces termini compatible with those of the DNA segment.

Synthetic linkers containing a variety of restriction endonuclease sites are commercially available from a number of sources including International Biotechnologies Inc, New Haven, CN, USA.

A desirable way to modify the DNA encoding the polypeptide of the invention is to use the polymerase chain reaction as disclosed by Saiki *et al* (1988) *Science* **239**, 487-491.

In this method the DNA to be enzymatically amplified is flanked by two specific oligonucleotide primers which themselves become incorporated into the amplified DNA. The said specific primers may contain restriction endonuclease recognition sites which can be used for cloning into expression vectors using methods known in the art. In relation to the above section on DNA expression the term "polypeptide" includes peptides and chimeric proteins.

Further the present invention provides host cells transformed with suitable expression vectors and able to express the peptides. The host cells may be prokaryotic (e.g. *E. coli*) or eukaryotic (e.g. yeast, mammalian cell cultures).

Bacterial cells are preferred prokaryotic host cells and typically are a strain of *E. coli* such as, for example, the *E. coli* strains DH5 available from Bethesda Research Laboratories Inc., Bethesda, MD, USA, and RR1 available from the American Type Culture Collection (ATCC) of Rockville, MD, USA (No ATCC 31343). Preferred eukaryotic host cells include yeast and mammalian cells, preferably vertebrate cells such as those from a mouse, rat, monkey or human fibroblastic cell line. Yeast host cells include YPH499, YPH500 and YPH501 which are generally available from Stratagene Cloning Systems, La Jolla, CA 92037, USA. Preferred mammalian host cells include Chinese hamster ovary (CHO) cells available from the ATCC as CCL61, NIH Swiss mouse embryo cells NIH/3T3 available from the ATCC as CRL 1658, and monkey kidney-derived COS-1 cells available from the ATCC as CRL 1650.

Transformation of appropriate cell hosts with a DNA construct of the present

invention is accomplished by well known methods that typically depend on the type of vector used. With regard to transformation of prokaryotic host cells, see, for example, Cohen *et al* (1972) *Proc. Natl. Acad. Sci. USA* **69**, 2110 and Sambrook *et al* (1989) *Molecular Cloning, A Laboratory Manual*, Cold Spring Harbor Laboratory, Cold Spring Harbor, NY. Transformation of yeast cells is described in Sherman *et al* (1986) *Methods In Yeast Genetics, A Laboratory Manual*, Cold Spring Harbor, NY. The method of Beggs (1978) *Nature* **275**, 104-109 is also useful. With regard to vertebrate cells, reagents useful in transfecting such cells, for example calcium phosphate and DEAE-dextran or liposome formulations, are available from Stratagene Cloning Systems, or Life Technologies Inc., Gaithersburg, MD 20877, USA.

Electroporation is also useful for transforming cells and is well known in the art for transforming yeast cell, bacterial cells and vertebrate cells.

For example, many bacterial species may be transformed by the methods described in Luchansky *et al* (1988) *Mol. Microbiol.* **2**, 637-646 incorporated herein by reference. The greatest number of transformants is consistently recovered following electroporation of the DNA-cell mixture suspended in 2.5X PEB using 6250V per cm at 25$\mu$FD.

Methods for transformation of yeast by electroporation are disclosed in Becker & Guarente (1990) *Methods Enzymol.* **194**, 182.

Successfully transformed cells, ie cells that contain a DNA construct of the present invention, can be identified by well known techniques. For example, cells resulting from the introduction of an expression construct of the present invention can be grown to produce the polypeptide of the invention. Cells can be harvested and lysed and their DNA content examined for the presence of the DNA using a method such as that described by Southern (1975) *J. Mol. Biol.*

98, 503 or Berent *et al* (1985) *Biotech.* 3, 208. Alternatively, the presence of the protein in the supernatant can be detected using antibodies as described below.

In addition to directly assaying for the presence of recombinant DNA, successful transformation can be confirmed by well known immunological methods when the recombinant DNA is capable of directing the expression of the protein. For example, cells successfully transformed with an expression vector produce proteins displaying appropriate antigenicity. Samples of cells suspected of being transformed are harvested and assayed for the protein using suitable antibodies.

Thus, in addition to the transformed host cells themselves, the present invention also contemplates a culture of those cells, preferably a monoclonal (clonally homogeneous) culture, or a culture derived from a monoclonal culture, in a nutrient medium.

In another aspect the present invention provides antibodies to PP1c which act in an analogous manner to the peptides of interest. Antibodies to the peptides themselves are also provided and these may themselves be used to affect cell metabolism or function.

Peptides in which one or more of the amino acid residues are chemically modified, before or after the peptide is synthesised, may be used providing that the function of the peptide, namely the production of specific antibodies *in vivo*, remains substantially unchanged. Such modifications include forming salts with acids or bases, especially physiologically acceptable organic or inorganic acids and bases, forming an ester or amide of a terminal carboxyl group, and attaching amino acid protecting groups such as N-t-butoxycarbonyl. Such modifications may protect the peptide from *in vivo* metabolism. The peptides

may be present as single copies or as multiples, for example tandem repeats. Such tandem or multiple repeats may be sufficiently antigenic themselves to obviate the use of a carrier. It may be advantageous for the peptide to be formed as a loop, with the N-terminal and C-terminal ends joined together, or to add one or more Cys residues to an end to increase antigenicity and/or to allow disulphide bonds to be formed. If the peptide is covalently linked to a carrier, preferably a polypeptide, then the arrangement is preferably such that the peptide of the invention forms a loop.

According to current immunological theories, a carrier function should be present in any immunogenic formulation in order to stimulate, or enhance stimulation of, the immune system. It is thought that the best carriers embody (or, together with the antigen, create) a T-cell epitope. The peptides may be associated, for example by cross-linking, with a separate carrier, such as serum albumins, myoglobins, bacterial toxoids and keyhole limpet haemocyanin. More recently developed carriers which induce T-cell help in the immune response include the hepatitis-B core antigen (also called the nucleocapsid protein), presumed T-cell epitopes such as Thr-Ala-Ser-Gly-Val-Ala-Glu-Thr-Thr-Asn-Cys (SEQ ID No 1), beta-galactosidase and the 163-171 peptide of interleukin-1. The latter compound may variously be regarded as a carrier or as an adjuvant or as both. Alternatively, several copies of the same or different peptides of the invention may be cross-linked to one another; in this situation there is no separate carrier as such, but a carrier function may be provided by such cross-linking. Suitable cross-linking agents include those listed as such in the Sigma and Pierce catalogues, for example glutaraldehyde, carbodiimide and succinimidyl 4-(N-maleimidomethyl)cyclohexane-1-carboxylate, the latter agent exploiting the -SH group on the C-terminal cysteine residue (if present).

If the peptide is prepared by expression of a suitable nucleotide sequence in a suitable host, then it may be advantageous to express the peptide as a fusion

product with a peptide sequence which acts as a carrier. Kabigen's "Ecosec" system is an example of such an arrangement.

The peptide of the invention may be linked to other antigens to provide a dual effect.

In a yet further aspect the present invention provides a method of diagnosis of abnormalities of cellular metabolism, said method comprising analysing the naturally occurring peptide(s) or the nucleotide sequences encoding therefore and comparing the results to the peptides described herein.

The peptides of the present invention may also be used in diagnosis and this aspect is also covered by the present invention.

The specificity of the catalytic subunit of protein phosphatase-1 (PP1c) is modified by regulatory subunits that target it to particular subcellular locations. For the first time we have identified PP1c-binding domains on $G_L$ and $G_M$, the subunits that target PP1c to hepatic and muscle glycogen, respectively, and on $M_{110}$, the subunit that targets PP1c to smooth muscle myosin. The peptide $G_M$-(G63-T93) interacted with PP1c and prevented $G_L$ from suppressing the dephosphorylation of glycogen phosphorylase, but it did not dissociate $G_L$ from PP1c or affect other characteristic properties of the $PP1_{GL}$ complex. These results indicate that $G_L$ contains two PP1c-binding sites, the region which suppresses the dephosphorylation of glycogen phosphorylase being distinct from that which enhances the dephosphorylation of glycogen synthase. At higher concentrations, $G_M$-(G63-N75) had the same effect as $G_M$-(G63-T93), but not if Ser67 was phosphorylated by cyclic AMP-dependent protein kinase. Thus phosphorylation of Ser67 dissociates $G_M$ from PP1c because phosphate is inserted into the PP1c-binding domain of $G_M$. The fragments $M_{110}$-(M1-E309) and $M_{110}$-(M1-F38), but not $M_{110}$-(D39-E309), mimicked the $M_{110}$ subunit in

stimulating dephosphorylation of the smooth muscle myosin P-light chain and heavy meromyosin *in vitro*. However, in contrast to the $M_{110}$ subunit and $M_{110}$-(M1-E309), neither $M_{110}$-(M1-F38) nor $M_{110}$-(D39-E309) suppressed the PP1c-catalysed dephosphorylation of glycogen phosphorylase. These observations suggest that the region which stimulates the dephosphorylation of myosin is situated within the N-terminal 38 residues of the $M_{110}$ subunit, while the region which suppresses the dephosphorylation of glycogen phosphorylase requires the presence of at least part of the region 39-296 which contains seven ankyrin repeats. $M_{110}$-(M1- F38) displaced $G_L$ from PP1c, while $G_M$-(G63-T93) displaced $M_{110}$ from PP1c *in vitro*. These observations indicate that the region(s) of PP1c that interact with $G_M/G_L$ and $M_{110}$ overlap, explaining why different forms of PP1c contain just a single targeting subunit.

We also disclose the structure of PP1c in complex with a portion of a targeting subunit, and show that changing key amino acid residues in the subunit disrupts its interaction with PP1c. These studies identify a critical structural motif in targeting subunits involved in the interaction with PP1c as well as the recognition site on PP1c itself. These findings will facilitate the rational design of agents such as peptides or other forms of small cell-permeant molecules that act by disrupting PP1-targeting subunit interactions. Given the structural motif and the coordinates of the atoms in the crystal structure, it is within the scope of the abilities of a skilled molecular modeller to produce small cell-permeant molecules, which can enter cells naturally, and possess either the same motif, or an analogous structure to give the same functional properties to the molecule. Thus the small cell-permeant molecule can have a precise copy of the motif, or one which is functionally equivalent. The molecule can be a peptide, but other types of molecules, which are transferred across the plasma membrane of cells, may be preferred.

Several mammalian PP1c targeting subunits have been isolated and

characterised, including the $G_M$ subunit that targets PP1c to both the glycogen particles and sarcoplasmic reticulum of striated muscles (Tang *et al.*, 1991; Chen *et al.*, 1994), the $G_L$ subunit that targets PP1c to liver glycogen (Moorhead *et al.*, 1995; Doherty *et al.*, 1995), the $M_{110}$ subunits responsible for the association of PP1c with the myofibrils of skeletal muscle (Moorhead *et al.*, 1994; Alessi *et al.*, 1992) and smooth muscle (Alessi *et al.*, 1992; Chen *et al.*, 1994), the p53 binding protein p53BP2 (Helps *et al.*, 1995) and the nuclear protein NIPP-1 (Jagiello *et al.*, 1995; Van Eynde *et al.*, 1995). PP1c is also reported to interact with other mammalian proteins such as the retinoblastoma gene product (Durphee *et al.*, 1993), an RNA splicing factor (Hirano *et al.*, 1996), ribosomal proteins L5 (Hirano *et al.*, 1995) and RIPP-1 (Beullens *et al.*, 1996), a 110 kDa nuclear protein yet to be identified (Jagiello *et al.*, 1995), kinesin-like proteins and small cytosolic proteins, inhibitor-1, DARPP-32 and inhibitor-2 (Cohen, 1989; Cohen, 1992, Hubbard and Cohen, 1993). Moreover, a number of distinct PP1-regulatory subunits have been identified in yeast (reviewed by Stark, 1996). We attempted to identify which regions of the $G_M$ and $M_{110}$ subunits were involved in binding to PP1c. These studies led to the identification of relatively small peptides from each targeting subunit that were capable of interacting with PP1c. Peptides comprising residues 63-93, 63-80 and 63-75 of $G_M$ bound to PP1c, dissociating it from $G_L$, while the N-terminal 38 residues of the $M_{110}$ subunit ($M_{110}$[1-38]) mimicked the intact $M_{110}$ subunit in enhancing the rate at which PP1c dephosphorylated the 20 kDa myosin light chain ($MLC_{20}$) subunit of smooth muscle myosin (Johnson *et al.*, 1996).

The present invention thus provides peptides comprising the N-terminal 38 residues of the $M_{110}$ subunit, and those comprising residues 63-93, 63-80 and 63-75 of $G_M$.

Phosphorylation of Ser 67 of $G_M$ by protein kinase A (PKA) disrupts the

interaction of $G_M$ with PP1c (Dent *et al.*, 1990) and a similar disruption is also observed following the phosphorylation of Ser 67 of the $G_M$[63-75] peptide (Johnson *et al.*, 1996). The finding that $G_M$[63-93] disrupted the interaction between PP1c and the $M_{110}$ subunit, and prevented $M_{110}$ from enhancing the $MLC_{20}$ phosphatase activity of PP1c implies that the binding of $M_{110}$ and $G_M$ to PP1c are mutually exclusive.

Thus the invention contemplates the substitution or modification of an amino acid in any such peptide.

To understand the basis for the recognition by PP1c of regulatory subunits, and peptides derived from these subunits, we co-crystallised a complex of PP1c with the $G_M$[63-75] peptide and determined the structure at 3.0 Å resolution. These experiments have demonstrated that residues 64 to 69 of the peptide are bound in an extended conformation to a hydrophobic channel within the C-terminal region of PP1c. The residues in $G_M$[63-75] that interact with PP1c lie in an Arg/Lys-Val/Ile--Xaa-Phe motif common to $M_{110}$[1-38] and almost all known mammalian PP1-binding proteins. Substituting Val or Phe by Ala in the $G_M$[63-75] peptide, and deleting the VxF motif from the $M_{110}$[1-38] peptide, abolished the ability of both peptides to interact with PP1c. These findings identify a recognition site on PP1c for a critical structural motif involved in the interaction of targeting subunits with PP1.

Particularly preferred peptides are derived from residues 63 to 69 of $G_M$ and comprise the motif Arg/Lys-Val/Ile-Xaa-Phe. Peptides derived from $M_{110}$ (or any other source) and also including the motif are also included in the scope of the invention.

Preferred peptides may also be substantially or wholly made up of hydrophobic residues.

The identification of this area of PP1c necessary for binding to the various subunits allows the design of agents to specifically disrupt the interaction at this area. Such disruption may, for example, increase the phosphorylation of the protein phospholamban in cardiac muscle and thus increase the force and rate of contraction of the muscle. This provides a possible treatment for congestive heart failure. Also, the specific disruption of the complex of PP1 and p53BP2 may prevent PP1 from dephosphorylating the tumour suppressor protein p53, thus enhancing phosphorylation of p53, its ability to bind to DNA, and thus its ability to act as a tumour suppressor.

The identification of the key motif in targetting subunits that bind to PP1 also provides the means to produce targetting subunits that can no longer interact with PP1. Over-expression of these mutant targetting subunits provides a powerful new way to determine the functions of different targetting subunits *in vivo*.

Abbreviations

PP1, protein phosphatase-1
PP1c, catalytic subunit of PP1
PP1, -isoform of PP1c
$PP1_G$, glycogen-associated form of PP1
$PP1_M$, myosin-associated form of PP1
$G_M$, glycogen-binding subunit of PP1 from striated muscle
$G_L$, glycogen-binding subunit of PP1 from liver
NIPP1, nuclear inhibitor of PP1
DARPP, dopamine and cyclic AMP-regulated phosphoprotein
$M_{21}$ and $M_{110}$, myofibrillar-binding subunits of PP1 with molecular masses of 21kDa and 110 kDa respectively.

PKA, cyclic AMP-dependent protein kinase

$PhMeSO_2F$, phenylmethylsuphonyl fluoride

GST, glutathione-S-transferase

$MLC_{20}$, myosin light chain of molecular mass 20 kDa.

The invention is now described in more detail by reference to the following Examples and Figures wherein:

Figure 1 shows that the N-terminal 118 residues of human $G_M$ interact with PP1c.

GST-$G_M$ fusion proteins were electrophoresed on 10% SDS/polyacrylamide gels and stained with Coomassie blue (lanes 1-3) or, after transfer to nitrocellulose, probed with digoxygenin-labelled PP1γ (lanes 4-6) as in [9]. Lanes 1 and 4, GST-$G_M$-(E2-D118); Lanes 2 and 5, GST-$G_M$-(H100-P350); Lanes 3 and 6, GST. The positions of the marker proteins glycogen phosphorylase (97 kDa), bovine serum albumin (66 kDa), ovalbumin (43 kDa), carbonic anhydrase (29 kDa) and soybean trypsin inhibitor (20 kDa) are indicated.

Figure 2 shows that synthetic peptides between residues 63 and 93 of rabbit $G_M$ stimulate the phosphorylase phosphatase activity of $PP1_{GL}$.

Hepatic glycogen particles were diluted in assay buffer to 0.6 phosphorylase phosphatase (PhP) mU per ml, incubated for 15 minutes at 30°C with $G_M$-(G63-T93) (closed circles), $G_M$-(G63-K80) (open circles) or $G_M$-(G63-N75) (closed triangles) and assayed as described in Example 1. The open triangles show the effect of $G_M$-(G63-N75) which had been phosphorylated at Ser67 by PKA ($pG_M$-(G63-N75)). Similar results were obtained in four experiments.

Figure 3 shows that removal of the $M_{21}$ subunit from smooth muscle $PP1_M$ does

not affect its $MLC_{20}$ phosphatase:phosphorylase phosphatase activity ratio.

(A) Purified smooth muscle $PP1_M$ was electrophoresed on a 12% SDS/polyacrylamide gel, and either stained with Coomassie blue (lane 1) or immunoblotted [32] with antibodies specific for the $M_{21}$ subunit (lane 2) or the $M_{110}$ subunit (lane 3). The positions of the $M_{110}$ subunit, the $M_{21}$ subunit and PP1c are marked.

(B) Purified $PP1_M$ (lane 1) or $PP1_M$ lacking the $M_{21}$ subunit (lane 2) were electrophoresed on a 12% SDS polyacrylamide gel, transferred to nitrocellulose and immunoblotted with mixed, affinity-purified antibodies to the $M_{110}$ and $M_{21}$ subunits. The $M_{110}$ and $M_{21}$ subunits are marked. The activity ratio, $MLC_{20}$ phosphatase (MP):phosphorylase phosphatase (PhP) of the two preparations is also shown. Similar results were obtained in three different experiments. The activity ratio MP:PhP of PP1c is 0.07.

Figure 4 shows expressed fragments of the $M_{110}$ subunit before and after cleavage of the GST-fusion proteins with thrombin .

Purified GST-fusion proteins were electrophoresed on a 15% SDS/polyacrylamide gel and stained with Coomassie blue. Lane 1, GST-$M_{110}$-(M1-A150); Lane 2, GST-$M_{110}$-(D39- E309); Lane 3, GST-$M_{110}$-(M1-E309); Lane 4, GST-$M_{110}$-(L24- Y496). Lanes 5-8 are the same as Lanes 1-4 except that the fusion proteins were cleaved with thrombin. The positions of the marker proteins glycogen phosphorylase (97 kDa), bovine serum albumin (66 kDa), ovalbumin (43 kDa), carbonic anhydrase (29 kDa), GST (26 kDa) and soybean trypsin inhibitor (20 kDa) are marked.

Figure 5 shows the effect of $M_{110}$ subunit fragments on PP1c-catalysed dephosphorylation of $MLC_{20}$ and glycogen phosphorylase

A,B; Effects of $M_{110}$-(M1-E309) (closed circles), $M_{110}$-(M1-F38) (open circles) and $M_{110}$-(D39-E309) (open triangles) on the $MLC_{20}$ phosphatase (B) and phosphorylase phosphatase (B) activities of PP1c were measured after incubating PP1c for 15 minutes at 30°C with each fragment. The results are presented as a percentage of those obtained in experiments where the $M_{110}$ fragments were omitted.

C,D; The effect of $M_{110}$-(M1-A150) (open circles) and $M_{110}$-(L24-Y496) (closed circles) on the $MLC_{20}$ phosphatase (C) and phosphorylase phosphatase (D) activities of PP1c were measured as in A,B.

Figure 6 shows the effect of $M_{110}$-(M1-F38) and $M_{110}$-(M1-E309) on the dephosphorylation of glycogen synthase by PP1c.

The glycogen synthase phosphatase activity of PP1c was measured after a 15 minute incubation at 30°C with the indicated concentrations of $M_{110}$-(M1-F38) and $M_{110}$-(M1-E309). Similar results were obtained in three different experiments.

Figure 7 shows that $G_M$-(G63-T93) dissociates $PP1_M$.

(A) The phosphorylase phosphatase (PhP) activity of $PP1_M$ (closed circles) and its $MLC_{20}$ phosphatase (MLCP) activity (open circles) were assayed after preincubation for 15 minutes at 30°C with the indicated concentrations of $G_M$-(G63-T93). Activities are shown relative to control incubations in which $G_M$-(G63-T93) was omitted. Similar results were obtained in three experiments.

(B,C) PPIM was incubated for 15 minutes at 30°C in the absence (B) and presence (C) of 10 M $G_M$-(G63-T93), then passed through a 30 x 1 cm column

of Superose 12 equilibrated at ambient temperature in 50 mM Tris/HCl pH 7.5, 0.2M NaCl, 0.1 mM EGTA, 0.1% (by vol) 2-mercaptoethanol, 0.03% (by mass) Brij 35 in the absence (B) or presence (C) of 1 $\mu$M $G_M$-(G63-T93). Fractions (0.25 ml) were assayed for $MLC_{20}$ phosphatase (MLCP) in B and for phosphorylase phosphatase (PhP) activity in C. The arrows denote the position of ferritin (450 kDa) and ovalbumin (43 kDa).

Figure 8 shows that $G_M$-(G63-T93) prevents $M_{110}$-(M1-F38) or $M_{110}$-(M1- E309) from modulating the substrate specificity of PP1c.

(A) The $MLC_{20}$ phosphatase activity of PP1c was assayed after incubation for 15 minutes at 30°C in the presence or absence of 1 $\mu$M $G_M$-(G63-T93) and either 0.1 $\mu$M $M_{110}$-(M1-F38) or 0.1 nM $M_{110}$-(M1-E309).

(B) The phosphorylase phosphatase activity of PP1c was assayed as in A in the presence or absence of 1 $\mu$M $G_M$-(G63-T93) and 1.0 nM $M_{110}$-(M1-E309). The results are presented (SEM for three experiments) as a percentage of the PP1c activity measured in the absence of $G_M$-(63-T93), $M_{110}$-(M1-F38) or $M_{110}$-(M1-E309).

Figure 9 shows the location of PP1c-binding domains on the $G_M$ and $M_{110}$ targeting subunits and their effects on PP1 activity.

The hatched boxes in the $M_{110}$ subunit denote the positions of the ankyrin repeats.

Figure 10 shows a stereo view of the electron density corresponding to the peptide. A: Initial 2-fold averaged electron map. B: map calculated using 3Fo-2Fc coefficients and phases calculated from the final refined model. Displayed using TURBO-FRODO.

Figure 11 shows the structure of PP1-$G_M$[63-75] peptide complex. A. Stereo view of a ribbons diagram of PP1c to indicate the position of the peptide binding channel at the interface of the two $\beta$-sheets of the $\beta$-sandwich. The peptide atoms are represented as ball-and-stick (MOLSCRIPT, Kraulis, 1991).

B. View of the surface of PP1c to show the hydrophobic peptide binding channel. Residues 63' to 69' (GRRVSFA) (SEQ ID No 2) of the $G_M$[63 75] peptide are shown as sticks. Drawn with TURBO-FRODO.

C. Stereo view of the $G_M$[63-75] peptide at the recognition site of PP1 to indicate polar interactions between peptide and protein and the formation of the $\beta$-sheet between Ser 67' - Ala 69' and 14 of PP1. Drawn with TURBO-FRODO.

D. Solvent accessible surface and surface electrostatic potential of PP1-$G_M$[63 75] peptide complex calculated with PP1 coordinates alone and showing the peptide as a stick representation in the vicinity of the peptide binding site. The figure was created with GRASP (Nicholls and Honig, 1991). The protein surface is coloured according to electrostatic potential from red (most negative) to blue (most positive). The figure shows pronounced negative electrostatic potential in the region surrounding the N-terminus of the peptide binding site that results from seven conserved acidic residues.

E. Details of the structure of the peptide binding site to show hydrophobic interactions between PP1c and Val 66', Phe 68' and Ala 69' of the $G_M$[68-75] peptide (MOLSCRIPT, Kraulis, 1991).

Figure 12 shows a sequence alignment of PP1-regulatory subunits in the vicinity of the (R/K)(V/I) x F motif. (A) mammalian PP1-binding subunits. $G_M$, Tang *et al.*, 1991; GL, Docherty *et al.*, 1995; $G_L$-related protein, Doherty

*et al.*, 1996; p53BP2, Helps *et al.*, 1995; NIPP-1, Bollen *et al.*, 1995; splicing factor PSF, Hirano *et al.*, 1996; $M_{110}$ subunit, Chen *et al.*, 1994; inhibitor-1, Aitken *et al.*, 1982; DARPP-32, Williams *et al.*, 1986. (B) PP1-binding proteins in *S. cerevisiae*. GAC1 (Francois *et al.*, 1992); PIG2 GIP1, GIP2, YIL045W (Tu *et al.*, 1996); REG1, REG2 (Tu and Carlson, 1995; Frederick and Tatchell, 1996); SCD5 (Nelson *et al* 1996; Tu *et al* 1996). The region homologous to the RRVSFA (SEQ ID No 3) motif in $G_M$ which intersects with PP1c is boxed.

Figure 13 shows the disruption of the interactions between PP1c and the $G_L$ and $M_{110}$ subunits by a synthetic peptide from p53BP2. (A) $PP1_M$ from chicken gizzard smooth muscle (Alessi *et al.*, 1992) was diluted and incubated for 15 min at 30°C with the peptide GKRTNLRKTGSERIAHGMRVKFNPLALLLDSC (SEQ ID No 4), corresponding to the sequence in p53BP2 that contains the RVxF motif. Reactions were started with either $^{32}$P-labelled $MLC_{20}$ or glycogen phosphorylase and the $MLC_{20}$ phosphatase (open circles) and phosphorylase phosphatase (PhP, closed circles) activities were determined. The results are expressed as a percentage of the activity determined in control incubations where the p53BP2 peptide was omitted (100%). Similar results were obtained in three separate experiments. (B) same as (A) except that the peptide was incubated with diluted hepatic glycogen particles containing PP1-$G_L$ before measuring the PhP activity. Similar results were obtained in three separate experiments.

Figure 14 shows the effect of $M_{110}$[M1-F38] and $M_{110}$[M1-K35] on the PP1c-catalysed dephosphorylation of $MLC_{20}$ $M_{110}$[M1-F38] (1-38, open circles) or $M_{110}$[M1-K35] (1-35, closed circles) were incubated with PP1c for 15 min at 30°C and reactions started with the $^{32}$P-labelled $MLC_{20}$ substrate. The results are expressed as a % of the activity determined in control incubations where

the $M_{110}$ peptides were omitted (100%). Similar results were obtained in three separate experiments.

Figure 15 shows the effect of synthetic peptides derived from the $M_{110}$ and $G_M$ subunits on the phosphorylase phosphatase activity of PP1-$G_L$. (A) Hepatic glycogen protein particles containing PP1-$G_L$ were diluted and incubated for 15 min at 30°C with the indicated concentrations of either $M_{110}$[M1-F38] (open circles) or $M_{110}$[M1-K35] (closed circles) and the phosphatase reactions were initiated by addition of $^{32}$P-labelled glycogen phosphorylase. The results are expressed as a percentage of the activity determined in control incubations where the $M_{110}$ peptides were omitted. Similar results were obtained in three separate experiments. (B) The experiment was carried out as in (A), except that the peptide $G_M$[G63-N75] ("wild type", WT) and variants in which either Val 66 (V66A) (closed triangles) or Phe 68 (F68A) (closed circles) were changed to Ala, were used instead of the $M_{110}$ peptides. Similar results were obtained in three separate experiments.

Figure 16 shows a stereo view of a ribbons diagram of a model of PP1-phospho-inhibitor-1 complex. The side chains of Ile 10, Phe 12 and pThr 35 of phospho-inhibitor-1 are shown with the main-chain atoms of residues 8 to 36 of the inhibitor indicated as a shaded ribbon. Drawn with MOLSCRIPT (Kraulis 1991).

Figure 17 shows a comparison of rat and chicken gizzard $M_{110}$ and $M_{21}$ subunits.

Vertical lines indicate identical residues, colons denote similar residues in the rat and chicken $M_{110}$ sequences and deletions are shown by dots. (A) Comparison of $M_{110}$ subunits. Underlined residues in the rat $M_{110}$ subunit (Rat1) are deleted in some rat aorta forms and underlined residues in the

chicken $M_{110}$ subunit (Ch1) are deleted in some chicken gizzard forms [5, 8]. Dashed lines above residues indicate amino acids deleted in the rat kidney $M_{110}$ subunit [9]. The alternative C-terminal sequences of rat uterus $M_{110}$ subunit are shown as Rat1 and Rat2. Leucine residues in the C-terminal leucine zipper motif are double underlined. **(B)**. The C-terminal sequence of the $M_{110}$ subunit is structurally related to the $M_{21}$ subunit. The sequence of the chicken $M_{21}$ subunit [5] is compared with the C-terminal sequences of Rat2 and Ch1 from A. Identities between Ch1 and Rat2 are shown in boldface type.

Figure 18 shows immunoprecipitation and immunoblotting of $PP1_M$ in extracts from chicken gizzard myofibrils.

**A.** Antibodies specific for the $M_{110}$ and/or $M_{21}$ subunits immunoprecipitate most of the myosin P-light chain phosphatase activity in myofibrillar extracts. $PP1_M$ was immunoprecipitated with either control IgG, antibody raised against the $PP1_M$ holoenzyme, antibody specific for the $M_{110}$ subunit or antibody specific for the $M_{21}$ subunit, as described under Methods in Example 3. The figure shows activity present in the supernatant (S, open bars) or pellet (P, filled bars) as a percentage of that measured before centrifugation. The results shown are the average (± S.E.M.) for three separate experiments each assayed in duplicate. **B,** The $M_{110}$ and $M_{21}$ subunits are present in similar molar proportions in myofibrillar extracts and in purified $PP1_M$. 10 ng (track 1) or 3 ng (track 3) of purified $PP1_M$ or 12 $\mu$g (track 2) or 3.6 $\mu$g (track 4) of myofibrillar extract was electrophoresed on a 12% SDS/polyacrylamide gel, transferred to nitrocellulose and immunoblotted with mixed affinity-purified antibodies to the $M_{110}$ and $M_{21}$ subunits as in [22]. The positions of the two subunits are marked. The results indicate that $PP1_M$ comprises about 0.1% of the myofibrillar protein.

Figure 19 shows the identification of the region on the $M_{110}$ subunit that

interacts with the $M_{21}$ subunit.

**A)** $PP1_M$ 5 μg (track 1), 10 μg bacterial extract containing $M_{110}$-(R714-I1004) (track 2), MBP-$M_{110}$-(R714-I1004) 1 μg (track 3), MBP-$M_{110}$-(R714-L934) 1 μg (track 4), MBP-$M_{110}$-(K933-I1004) 1 μg (track 5), MBP 1μg (track 6), $M_{110}$-(M1-E309) 2 μg (lane 7) and $M_{110}$-(M1-S477) 2 μg (track 8) were run on a 12% SDS/polyacrylamide gel and stained with Coomassie Blue. **B)** same as **A)** except that 10-fold less protein was electrophoresed and after transfer to nitrocellulose the proteins were probed with digoxigenin-labelled $M_{21}$ subunit (0.2 μg/ml). **C)** same as **B)** except that, after electrophoresis, the proteins were transferred to nitrocellulose and probed with digoxigenin-labelled $M_{21}$-(M1-L146) (0.2 μg/ml).

Figure 20 shows the identification of the region of the $M_{21}$ subunit involved in interaction with the $M_{110}$ subunit and in dimerization.

**A)** GST-$M_{21}$ 5 μg (track 1), $M_{21}$ 5 μg (track 2), $M_{21}$-(M1-L146) 5 μg (track 3), $M_{21}$-(M1-E110) 20 μg (track 4) and $M_{21}$-(E110-K186) 5 μg (track 5) were run on 16.5% polyacrylamide gels and stained with Coomassie Blue. The marker proteins ovalbumin (43 kDa) and carbonic anhydrase (29 kDa) are indicated. **B)** GST-$M_{21}$ 0.5 μg (track 1), $M_{21}$ 0.5 μg (track 2), $M_{21}$-(M1-L146) 0.5 μg (track 3), $M_{21}$-(M1-E110) 5 μg (track 4) and $M_{21}$-(E110-K186) 5 μg (track 5) were electrophoresed as in **A)** and after transfer to nitrocellulose the blots were probed with digoxigenin-labelled MBP-$M_{110}$-(K933-I1004) (0.2 μg/ml). **C)** same as **B)** except that, after electrophoresis, the proteins were transferred to nitrocellulose and probed with digoxigenin-labelled $M_{21}$ subunit (0.2 μg/ml).

Figure 21 shows that the $M_{21}$ subunit and $M_{21}$-(M1-L146) interact with the $M_{110}$ subunit and themselves, but not with PP1.

$PP1_M$ (0.5 $\mu$g) was electrophoresed on a 12% SDS/polyacrylamide gel, transferred to nitrocellulose and probed with digoxigenin-labelled $M_{21}$ subunit (0.2 $\mu$g/ml) (track 1) or digoxigenin-labelled $M_{21}$-(M1-L146) (0.2 $\mu$g/ml) (track 2). The positions of the $M_{110}$ subunit, the $M_{21}$ subunit and PP1c are marked.

Figure 22 shows that removal of the $M_{21}$ subunit from smooth muscle $PP1_M$ does not prevent it from being pelleted with myosin.

The PP1 catalytic subunit (PP1c), $PP1_M$, or $PP1_M$ lacking the $M_{21}$ subunit, $PP1_M(\Delta M_{21})$, each at 30 nM, were incubated for 15 min at 0°C with 1 $\mu$M myosin and centrifuged (see Methods of Example 3). The figure shows the myosin P-light chain phosphatase activity present in the supernatant (S, open bars) or pellet (P, filled bars) as a percentage of that measured before centrifugation. The results shown are the average (± S.E.M.) for three separate experiments each assayed in duplicate.

Figure 23 shows the identification of a region of the $M_{110}$ subunit which binds to myosin.

(A); $PP1_M$, $M_{110}$-(M1-S477) and GST-$M_{110}$-(M377-K976), each at 30 nM were incubated for 15 min at 0°C with 1 $\mu$M myosin and centrifuged. The supernatants (S), resuspended pellets (P) and the suspension before centrifugation (T, total) were electrophoresed on 12% SDS/polyacrylamide gels, transferred to nitrocellulose and immunoblotted with antibodies raised against the $PP1_M$ holoenzyme. No protein was pelleted in the absence of myosin (not shown). The positions of the marker proteins myosin heavy chain (200 kDa), glycogen phosphorylase (97 kDa), bovine serum albumin (66 kDa), ovalbumin (43 kDa), carbonic anhydrase (29 kDa) and soybean trypsin inhibitor (20 kDa) are indicated. (B) The experiments were carried out as in (A), except that the $M_{110}$ fragments and $M_{21}$ subunit were used at 100 nM, the 8.5 kDa

$M_{110}$-(K933-I1004) fragment was electrophoresed on a 16.5% polyacrylamide gel and immunoblotting was carried out with affinity purified antibodies (see Methods). A small amount of $M_{110}$-(R714-I1004) pelleted in the absence of myosin. This was probably due to aggregation in the bacterial extract since this did not happen when it was complexed to the $M_{21}$ subunit (data not shown). No other protein was pelleted in the absence of myosin.

Figure 24 shows that the isolated $M_{21}$ subunit binds to myosin.

**(A)**; Myosin (1 $\mu$M) was mixed with 50 $\mu$M, 20 $\mu$M or 10 $\mu$M $M_{21}$ subunit to give the molar ratios $M_{21}$:myosin dimer indicated. After 15 min at 0°C, the solutions were centrifuged and the supernatants (S), resuspended pellets (P) and the suspension before centrifugation (T, total) were electrophoresed on 12% SDS/polyacrylamide gels and stained with Coomassie blue. The positions of the myosin heavy chain (MHC) and the $M_{21}$ subunit are indicated. The myosin light chains migrate faster than the $M_{21}$ subunit and are not visible at these loadings.

**(B)**; Myosin (track A) was purified from chicken gizzard, and the myosin "rod" domain (track B) and light meromyosin (track C) produced by digestion of myosin with papain and chymotrypsin, respectively. These three proteins, all at 1 $\mu$M, were then mixed with $M_{21}$ subunit (track D) to give a molar ratio $M_{21}$:myosin dimer of 10:1 and, after 15 min at 0°C, the solutions were centrifuged and the supernatants (S), resuspended pellets (P) and the suspension before centrifugation (T, total) were electrophoresed on 12% SDS/polyacrylamide gels and stained with Coomassie blue. The slightly faster migrating band in the $M_{21}$ subunit preparation was shown by amino acid sequencing to be N-terminally truncated commencing at residue 16. **(C)**; same as **(B)**, except that $M_{21}$-(M1-L146) (track D) replaced the $M_{21}$ subunit.

Figure 25 gives a schematic representation of the regions on the $M_{110}$ subunit from chicken gizzard that interact with PP1c, myosin and the $M_{21}$ subunit.

PP1c binds to the KVKF (SEQ ID No 5) motif between residue 35 and 38, just N-terminal to the seven ankyrin repeats (hatched vertical lines) that suppress the dephosphorylation of substrates other than myosin. Residues 1-38 of the $M_{110}$ subunit enhance the dephosphorylation of myosin. The $M_{21}$ subunit binds to the C-terminal 72 residues of the $M_{110}$ subunit which are 43% identical in amino acid sequence to residues 87-161 of the $M_{21}$ subunit. The dephosphorylated form of myosin binds to $M_{110}$-(R714-I1004) but not to $M_{110}$-(K933-I1004), suggesting that myosin binds N-terminal to the $M_{21}$ subunit.

**Example 1: Identification of protein phosphatase 1-binding domains on the glycogen and myofibrillar targeting subunits**

MATERIALS AND METHODS

*Materials.*

The myosin-associated form of PP1 ($PP1_M$) was from chicken gizzard [9] and the glycogen-associated form of PP1 ($PP1_G$) from rabbit skeletal muscle [21]. The $\beta$ isoform of PP1c was released from $PP1_G$ by incubation for 2 hours in 2M LiBr, then purified by gel-filtration on a 30 x 1 cm column of Superose 12 (Pharmacia, Milton Keynes, U.K.) in the presence of 0.5M LiBr. Glycogen protein particles from rat liver [22] were used as the source of hepatic $PP1_G$. Digoxygenin-labelled PP1c ($\gamma_1$-isoform, hereafter termed PP1) was prepared as in [9]. $G_L$ was expressed in *E. coli* as a glutathione-S-transferase (GST) fusion protein [7], termed GST-$G_L$. The catalytic subunit of PP2A from bovine heart (PP2AC) was provided by Dr R. MacKintosh in this Unit. The phosphorylatable myosin light chain ($MLC_{20}$) and heavy meromyosin from chicken gizzard were a gift from Dr M. Ikebe (Case Western Reserve

University, Cleveland, USA). Thrombin and benzamidine-Agarose were purchased from Sigma (Poole, UK).

*Peptide synthesis.*

Peptides were synthesised on an Applied Biosystems 430A peptide synthesiser and their purity and concentration established by high performance liquid chromatography, mass spectrometry and amino acid analysis. The sequence of rabbit $G_M$-(G63-T93) is GRRVSFADNFGFNLVSVKEFDTWELPSVSTT (SEQ ID No 6) and the sequence of $M_{110}$-(M1-F38) is MKMADAKQKRNEQLKRWIGSETDLEPPVVKRQKTKVKF (SEQ ID No 7). The peptide $G_M$-(G63-T93) was cleaved with Lys-C endoproteinase (Boehringer) and the peptide $G_M$-(E81-T93) thus generated was purified on a $C_{18}$ column. The peptides $G_M$-(G63-K80) and $G_M$-(G63-N75), were synthesised, and the latter phosphorylated at Ser67 with the catalytic subunit of cyclic AMP-dependent protein kinase (PKA), then bound to a 1 ml $C_{18}$ column equilibrated in 0.1% (v/v) trifluoroacetic acid, washed with 0.1% trifluoroacetic acid to remove excess ATP, eluted with 0.1% trifluoroacetic acid containing 70% acetonitrile, dried and dissolved in water. The peptide $G_M$-(S40-Y55) was a gift from Dr Bruce Kemp (St Vincent's Institute, Australia).

*Preparation of phosphorylated proteins and phosphatase assays.*

$^{32}$P-labelled rabbit skeletal muscle phosphorylase a (containing 1.0 mol phosphate per mol subunit) was prepared by phosphorylation with phosphorylase kinase [23], $^{32}$P-labelled rabbit skeletal muscle glycogen synthase (containing 1.5 mol/mol subunit in the sites 3 region) was prepared by phosphorylation with glycogen synthase kinase-3 [24]), $^{32}$P-labelled chicken gizzard $MLC_{20}$ and $^{32}$P-labelled chicken gizzard heavy meromyosin (containing 1.0 mol phosphate per mol subunit) were prepared by phosphorylation with smooth muscle myosin light chain kinase [9]. The dephosphorylation of

phosphorylase a (10 $\mu$M), glycogen synthase (1 $\mu$M) and $MLC_{20}$ (1 $\mu$M) and heavy meromyosin (1 $\mu$M) was carried out as in [24]. One unit of activity (U) was that amount which released 1 mole of phosphate in one minute.

*Construction of vectors for the expression of N-terminal fragments of the $G_M$ subunit as glutathione-S-transferase (GST) fusion proteins in E. coli.*

$G_M$-(E2-R575) was produced by inserting a SmaI-SmaI restriction fragment, encoding amino acids 2-575 of human $G_M$, from clone H1G11 [5] into the SmaI site of pGEX-KG (Pharmacia, Milton Keynes, U.K.). This resulted in the addition after residues 2-575 of amino acids EFPVVVVEF (SEQ ID No 8) before the stop codon. $G_M$-(E2-P243) was made by deleting an NcoI-HindIII fragment of the $G_M$-(E2-R575) construct, resulting in termination after residue 243. $G_M$-(E2-D118), encoding amino acids 2-118, with a C-terminal addition of QLNSS was produced by deleting a BglII-HindIII fragment of the $G_M$-(E2-R575) construct. $G_M$-(H100-P350) encoding amino acids 100-350 was made by inserting an EcoRI-HindIII digested PCR fragment prepared using primers

5′ GCCGAATTCACACAGAAGAATATGTTTTAGCC 3′ (SEQ ID No 9) and

5′ GCCGAAGCTTATGGAAAATTGACTGGATCTGTTG 3′ (SEQ ID No 10)

into the same sites of pGEX-KG. Restriction sites in the primers are underlined.

*Construction of vectors for the expression of the chicken gizzard $M_{21}$ subunit in E. coli.*

The entire coding region (M1-K186) of the $M_{21}$ subunit [10] was amplified by PCR using primers

5′ CGCGCATATGTCGTCGCTGTTCACCAGG 3′ (SEQ ID No 11) and

5′ GGCGGATCCCTACTTGGAGAGTTTGC 3′ (SEQ ID No 12), containing

restriction sites NdeI and BamH1 (underlined). After cleavage with the restriction enzymes, the PCR fragment was cloned into the same sites of the bacterial expression vector pT7-7.

*Production of fragments of the chicken gizzard and rat aorta $M_{110}$ subunits.*

The C-terminal 291 residues $M_{110}$-(R714-I1004) of the chicken gizzard $M_{110}$ subunit were amplified by PCR using a primer 5′ AGGAAGAATTCGTTCCACACGAAC 3′ (SEQ ID No 13) containing an EcoRI restriction site (underlined) and a KS primer in the Bluescript vector of the cDNA clone [10]. The EcoRI digested PCR fragment was subcloned into the same site of pT7-7.

Rat aorta $M_{110}$ fragments were produced as GST-fusion proteins. $M_{110}$-(M1-A150) was amplified by PCR using primers A (5′ CCTAGCCCGGGGATGAAGATGGCGGAC 3′) (SEQ ID No 14) and B (5′ GCGGAAGCTTATGCTTCCTCCTCTGCAATATC 3′) (SEQ ID No 15), containing SmaI and HindIII restriction sites (underlined) and the SmaI-HindIII digested PCR fragment subcloned into the same sites of pGEX-KG. $M_{110}$-(M1-E309) was produced by subcloning a SmaI-HindIII digested PCR fragment amplified using primers A and C (5′ CTAGAAGCTTCCATATTTGCTGTTGATTCAATC 3′) (SEQ ID No 16) into the same sites of pGEX-KG. This resulted in one amino acid (A) being added after E309. $M_{110}$-(D39-E309) was produced by subcloning a SmaI-HindIII digested PCR fragment amplified using primers D (5′ CCTAGCCCGGGGGACGATGGCGCCGTCTTCC 3′) (SEQ ID No 17) and C into the same sites of pGEX-KG. An $M_{110}$-(L24-K976) was prepared by inserting a XhoI-XhoI restriction fragment of the entire $M_{110}$ cDNA in Bluescript into XhoI site of pGEX-KG, and $M_{110}$-(L24-Y496) expressed by deleting a NdeI-NdeI fragment of the L24-K976 construct and filling the

overhanging ends before ligating them. This resulted in the addition after Y496 of amino acids MVAD (SEQ ID No 18) before the stop codon. The sequence of all subclones produced after PCR amplification were verified using an Applied Biosystems 373A automated DNA sequencer and Taq dye terminator cycle sequencing according to the manufacturer's instructions.

*Expression of proteins in E.coli.*

All constructs were expressed in *E. coli* strain BL21(DE3)plysS. Cultures were grown at 37°C in Luria-Bertani medium in the presence of 100 μg/ml ampicillin and 30 μg/ml chloramphenicol to an A600 of 0.4-0.6, and induced with 50 μg/ml isopropylthiogalactoside for 8 hours at 25°C or overnight at ambient temperature. After centrifugation for 10 minutes at 7000 x g (4°C), cells from one litre of culture were resuspended in 20 ml of 50 mM Tris-HCl pH 8.0, 0.1 M NaCl, 1 mM EDTA, 0.1% (by vol) 2-mercaptoethanol, 0.2 mM phenylmethylsulphonylfluoride ($PhMeSO_2F$), 1 mM benzamidine (buffer A) and frozen at -80°C. After thawing, sodium deoxycholate (1 mg/ml ), 8 mM MgSO4 and 10 g/ml DNAase I were added, the extract incubated until it was no longer viscous, then made 6 mM in EDTA, 1 mM in benzamidine and 0.2 mM in $PhMeSO_2F$ and centrifuged for 10 minutes at 10,000 x g. The soluble GST-fusion proteins were then purified from the supernatant by affinity chromatography on glutathione-Sepharose (Pharmacia).

The $M_{21}$ subunit and $M_{110}$-(R714-I1004) C-terminal fragment from chicken gizzard $M_{110}$ subunit, which were used for affinity purification of the anti-$M_{21}$ and anti-$M_{110}$ antibodies (see below) were obtained in inclusion bodies and therefore recovered in the pellets after centrifuging *E. coli* extracts at 10,000 x g. $M_{110}$-(R714-I1004) was solubilised by resuspension in Buffer A containing 0.5% (by mass) Triton X-100 and was >95% pure. The $M_{21}$ subunit was not solubilised by this procedure but, after washing the pellets in 0.5% Triton

X-100, was dissolved by sonication in 0.5% trifluoroacetic acid; its purity was about 20%.

$M_{110}$ GST-fusion proteins (1-9 mg/ml in 50 mM Tris/HCl, 2.5 mM CaCl2, 150 mM NaCl and 0.1% (by vol) 2-mercaptoethanol) were cleaved by incubation for 20 minutes at 30°C with 20 μg/ml thrombin. Benzamidine-Agarose (0.2 ml) was added and, after incubation (with rotation) for 30 minutes at ambient temperature, the benzamidine-Agarose containing the attached thrombin was removed, and the supernatant dialysed against 50 mM Tris-HCl pH 7.5, 0.1 mM EGTA, 0.1% (by vol) 2-mercaptoethanol, 10% glycerol and stored in aliquots at -80°C. After cleavage with thrombin, all fragments of the $M_{110}$ subunit, except $M_{110}$-(L24-Y496), commenced with the sequence GSPG (SEQ ID No 19) before the initiating residue of the GST-fusion proteins. The $M_{110}$-(24-Y496) was preceded by the sequence GSPGISGGGGGILDSMGR (SEQ ID No 20).

*Production of antibodies that recognise the $M_{110}$ and $M_{21}$ subunits of chicken gizzard $PP1_M$.*

Polyclonal sheep antibodies to the $PP1_M$ holoenzyme were raised in the Scottish Antibody Production Unit (Carluke, Ayrshire, U.K.). Antibodies which recognise the $M_{110}$ subunit specifically were obtained by passing the antiserum down a 4 ml affinity column comprising 40 mg of $M_{110}$-(R714-I1004) coupled covalently to 1g of dried CNBr-activated Sepharose 4B (Sigma). After washing with 10 column volumes of 50 mM Tris/HCl pH 7.5, 1% (by mass) Triton X-100, 0.1 mM EGTA, 0.1% (by vol) 2-mercaptoethanol (Buffer B) plus 0.5 M NaCl, followed by 10 volumes of Buffer B plus 1 M LiBr, the anti-$M_{110}$ antibody was eluted with 50 mM glycine pH 2.0, neutralised immediately with 1 M Tris/HCl pH 8.0 and stored in aliquots at -80°C. Antibodies which recognise the $M_{21}$ subunit specifically were obtained in an

identical manner, except that the affinity column comprised about 40 mg of the expressed chicken gizzard $M_{21}$ subunit coupled to 6 g (dry weight) of CNBr-activated Sepharose.

*Removal of the $M_{21}$ subunit from $PP1_M$.*

$PP1_M$ (0.01 ml, 0.4U/ml) was dissociated by incubation for 30 minutes with 500 $\mu$M arachidonic acid [25] and then for 30 minutes with 0.08 ml of packed Protein G-Sepharose coupled to 0.08 mg of affinity purified anti-$M_{21}$ antibody. The Protein G-Sepharose was pelleted, and the supernatant diluted at least 15-fold to allow the $M_{110}$ subunit and PP1c to recombine. The $M_{110}$-PP1c complex was further purified by gel filtration on Superose 12 (30 x 1 cm) to ensure complete removal of any free PP1c.

RESULTS.

*Identification of a PP1c-interaction domain on the $G_M$-subunit of $PP1_{GM}$.*

The amino acid sequence of rat hepatic $G_L$ is 23% identical (39% similar) to residues 1-286 of $G_M$ from human skeletal muscle [7]. There is no homology over the first 63 residues but identity is >40% over the regions 63-86, 144-166 and 186-227 of $G_M$ suggesting that one or more of these sequences comprise a PP1-binding domain. Fusion proteins in which GST was linked to fragments of $G_M$ were therefore tested for their ability to bind to PP1c. GST-$G_M$-(E2-D118) (Fig 1) and GST-$G_M$-(E2-P243) (data not shown), but not GST-$G_M$- (H100-P350) or GST itself (Fig 1) interacted with PP1 in Far Western experiments, indicating that the first 118 residues of $G_M$ contain a PP1c-binding domain. Moreover, a proteolytic fragment derived from GST-$G_M$-(E2-D118) whose molecular mass was 5 kDa less than GST-$G_M$-(E2-D118), but not a proteolytic fragment that was 6 kDa smaller, also interacted with PP1c (Fig 1). Taken together, the observations suggested that the region comprising residues 63-86 was likely to bind to PP1c. We

therefore synthesised $G_M$-(G63-T93) and examined its effect on the enzymatic properties of $PP1_{GL}$, the form of PP1 associated with rat hepatic protein-glycogen particles.

The interaction of PP1c with $G_L$ suppresses the dephosphorylation of muscle glycogen phosphorylase by 80% and enhances the dephosphorylation of muscle glycogen synthase by 2-3 fold [21, 26]. Disruption of the characteristic properties of hepatic $PP1_{GL}$ can therefore be monitored very simply by changes in its specificity. $G_M$-(G63-T93) induced a sixfold increase in the phosphorylase phosphatase activity of $PP1_{GL}$, the concentrations required for 50% activation being 30 nM (Fig 2). $G_M$-(G63-T93) also prevented bacterially expressed GST-$G_L$ from suppressing the phosphorylase phosphatase activity of PP1c (data not shown). However, $G_M$-(G63-T93) had no effect on the glycogen synthase phosphatase activity of $PP1_{GL}$, nor was there any alteration of the other characteristic properties of $PP1_{GL}$, namely allosteric inhibition of the glycogen synthase phosphatase activity by phosphorylase a and binding to glycogen (data not shown). Thus the interaction of $G_M$-(G63-T93) with $PP1_{GL}$ does not displace $G_L$ from PP1c.

$G_M$-(G63-T93) also increased the phosphorylase phosphatase activity of PP1c, indicating that it binds to PP1c, rather than to $G_L$. However, the maximal stimulation was only 37 + 1.4% (SEM for three experiments), establishing that far greater activation of $PP1_{GL}$ is explained by the ability of $G_M$-(G63-T93) to overcome the suppressive effect of $G_L$ on the phosphorylase phosphatase activity of PP1c. Several other peptides, including a 32 residue peptide related to the C-terminus of ribosomal protein S6([G245,G246]S6[218-249]), $G_M$-(S40-Y55) and $G_M$-(E81-T93) (data not shown), had no effect on the phosphorylase phosphatase activity of $PP1_{GL}$ or PP1c at concentrations up to 10 $\mu M$.

The peptides $G_M$-(G63-K80) and $G_M$-(G63-N75) also increased the phosphorylase phosphatase activity of $PP1_{GL}$, but were less effective than $G_M$-(G63-T93) and higher concentrations were needed (Fig 2). $G_M$-(G63-K80) and $G_M$-(G63-N75) did not increase the phosphorylase phosphatase activity of PP1c significantly at concentrations up to 10 $\mu$M (data not shown). The phosphorylation of $G_M$ at Ser67 by cyclic AMP-dependent protein kinase (PKA) triggers the dissociation of PP1 from $G_M$ *in vitro* and *in vivo* [18] and phosphorylation of the peptide $G_M$-(G63-N75) at Ser67 prevented it from increasing the phosphorylase phosphatase activity of $PP1_{GL}$ (Fig 2A). The increase in phosphorylase phosphatase activity observed at the highest phosphopeptide concentrations (10 $\mu$M) may be explained by trace contamination (< 10%) with dephosphopeptide, resulting either from incomplete phosphorylation of Ser67 or slight dephosphorylation during the assay.

*Identification of a PP1-interaction domain on the $M_{110}$ subunit.*

Antibodies were prepared that recognised either the $M_{110}$ or $M_{21}$ subunits of the myosin-associated form of PP1 ($PP1_M$) from chicken gizzard (Fig 3A). Removal of the $M_{21}$ subunit using the $M_{21}$-specific antibody (Fig 3B and see Methods) did not affect the activity of $PP1_M$ towards $MLC_{20}$ or phosphorylase, the $MLC_{20}$ phosphatase:phosphorylase phosphatase activity ratio (0.95 ± 0.03) remaining 15-fold higher than PP1c (Fig 3B). The $M_{21}$ subunit bound to $M_{110}$, but had no effect on the $MLC_{20}$ phosphatase or phosphorylase phosphatase activity of PP1c and did not bind to PP1c (D. Johnson unpublished). Thus $M_{110}$ is solely responsible for enhancing the dephosphorylation of $MLC_{20}$ and suppressing the dephosphorylation of glycogen phosphorylase by PP1c [9].

In order to identify which region(s) of $M_{110}$ modulates the specificity of PP1c, fusion proteins were constructed consisting of glutathione S-transferase (GST) followed by fragments of the $M_{110}$ subunit. After expression in *E. coli* and

purification by affinity chromatography on glutathione-Sepharose, the fusion proteins were cleaved with thrombin to release GST from fragments of the $M_{110}$ subunit (Fig 4 and see Methods). $M_{110}$-(M1-E309), which contains seven 33 residue ankyrin repeats located between residues 39-296, modified the specificity of PP1c in a similar manner to $M_{110}$ itself, increasing activity towards $MLC_{20}$ about 3-fold (Fig 5A) and suppressing activity towards glycogen phosphorylase by about 80% (Fig 5B). The concentration of $M_{110}$-(M1- E309) required to activate the $MLC_{20}$ phosphatase activity maximally (0.1 nM) was similar to the PP1c concentration in the assay, indicating an extremely high affinity for PP1c. $M_{110}$-(M1-A150) modified the specificity of PP1 similarly, but 10-fold higher concentrations were needed compared to $M_{110}$-(M1-E309) (Figs 5C and 5D).

If the GST tags were not cleaved with thrombin, a 10-fold higher concentration of $M_{110}$-(M1-E309) was needed to modulate the substrate specificity of PP1c, while $M_{110}$-(M1-A150) was unable to stimulate the $MLC_{20}$ phosphatase activity of PP1c at all (data not shown). GST itself did not interact with PP1c (Fig 1), had no effect on either the $MLC_{20}$ phosphatase or phosphorylase phosphatase activity of PP1c (data not shown), and therefore was not removed from the solution after cleavage of the fusion proteins with thrombin.

In contrast to $M_{110}$-(M1-E309), $M_{110}$-(D39-E309) failed to stimulate the $MLC_{20}$ phosphatase activity of PP1c, or to inhibit its phosphorylase phosphatase activity (Figs 5A and 5B), suggesting that the extreme N-terminus of the $M_{110}$ subunit (i.e. before the start of the ankyrin repeats) might be important in modulating the specificity of PP1c. The peptide $M_{110}$-(M1-F38) was therefore synthesized and found to stimulate the $MLC_{20}$ phosphatase activity of PP1c to the same extent as $M_{110}$-(M1-E309), although the concentration required for half maximal activation (10 nM) was at least 100-fold higher (Fig 5A). $M_{110}$-(M1-F38) stimulated the dephosphorylation of heavy meromyosin in a

similar manner to the dephosphorylation of $MLC_{20}$ (data not shown). However, like $M_{110}$-(D39-E309), $M_{110}$-(M1-F38) did not inhibit the phosphorylase phosphatase activity of PP1c (Fig 5B). These observations suggested that residues beyond 38 were needed to suppress phosphorylase phosphatase activity. Consistent with this, $M_{110}$-(L24-Y496) was less effective than $M_{110}$-(M1-A150) or $M_{110}$-(M1-E309) in stimulating the $MLC_{20}$ phosphatase activity of PP1c, but inhibited the phosphorylase phosphatase activity of PP1c in a similar manner to $M_{110}$-(M1-A150) (Figs 5C and 5D).

Although $M_{110}$-(D39-E309) and $M_{110}$-(M1-F38) had no effect on the phosphorylase phosphatase activity of PP1c when each peptide was included individually in the assays at concentrations up to 1 $\mu$M (Fig 5), a 39 $\pm$ 2% inhibition (SEM n=4) was observed when both peptides were both present at 1 $\mu$M. Surprisingly, $M_{110}$-(D39-E309) prevented (IC50 = 0.1 M) $M_{110}$-(M1-F38) from stimulating the $MLC_{20}$ phosphatase activity of PP1c (data not shown). Thus $M_{110}$-(D39-E309) plus $M_{110}$-(M1-F38) do not faithfully mimic the effect of $M_{110}$-(M1-E309).

We have reported previously that the $M_{110}/M_{21}$ complex suppresses the dephosphorylation of glycogen synthase by PP1c [9] and, consistent with this finding, the dephosphorylation of glycogen synthase was also inhibited by $M_{110}$-(M1-E309) (Fig 6B). However, the dephosphorylation of glycogen synthase was greatly enhanced by $M_{110}$-(M1-F38) (Fig 6A).

*The binding of $G_M$ and the $M_{110}$ subunit to PP1c is mutually exclusive.*

In order to investigate whether $G_M$ binds to the same region of PP1c as $M_{110}$, we next examined the effect of $G_M$-(G63-T93) on the properties of $PP1_M$. $G_M$-(G63-T93) at 10 $\mu$M increased the phosphorylase phosphatase activity of $PP1_M$ by about 7-fold and suppressed its $MLC_{20}$ phosphatase activity by 60-65 %

(Fig 7A), indicating that the distinctive properties of $PP1_M$ had been disrupted. Gel-filtration experiments confirmed that $G_M$-(G63-T93) had displaced the $M_{110}$ subunit from $PP1_M$, dissociating it to PP1c (Figs 7B and 7C). $G_M$-(G63-T93) also prevented $M_{110}$-(M1-F38) or $M_{110}$-(M1-E309) from stimulating the $MLC_{20}$ phosphatase activity of PP1c (Fig 8A), and prevented $M_{110}$-(M1-E309) from suppressing the phosphorylase phosphatase activity of PP1c (Fig 8B).

Conversely, the presence of 10 $\mu$M $M_{110}$-(M1-F38) increased the phosphorylase phosphatase activity of $PP1_{GL}$ by 3.5- fold. This resulted from the partial dissociation to PP1c, because the enhanced phosphorylase phosphatase activity was not associated with glycogen, but recovered in the supernatant after centrifugation of the glycogen-protein particles (not shown).

DISCUSSION.

We have identified a region on $G_M$ that binds to PP1c (Fig 9). The peptides $G_M$-(G63-T93), $G_M$-(G63-K80) and $G_M$-(G63-N75) all prevented $G_L$ from suppressing the dephosphorylation of glycogen phosphorylase by PP1c and two lines of evidence indicate that these peptides interact with PP1c and not with $G_L$.

Firstly, the PP1c-catalysed dephosphorylation of glycogen phosphorylase is stimulated slightly by $G_M$-(G63-T93).

Secondly, PP1c crystallises in the presence of $G_M$-(G63-K80) or $G_M$-(G63-N75) in a different form than is observed in the absence of these peptides. PKA phosphorylates $G_M$ at Ser67 and the introduction of a negative charge directly into the PP1c-binding domain explains why phosphorylation of Ser67 triggers the dissociation of $G_M$ from PP1c [18]. Phosphorylation of $G_M$-(G63-N75) at Ser67 also prevented this peptide from interacting with PP1 in the $PP1_{GL}$

complex (Fig 2).

Although $G_M$-(G63-T93) prevented $G_L$ from suppressing the dephosphorylation of glycogen phosphorylase by PP1c, it did not dissociate $G_L$ from PP1c, nor did it affect the other characteristic properties of $PP1_{GL}$. Moreover, unlike $G_L$, $G_M$-(G63-T93) did not itself suppress the phosphorylase phosphatase activity of PP1c, but actually enhanced it slightly. These observations demonstrate that another region(s) on $G_L$ must interact with PP1c and that this other region(s) may play an important role in modulating the substrate specificity of PP1c. The presence of a second PP1c binding site in $G_M/G_L$ would be somewhat analogous to the situation found in inhibitor-1 and DARPP which also contain two PP1-binding sites, high (nM) affinity binding being generated by the conjugation of two low affinity binding sites that, individually, only interact with PP1 at $\mu$M concentrations [28]. The second PP1c-binding site on $G_M/G_L$ might correspond to one of the other regions where $G_M$ and $G_L$ show $>40\%$ identity (residues 144-166 and 186-227 of human $G_M$). Although $G_M$-(H100-P350) was not recognised by PP1c in Far Western experiments (Fig 1) this result is not definitive because $G_M$-(H100-P350) may only interact with PP1c weakly. Alternatively, $G_M$-(H100-P350) might not fold correctly or fail to renature after SDS/polyacrylamide gel electrophoresis.

However, it is also possible that residues 144-166 and 186-227 of $G_M$ do not represent part of the second PP1c-binding domain, but part of the glycogen-binding domain. In this connection it should be recalled that residues 144-166 and 186-227 are the regions showing greatest similarity (25% identity) to GAC1, which appears to be a homologue of $G_M/G_L$ in budding yeast [7, 27, 28]. Curiously, GAC1 does not contain a region homologous to residues 63-93 of $G_M/G_L$. It would clearly be of interest to compare the effect of GAC1 on the enzymatic properties of PP1c with those of $G_M$ and $G_L$.

We have also identified a region on the $M_{110}$ subunit that binds to PP1c. An N-terminal fragment, M100-(M1-E309), enhanced the PP1c-catalysed dephosphorylation of $MLC_{20}$ and suppressed the dephosphorylation of glycogen phosphorylase in a similar manner to $M_{110}$ itself (Fig 5). However, unlike $M_{110}$, this fragment does not bind to myosin. Thus the region which enhances the dephosphorylation of $MLC_{20}$ is distinct from the myosin-binding domain.

The fragment $M_{110}$-(M1-E309) contains seven ankyrin repeats lying between residues 39 and 296. However, $M_{110}$-(D39-E309) was ineffective as an activator of the $MLC_{20}$ phosphatase activity of PP1c or as an inhibitor of the phosphorylase phosphatase activity, and this led to the finding that a peptide comprising the N-terminal 38 residues of the $M_{110}$ subunit enhances the dephosphorylation of $MLC_{20}$ to the same extent as $M_{110}$-(M1-E309), although with lower potency. However, $M_{110}$-(M1-F38) did not inhibit the dephosphorylation of glycogen phosphorylase by PP1c suggesting that residues beyond 38 are required to suppress this activity. This view was reinforced by the finding that, although neither $M_{110}$-(M1-F38) nor $M_{110}$-(D39-E309) inhibited the phosphorylase phosphatase activity of PP1c when present individually, inhibition was observed in the presence of both peptides. Moreover $M_{110}$-(D39-E309) actually prevented $M_{110}$-(M1-F38) from stimulating the dephosphorylation of $MLC_{20}$.

These observations suggest that $M_{110}$-(D39-E309) can bind to $M_{110}$-(M1-F38) and/or PP1c. An interaction with PP1c seems likely because it has been found that $M_{110}$-(D39-E309) can enhance the phosphorylase activity of $PP1_{GL}$. The presence of a second PP1-binding site in the ankyrin-repeat domain of the $M_{110}$ subunit is also supported by the observation that higher concentrations of $M_{110}$-(M1-A150) and $M_{110}$-(M1-E309) are needed to inhibit the phosphorylase phosphatase activity of PP1c than are required to stimulate its $MLC_{20}$ phosphatase activity (see Fig 5). The presence of at least two PP1-binding sites

may explain why the $M_{110}$ subunit and PP1c interact at picomolar concentrations. The ankyrin repeat domain might suppress the dephosphorylation of some substrates (such as glycogen phosphorylase) by a steric mechanism, preventing them from gaining easy access to the catalytic centre. This scenario could explain why the dephosphorylation of glycogen synthase is greatly enhanced by $M_{110}$-(M1-F38) yet suppressed by $M_{110}$-(M1-E309) (Fig 6).

$G_M$-(G63-T93) abolished the distinctive properties of $PP1_M$ (Fig 7A), prevented $M_{110}$-(M1-F38) or $M_{110}$-(M1-E309) from modulating the substrate specificity of PP1c (Fig 8) and displaced the $M_{110}$ subunit from $PP1_M$ (Fig 7B). In addition, the peptide $M_{110}$-(M1-F38), was capable of displacing $G_L$ from $PP1_{GL}$. These findings indicate that the binding site(s) on PP1c for $G_M$ and the $M_{110}$ subunit are likely to overlap, explaining why different forms of PP1 contain a single PP1-targeting subunit. The three-dimensional structure of PP1c isoforms have recently been solved to high resolution [29,30], and PP1c crystallises in different forms in the presence of $G_M$-(G63-N75) or $G_M$-(G63-K80) or $M_{110}$-(M1-F38) than in the absence of these peptides.

Consistent with the results presented here, Gailly *et al* [31] have recently shown that $M_{110}$-(M1-F38) or $M_{110}$(M1-E309) enhance the ability of PP1c to stimulate the relaxation of microcystin-contracted permeabilised portal vein, while $G_M$-(G63-T93) inhibits the ability of $PP1_M$ to induce the relaxation of this smooth muscle. $G_M$-(G63-T93) also slowed the relaxation of permeabilised femoral artery, indicating that it competes with the endogenous $M_{110}$ subunit for PP1c [31]. Thus the PP1c-binding peptides described constitute useful pharmacological agents with which to explore the role and regulate the activity of PP1 in cell regulation.

**Example 2: Structural basis for the recognition of regulatory subunits by the catalytic subunit of protein phosphatase 1**

MATERIALS AND METHODS

*Crystallisation and Data Collection*

The catalytic subunit of PP1 1 was overproduced in *Escherischia coli* and purified as described previously (Alessi *et al.*, 1993; Barford and Keller, 1994). The $G_M$[G63-N75] peptide, variants of this peptide in which Val 66' or Phe 68' were changed to Phe, and the peptides $M_{110}$[1-38] and $M_{110}$[1-35] were synthesised on an Applied Biosystems 430A peptide synthesiser and purified by chromatography on a C18 column (Johnson *et al.*, 1996) by Mr F.B. Caudwell at Dundee. A three-fold molar excess of $G_M$[G63-N75] was added to the protein solution (8 mg/ml), which had been previously dialysed against 10 mM Tris-HCl (pH 7.8), 0.3 M NaCl, 0.4 mM $MnCl_2$ and 2 mM DTT. The complex was crystallised at 20°C using the hanging drop vapour diffusion method, by mixing 2 ml of the protein-peptide solution and 2 ml of the precipitant solution containing 2.0 M ammonium sulphate, 2% (w/v) polyethylene glycol 400,100 mM HEPES (pH 7.5) and 2 mM DTT. These conditions are very much in contrast to the relatively low ionic strength conditions from which the monoclinic PP1c crystals grew (Barford and Keller, 1994; Egloff *et al.*, 1995). Crystals appeared after 3 months as a cluster. Individual crystals removed from the cluster had dimensions of ~25 μm x 25 μm x 5 μm. Crystals were frozen in a 100 K nitrogen gas stream and stored. Prior to freezing, crystals were incubated in a cryoprotectant solution consisting of an equilibration buffer; 2.0 M ammonium sulphate, 2% (w/v) PEG 400, 100 mM HEPES (pH 7.5) with increasing amounts of glycerol in steps of 7%, 15%, 22% and 30% (v/v).

A partial data set to 3.0 Å was collected on Beam Line PX 9.6, SRS,

Daresbury, using a 30 cm diameter Mar Research image plate system. Data were processed and scaled using DENZO and SCALEPACK (Otwinowski, 1993). The crystal system is tetragonal with point group symmetry P422 and unit cell dimensions a = b = 62.50Å, c = 361.30Å. Systematic absences indicate a 21 screw axis along b. The Matthews coefficient was 2.38 $Å_3$ per Dalton, assuming 2 molecules per asymmetric unit. A second data-set was collected on BL4 at the ESRF, Grenoble. Substantial radiation damage was observed during data collection requiring that three crystals were used in total. Data collected from four crystal at Daresbury and the ESRF were merged together in SCALEPACK. Details of the data collection and processing statistics are given in Table 1.

*Structure determination*

The structure of the PP1-$G_M$[63-75] complex was solved by molecular replacement using as a model the protein atoms coordinates of the 2.5Å refined structure of the catalytic subunit of PP1γ1 determined by MAD methods (Egloff *et al.*, 1995). Rotation and translation functions searches were performed with AMORE (Navaza, 1992). Using data between 8 and 3 Å resolution, the peak in the rotation search was 6.7 standard deviations (SD) above the mean. The translation search was best performed using data between 8 and 3.5 Å, giving a maximal peak at 13.8 SD above the mean for the space group P41212. After the first rigid body refinement performed in AMORE, the R-factor was 0.494 and the correlation factor 0.30.

*Crystallographic Refinement*

The solution from molecular replacement was optimized by 20 cycles of rigid body refinement performed with X-PLOR version 3.1 (Brunger, 1992), using data between 8.0 Å and 3.0 Å resolution. After a round of conjugate gradient

positional refinement and simulated annealing molecular dynamics to 2000 K, followed by 25 cycles of grouped B-factor refinement (2 B-factor groups for each residue), the R factor (respectively free-R) was 0.295 (0.367). Fourier difference maps (Fo-Fc) and (3Fo-2Fc) revealed the presence of three strong peaks at (over three-times the sigma level of the map) at the catalytic site of PP1c. From the previously refined PP1c-structure, we identified two as manganese and iron ions. The third one, occupying the position of the tungstate ion in the PP1c-WO4 complex, was identified as sulphate. The initial difference Fourier maps also revealed strong electron density near the N-terminus of β14. The maps were improved by applying non-crystallographic symmetry 2-fold averaging using PHASES (Furey and Swaminathan, 1990). As shown in Fig. 1A, residues Val 66', Ser 67' and Phe 68' of the $G_M$[63-75] peptide were identified in the averaged map. These 3 residues, as well as the 2 metal and sulphate ions were built in each molecule, using the program TURBO-FRODO (Roussel and Cambillau, 1992). Refinement of this structure was performed by repeated rounds of manual rebuilding followed by conjugate gradient positional refinement and grouped B-factor refinement using X-PLOR. The final model contains protein residues Lys 6 to Ala 299 and peptide residues Arg 65' to Ala 69' in molecule 1, and protein residues Asn 8 to Lys 297 and peptide residues Gly 63' to Ala 69' in molecule 2. A few well defined water molecules were also observed in both initial (3Fo-2Fc) and (Fo-Fc) electron density maps. Eventually, 14 water molecules that were above 3 sigma in the (Fo-Fc) difference map, within hydrogen bond of the PP1-peptide complex or another solvent molecule and present in both molecules, were included in the model. The crystallographic and refinement data are summarized in Table 1. Representative electron density from the peptide before and after refinement is shown in Figure 10A and 10B, respectively. Solvent accessible surface areas were calculated using the method of Lee and Richards (1974).

*Purification and assay of PP1.*

PP1c was isolated from the rabbit skeletal muscle PP1-$G_M$ complex as described previously (Johnson *et al*, 1996). Glycogen particles isolated from rat liver (Schelling *et al*, 1988) served as the source of PP1-$G_L$. The dephosphorylation of glycogen phosphorylase (10 $\mu$M) and the isolated $MLC_{20}$ of smooth muscle myosin (1 $\mu$M) by PP1c was carried out as described previously (Cohen *et al.*, 1988; Alessi *et al.*, 1992).

**Table 1. Crystallographic data and refinement statistics**

| | |
|---|---|
| **Crystallographic data:** | |
| Space group | $P4_12_12$ |
| Unit cell parameters (Å) | a = b = 62.50; c = 361.30 |
| Number of molecules per asymmetric unit | 2 |
| Temperature (K) | 100 |
| Total measured reflections | 290671 |
| Number of unique reflections | 15509 |
| Mean I/s(I) | 7.5 |
| Completeness (%) | 87 |
| Overall R-merge (%) | 14.7 |
| **Refinement statistics:** | |
| Number of reflections used for refinement | 13078 |
| Resolution range (Å) | 8.0-3.0 |
| R-work | 0.223 |
| R-free | 0.308 |
| Number of residues | protein peptide |

| | |
|---|---|
| Molecule 1 | 294 (Lys 6 to 6 (ARVSFA) (SEQ ID No 21) Ala 299) 6 (RRVSFA) SEQ ID No 3) |
| Molecule 2 | 290 (Asn 8 to Lys 297) |
| R.m.s.d. from ideal bond lengths (Å) | 0.012 |
| R.m.s.d. from ideal angles (°) | 1.863 |
| Number of water molecules | |
| Molecule 1 | 7 |
| Molecule 2 | 7 |

**Table 2. PP1-peptide polar interactions**

| | **Peptide atom** | **Protein atom** | **Water molecule** | **Distance (Å)** |
|---|---|---|---|---|
| Molecule 1 | Arg 65′ O | - | 7W | 3.2 |
| | Val 66′ N | Asp 242OD2 (**) | | 3.0 |
| | Ser 67′ N | Leu 289 O | | 3.3 |
| | Ser 67′ OG | | 7W | 2.7 |
| | Ser 67′ O | Cys 291 N (*) | | 3.2 |
| | Ala 69′ N | Cys 291 O (*) | | 2.8 |
| Molecule 2 | Arg 64′ NH1 | Glu 287 O | | 2.6 |
| | | (**) | | |
| | Arg 65′ O | | 7W | 2.8 |
| | Val 66′ N | Asp 242 OD2 (**) | | 3.2 |
| | Ser 67′ N | Leu 289 O (*) | | 3.1 |
| | Ser 67′ OG | | 7W | 2.6 |
| | Ser 67′ | Cys 291 N (*) | | 3.0 |

| | | | | |
|---|---|---|---|---|
| | Ala 69′ N | Cys 291 O (*) | | 3.3 |

**Table 2. PP1-peptide hydrophobic interactions**

| | **Peptide residues** | **Protein residues** | | |
|---|---|---|---|---|
| | Val 66′ | Ile 169 (*), Leu 243 (*), D242 (**), Leu 289 (*), Cys 291 (*) | | |
| | Phe 68′ | Phe 257 (*), Cys 291 (*), Phe 293 (*) | | |
| | Ala 69′ | Met290 (**) | | |

The star (*) indicates residues absolutely conserved in all protein phosphatase 1 sequences available so far, the double start (**) the residues mostly conserved (from sequence alignment from Barton *et al*, 1994).

## RESULTS AND DISCUSSION

*Structure Determination.*

Crystallographic data to 3.0 Å were measured at the ESRF beam-line BL4 at Grenoble and at PX9.6, Daresbury (Table 1). The relatively high merging R-factors and low I/(I values of the crystallographic data results from the weak diffraction observed from the PP1-$G_M$[63-73] crystals. This is attributable to both the small crystal size ( ~ 25 $\mu$m by 25 $\mu$m by 5 $\mu$m) and long c-axis of the unit cell. In addition, the high x-ray photon dose required to obtain usable diffraction images resulted in x-ray radiation damage to the crystals, despite being maintained at a temperature of 100 K during the course of the experiment. The structure was solve by the molecular replacement method using as a search model the 2.5 Å refined coordinates of PP1c (Egloff *et al.*, 1995). Phases obtained from a single cycle of simulated annealing refinement

of the protein coordinates alone using X-PLOR Brunger, 1992), and improved by 2-fold non-crystallographic symmetry averaging and solvent flattening, were used to calculate an electron density map. This map revealed clear density corresponding to residues Val 66', Ser 67' and Phe 68' (where ' denotes residues of the peptide) of the $G_M$ peptide and provided a starting point for further refinement of the PP1-$G_M$ peptide complex (Fig. 10A). The final model of the complex was refined at 3.0 Å resolution with a crystallographic R-factor of 0.22 and R-free of 0.31 (Fig. 10B). The two molecules of PP1c within the asymmetric unit are similar with a root mean square deviation between main chain atoms of 0.6 Å. Residues 6 to 299 and 8 to 297 from molecules 1 and 2 respectively, are visible in the electron density map. Similar to the structures of native $PP_{\gamma 1}$ (Egloff *et al.*, 1995) and PP1$\alpha$ in complex with microcystin LR (Goldberg *et al.*, 1995), residues C-terminal to 299 are disordered.

*Overall Structure of PP1*

The conformation of PP1c in the PP1-$G_M$ complex is virtually identical to that of native PP1c in complex with tungstate (Egloff *et al.*, 1995) with a root mean square deviation between equivalent main-chain atoms of 1.0 Å. PP1c is folded into a single elliptical domain consisting of a central $\beta$-sandwich of two mixed $\beta$-sheets surrounded on one side by 7$\alpha$-helices and on the other by a sub-domain consisting of 3$\alpha$-helices and a 3 stranded mixed $\alpha$-sheet (Fig. 2A, B). The interface of the three $\beta$-sheets at the top of the $\beta$-sandwich creates a shallow catalytic site channel. Three loops connecting $\beta$-strands with $\alpha$-helices within a $\beta$-$\alpha$-$\beta$-$\alpha$-$\beta$ motif in sheet 1 (strand order $\beta$4-$\beta$3-$\beta$2-$\beta$13-$\beta$14) together with loops emanating from the opposite $\beta$-sheet (sheet 2; strand order, $\beta$1-$\beta$5-$\beta$6-$\beta$10-$\beta$12-$\beta$11) provide the catalytic site residues. The catalytic site of PP1 contains a binuclear metal site consisting of $Mn^{2+}$ and $Fe^{2+}$ (Egloff *et al.*, 1995) and, in the PP1-$G_M$ complex, oxygen atoms of a sulphate ion of crystallisation coordinate both metal ions, similar to that seen in the PP1-tungstate (Egloff *et al.*, 1995) and PP2B-phosphate complexes (Griffith *et*

*al*, 1995).

*PP1c-$G_M$[63-75] Peptide Interactions*

Six residues of the $G_M$[63-75] peptide (Arg 64' to Ala 69') are clearly visible in the electron density map of the complex of molecule 2, the remaining residues are not visible and assumed to be disordered (Fig. 10B). Density is not visible for Arg 64' of the peptide bound to molecule 1, otherwise equivalent residues of the peptide are similar within the two complexes. The six residues (RRVSFA) (SEQ ID No 3) of the $G_M$[63-75] peptide in complex 2 adopt an extended conformation and bind to a hydrophobic channel on the protein surface with dimensions 25 Å by 10 Å that is formed at the interface of the two $\beta$-sheets of the $\beta$-sandwich opposite to the catalytic site channel and therefore remote from the catalytic site (Fig. 11A). The residues that form this channel occur on three regions of PP1c, namely (i) the N-terminus of 5 and $\beta$5/$\beta$6 loop of sheet 2; (ii) the three edge $\beta$-strands of sheet 2: $\beta$10, $\beta$12, $\beta$11 and (iii) $\beta$13, the $\beta$13/$\beta$14 loop and $\beta$14 of the edge of sheet 1 (Fig. 11A). The total solvent accessible surface area buried on formation of the complex is 980 Å2. Three residues of the peptide (Ser 67' to Ala 69') form a $\beta$-strand which is incorporated into $\beta$-sheet 1 of PP1c as a sixth $\beta$-strand parallel to the N-terminus of the edge $\beta$-strand, $\beta$14 (residues Leu 289 to Leu 296) (Fig. 11C). Main-chain atoms of Ser 67' and Ala 69' form H-bonds to the main-chain atoms of residues of $\beta$14. In addition, the main-chain nitrogen of Val 66' forms a H-bond with the side-chain of Asp 242. Other polar interactions include the guanidinium group of Arg 64' with the mainchain carbonyl of Glu 287 and a salt bridge to Asp 166. Both Asp 166 and Asp 242 are invariant in mammalian PP1 genes. A water molecule bridges the main-chain carbonyl of Arg 65' and side-chain hydroxyl of Ser 67' with the main-chain carbonyl of Thr 288 of PP1c (Fig. 11C). A notable feature of the peptide binding site is the presence of a negatively charged region created by seven acidic residues (with one Lys residue) surrounding the hydrophobic

channel at the N-terminus of the peptide in the vicinity of Arg 64' and Arg 65' that includes Asp 166 and Asp 242 (Fig. 11D). This would suggest a favourable electrostatic environment for the side chains of Arg 64' and Arg 65'.

The predominant interactions between the peptide and PP1c involve hydrophobic contacts between the side chains of Val 66' and Phe 68' and solvent exposed, invariant, hydrophobic residues of PP1c that form the hydrophobic channel (Fig. 11C, E). In particular, the binding site for the side chain of Val 66' is formed from the side chains of Ile 169, Leu 243, Leu 289 and Cys 291, whereas that for the side chain of Phe 68' is formed from the side chains of Phe 257, Cys 291 and Phe 293. Details of peptide-PP1c contacts are given in Table 2. The structure of the $G_M$[63-75] peptide binding site is likely to be conserved in other forms of PP1 from diverse species. Each hydrophobic residue of PP1c that interacts with the Val 66' and Phe 68' residues of the $G_M$[63-75] peptide are invariant and the acidic residues that surround the N-terminus of the peptide binding site are highly conserved amongst all isoforms of PP1 from species as diverse as yeast, *Drosophila*, mammals and higher plants (Barton *et al.*, 1994). However, since these residues are not conserved within the PP2A and PP2B sequences, these proteins will not recognise PP1-regulatory subunits.

*Presence of an (R/K) (V/I) x F Motif in other PP1c Regulatory Proteins*

Over a dozen regulatory subunits of PP1c are now known which appear to bind to PP1c in a mutually exclusive manner that suggests either an overlapping binding site or sites. Sequence comparisons of these subunits reveals little similarity except for the motif (R/K) (V/I) x F, that is not only present in $G_M$[63-75] but also in $G_M$, $G_L$, $M_{110}$, NIPP-1, p53BP2, and an RNA splicing factor (Fig. 12A). Moreover, a 38 residue peptide from the 110kDa $M_{110}$ subunit that binds to PP1c contain this motif (Johnson *et al*, 1996), as do

fragments of NIPP-1 (Beullens *et al.*, 1992; Van Eynde *et al*, 1995), an RNA splicing factor (Hirano *et al.*, 1996) and p53BP2 (Helps *et al.*, 1995). A 32 residue peptide from p53BP2, which contains this motif, disrupted the interaction of the $M_{110}$ subunit with PP1c, as shown by a decrease in the rate of dephosphorylation of the $MLC_{20}$ subunit of smooth muscle myosin and by an increase in the rate of dephosphorylation of glycogen phosphorylase (Fig. 13A). This peptide also disrupted the interaction of the $G_L$ subunit with PP1c, as shown by an increase in the rate of dephosphorylation of glycogen phosphorylase (Fig. 13B). Peptides comprising the motif (R/K) (V/I) x F are thus encompassed within the scope of the invention.

In further support of the notion of a common PP1c recognition motif present within PP1-binding proteins, previous studies had revealed that the sequence KIQF (SEQ ID No 22) (similar to the R/KVxF motif) at the N-terminus of inhibitor 1 and its homologue DARPP-32 (Fig. 12A) is necessary for mediating the inhibitory effects of these proteins. Loss of Ile 10 of the KIQF (SEQ ID No 22) motif of inhibitor 1 disrupts the inhibitory effects on PP1c by phospho-inhibitor-1 (Aitken and Cohen, 1984; Endo *et al.*, 1996) and the binding of either dephospho-inhibitor-1 or phospho-inhibitor-1 to PP1c (Endo *et al.* , 1996). A similar result was found on disrupting the equivalent residue (Ile 9) of DARPP-32 (Hemmings *et al.*, 1990; Desdouits *et al.*, 1995). These results were interpreted to indicate that inhibitor-1 and DARPP-32 bind to PP1 through two low affinity binding sites, one that encompasses the sequence KIQF (SEQ ID No 22) and another which includes the phosphorylated Thr residue (35 in I-1, 34 in DARPP-32) and which presumably binds at the catalytic site. Analysis of the PP1-$G_M$[63-75] complex structure suggests that an isoleucine residue could be readily accommodated within the peptide binding site in place of Val 66' such that the additional methyl group on Ile compared to Val would contribute to favourable van der Waals interactions between the peptide and Leu 243 and Cys 291 of PP1. More bulky hydrophobic residues

such as Leu, Met and Phe cannot be accommodated, however. It is interesting to note that as well as the (R/K) (V/I) x F motif shared by PP1-regulatory subunits, the four residues N-terminal to this motif contain an abundance of basic residues. These residues may provide further favourable interactions with the negative electrostatic surface potential at the N-terminus of the $G_M$(63-75] peptide binding site of PP1c (Fig. 11D).

*Mutagenesis of the R/K) (V/I) x F motif*

The structural studies presented here suggest a dominant role for Val 66' and Phe 68' in stabilising the interaction between $G_M$[63-75] and PP1c and this notion is further reinforced by the finding that other PP1-regulatory subunit sequences contain an (R/K)(V/I) x F motif yet share little overall sequence similarity. To test the hypothesis that Val 66' and Phe 68' are required for the interaction of $G_M$[63-75] with PP1c and also that the KVKF (SEQ ID No 5) sequence present within the $M_{110}$[M1-F38) peptide is important in mediating its interaction with PP1c, we synthesised variations of the $G_M$ and $M_{110}$ peptides where the R/KVxF motif was disrupted. The two variants of the $G_M$ peptide were Val 66' and Phe 68' to Ala substitutions. In order to disrupt the (R/K)(V/I) x F present within the $M_{110}$ peptide, a peptide corresponding to residues Met 1 to Lys 35 was synthesised which no longer contains the sequence VKF of the VxF motif, which is present at residues 36-38.

The results for the $M_{110}$[1-38] and $M_{110}$[1-35] peptides (Figs. 14, 15) are unequivocal. Whereas $M_{110}$[1-38] stimulates the myosin light chain phosphatase activity of PP1c with a half-maximal effect at 10 nM reaching maximal (3-fold) activation at a peptide concentration of 1 $\mu$M as reported previously (Johnson *et al*, 1996), the $M_{110}$[1-35] peptide was at least 104-fold less effective at activating PP1c (Fig. 14). Unlike $M_{110}$[1-38], the $M_{110}$[l-35] peptide was also unable to activate the phosphorylase phosphatase activity of liver PP1-$G_L$. This latter result suggests two conclusions. Firstly, that although $M_{110}$[1-38] is able

to bind to PP1c and disrupt the interactions between PP1c and the $G_L$-subunit, hence reversing the inhibitory effects of $G_L$ on the ability of PP1c to dephosphorylate phosphorylase, loss of the VKF sequence in the $M_{110}$[1-38] peptide abolishes the ability of the peptide to disrupt this interaction. Secondly, the recognition site on PP1c for the VKF sequence of the $M_{110}$[1-38] peptide must overlap with the binding site for the $G_L$ subunit, suggesting that the VKF sequence binds to the same site as the VSF sequence of $G_L$ that is identical with that present in the $G_M$[63-75] peptide. Similar conclusions may be reached from the results obtained from disrupting the VxF motif within the $G_M$[63-75] peptide (Fig. 16B). Substitution of Phe 68' for Ala abolishes completely the ability of $G_M$[63-75] to disrupt the PP1-$G_L$ complex, whereas replacement of Val 66' with Ala reduced the effectiveness of the disruption 100-fold.

Thus preferred peptides may comprise analogues of $G_M$ with substitutions at Val 66' and Phe 68' to some other amino acid such as Ala, so that binding of the PP1c to $G_M$ does not occur and the PP1c is not suitably directed or controlled. Alternatively, suitable peptides could comprise peptides suitable to compete for the binding site(s) of Val 66' and Phe 68' on PP1c. Such peptides can be added in sufficient quantities to compete for the Phe 68' and Val 66' binding site(s) on the PP1c, thereby disrupting the interaction of PP1c and natural $G_M$. Such peptides could comprise structural analogues of $G_M$ with Phe 68' and Val 66' in the same positions as $G_M$. Alternatively, other amino acids capable of mimicking the binding of Phe 68' and Val 66' could be used in these locations.

*Regulation of the PP1-$G_M$ Complex by Phosphorylation of Ser 67'*

Phosphorylation of Ser 67', corresponding to x of the VxF motif, by PKA promotes dissociation of both $G_M$ and $G_M$[63-75] from PP1c. *In vivo*, this provides a mechanism of inhibiting PP1c during stimulation of skeletal muscle

by adrenalin (Dent *et al.*, 1990). The sequence of $G_M$ surrounding Ser 67' (RRVSFA) (SEQ ID No 3) conforms to a consensus PKA recognition sequence. Interestingly, the conformation of the peptide is similar to that of residues 18 to 23 corresponding to the pseudo-substrate sequence of PKI bound to the catalytic site of PKA (Knighton *et al.*, 1990). Although the side chain of Ser 67' is exposed within the PP1c-peptide complex, overall the $G_M$ peptide is buried, and it is unlikely that Ser 67' would be a substrate for PKA when the peptide is bound to PP1c. This would suggest that PKA phosphorylates Ser 67' when $G_M$ is not associated with PP1c and that this phosphorylation prevents the re-association of PP1c with $G_M$. Since phosphorylation of Ser 67' promotes the dissociation of the PP1-$G_M$ complex both *in vivo* and *in vitro*, it is most likely that PKA phosphorylates Ser 67' of $G_M$ by competing with PP1c for the RRVSFA (SEQ ID No 3) sequence. This is consistent with a notion that the PP1-$G_M$ complex exists in dynamic equilibrium with free PP1c and $G_M$ subunits and that phosphorylation occurs on the regulatory subunit during transient dissociation from PP1c. In the PP1c-peptide complex, the side-chain of Ser 67' adopts the most favourable rotamer conformation. Analysis of the PP1c peptide complex structure suggests that incorporation of a phosphate group onto the side chain of Ser 67' with the same side-chain rotomer conformation would cause steric hindrance between the peptide and Met 290 of PP1 and also introduce a phosphate group into a region of negative charge at the PP1c surface (Fig. 11C, D). This may explain how phosphorylation of Ser 67' prevents peptide association with PP1c, although it should be noted that rotation of the side-chain of Ser 67' would relieve this steric clash.

A similar mechanism of control may also operate for other PP1-regulatory subunits. For example, NIPP-1 a nuclear inhibitor of PP1, inhibits PP1 with an inhibitory constant of 1 pM (Beullens *et al.*, 1992). Phosphorylation of NIPP-1 by PKA and/or casein kinase 2 *in vitro* abolishes this inhibition (Beullens *et al.*, 1993; Van Eynde *et al.*, 1994). Although the sites of

phosphorylation on NIPP-1 that mediate these effects are not yet fully characterised it is known that these sites occur within the central ~120 residues of NIPP-1 that incorporates the (R/K)(V/I) x F motif (Van Eynde *et al.*, 1995). Interestingly, a consensus phosphorylation site for PKA (RKNS) (SEQ ID No 23) occurs immediately N-terminal to this motif whereas one casein kinase 2 consensus phosphorylation site occurs between the Val and Phe of the motif and another occurs immediately C-terminal to the Phe residue (TFSEDDE) (SEQ ID No 24) (Van Eynde *et al.*, 1995) (Fig. 12A). It is possible that PKA, casein kinase II or other kinases with similar specificity, release PP1c from inhibition by NIPP-1 by phosphorylating NIPP-1 at sites that block its interaction with the (R/K)(V/I) x F motif recognition site on PP1c.

*Model of the PP1c-Phospho-Inhibitor 1 Complex*

Our model for the interaction of a (R/K)(V/I) x F motif with PP1c, together with previous kinetic data suggesting that the sequence KIQF (SEQ ID No 22) of inhibitor-1 (Aitken and Cohen, 1984; Endo *et al.*, 1996) and DARPP-32 (Hemmings *et al.*, 1990; Desdouits *et al*, 1995) interacts with PP1c, allowed us to construct a plausible model of a complex of PP1c with phospho-inhibitor 1. The major assumptions of this model were (1) the KIQF (SEQ ID No 22) sequence of inhibitor-1 binds to the same site as RVSF (SEQ ID No 25) of the $G_M$[63-75] sequence and (2) that the phosphothreonine residue 35 of phospho-inhibitor 1 binds at the phosphate binding site of the PP1c-catalytic site. Secondary structure predictions of inhibitor 1 (Rost and Sander, 1993; Rost, 1996) suggested that residues 9 to 14 and 23 to 31 adopt $\beta$-strand and $\alpha$-helical conformations, respectively. The prediction of the sequence KIQF (SEQ ID No 22) as a $\beta$-strand is consistent with our assumption that this region of inhibitor-1 adopts the same conformation as RVSF (SEQ ID No 25) of the $G_M$ peptide when bound to the VxF recognition site of PP1c. We have positioned the residues RRPpTP (SEQ ID No 26) encompassing the pThr 35

site within the catalytic site channel in an extended conformation, with the phosphate group of the pThr 35 occupying the phosphate binding site of the catalytic site and the Oγ-atom of Thr 35 equivalent to the solvent exposed oxygen of a dianion that forms a H-bond to the side-chain of the putative general acid His 125 (Egloff *et al.*, 1995; Griffith *et al.*, 1995). The four consecutive Arg residues N-terminal to pThr 35 interact with Asp and Glu residues within an acidic groove of PP1c formed from the β7/β8 loop on one side and the β10/β11 loop and β11 strand on the other, similar to that proposed by Goldberg *et al.*, (1995) for their model of DARPP-32 bound to PP1c. We propose that residues 20 to 30 of inhibitor-1 form an amphipathic helix which folds around the edge of the β-sandwich of PP1c. The N-terminus of this helix is disrupted by prolines at residues 19 and 23. Pro 19 and Pro 15 are probably responsible for introducing turns into the polypeptide chain that allows the β-strand encompassing the KIQF (SEQ ID No 22) sequence (residues 9 to 14) to connect with the α helix. The model of the phospho-inhibitor 1-PP1c complex is shown in Fig. 16.

*Prediction of PP1 Recognition Motifs in Yeast PP1-Binding Proteins*

The residues in mammalian PP1c that interact with the sequence RRVSFA (SEQ ID No 3) are conserved in *S. cerevisiae* PP1 suggesting that the proteins in *S. cerevisiae* known to interact with PP1 (reviewed by Stark, 1996) probably bind to a similar hydrophobic groove on the surface of the enzyme. Examination of their amino acid sequences revealed that a number of PP1-binding proteins in *S. cerevisiae* contained putative PP1-binding motifs that were similar to those present in mammalian PP1-binding proteins (Fig. 12A, B). The *S. cerevisiae* PP1-binding proteins not only contain a V/I x F motif, but also a basic residue equivalent to Arg 64' of $G_M$V the residue that contacts Asp 166, Leu 289 and the main-chain carbonyl of Glu 287 of PP1c. Several of the *S. cerevisiae* proteins also contain a further basic residue (His or Lys) at the position equivalent to Arg 65' of $G_M$. Another striking feature of the

putative PP1-binding sequences in *S. cerevisiae* is the presence of a basic amino acid between the Val/Ile and Phe residues, as is also found in two mammalian PP1-regulatory subunits, the $M_{110}$ subunit and the p53BP2 (Fig. 12A).

The *S. cerevisiae* proteins GAC1 and PIG2 show some homology to residues 140-230 of mammalian $G_M$V and there is genetic and biochemical evidence that they may function to regulate glycogen metabolism in budding yeast (Francois *et al.*, 1992). GIP2 also shares sequence similarity with residues 140-230 of mammalian $G_M$, while YIL045W is an open reading frame in the *S. cerevisiae* genome whose predicted amino acid sequence shows 41% sequence identity to GIP2. YIL045W contains two putative PP1-binding motifs and site directed mutagenesis will be needed to establish which (if either) of these sequences binds to PP1c. REG1 and REG2 are PP1-binding proteins that play a role in cell growth and, in the case of REG1, glucose repression (Tu and Carlson, 1995; Tu *et al.*, 1996; Frederick and Tatchell, 1996). GIP1, which also contains two putative PP1-binding motifs, is expressed specifically during meiosis, affects the transcription of late meiotic genes and is essential for sporulation (Tu and Carlson, 1996). SCD5 is a PP1-interacting protein (Tu *et al.*, 1996) that was first isolated as a multicopy suppressor of the inviability of clathrin heavy chain-deficient yeast (Nelson *et al.*, 1996).

The findings herein demonstrate that the short peptide sequence, the (R/K)(V/I)XF motif, is critical for PP1c to interact with its regulatory subunits. PP1c (when complexed to its targeting subunits) plays key roles in the control of many cellular processed and it is reasonable to predict that over 100 pp1-binding proteins may exist in mammalian cells. Protein sequence data-base searching has revealed that the (R/K)(V/I)XF motifs are found in 10% of proteins. Thus if ~100 PP1-binding proteins occur in mammalian cells, only 1% of proteins with the (R/K)(V/I)XF motif will be PP1-binding proteins. The

reasons why only a few proteins with the (R/K)(V/I)XF motif bind to PP1 are numerous. For example, not every residue may be tolerated at position X or immediately N-terminal or C- terminal to this motif. This study has shown that phosphoserine is not tolerated at position X and it is therefore likely that Asp or Glu will not be tolerated either. The structure of the PP1-$G_M$[63-75] complex suggests that large hydrophobic residues will also be excluded from position X. Moreover, the Val (or Ile) and Phe residues in many (R/K)(V/I)XF motifs will be buried in the hydrophobic core of the protein and hence be unable to interact with PP1, since this motif is predicted to form an amphipathic $\beta$-strand conformation. Thirdly, many of the (R/K)(V/I)XF motifs will be in extracellular proteins or extracelluar domains of transmembrane proteins and hence be unable to bind to PP1. Particular feature so the tertiary structure of PP1-binding proteins may allow exposure of this motif on the surface to allow interaction with PP1. Finally, there is evidence that a second PP1-binding site exists on the $G_M$ and $M_{110}$ subunits (Johnson *et al.*, 1996) and the high affinity interaction of PP1c with protein inhibitor-1 is generated by the binding of PP1c to two low affinity sites (Desdouits *et al.*, 1995), one of which is the KIQF sequence belonging to the (R/K)(V/I)XF motif.

The question of how regulatory subunits modulate the substrate specificity of PP1c requires the co-crystallisation of PP1c with a diverse array of regulatory subunits and substrates and is beyond the scope of this paper. However, two models to account for this property of regulatory subunits are that these subunits either alter the conformation of PP1c or simply target PP1 to its substrates. Both mechanisms may operate *in vivo* depending on the regulatory subunits and substrates. For example, evidence for the former model has recently been reported for the enhancement of myosin dephosphorylation by a complex of PP1c and the $M_{110}$ subunit (Johnson *et al.*, 1996, 1997), whereas the enhancement of the dephosphorylation of glycogen phosphorylase and glycogen synthase by the PP1-$G_M$ complex is more consistent with the second

model (Hubbard and Cohen, 1989).

The identification of the (R/K)(V/I)XF motif also suggests a new approach for determining the physiological roles of PP1-targeting subunits whose functions are unknown. Thus mutation of the (R/K)(I/V)XF motif should disrupt the interaction of many targeting subunits with PP1c without affecting their binding to the target locus. Expression of these mutated proteins under an inducible promoter should lead to displacement of the normal targeting subunit (complexed to PP1c) from its target locus, without disrupting the functions of any other PP1c-targeting subunit complex. Finally, the structural information described here will also facilitate the rational design of drugs that act by disrupting PP1-targeting subunit interactions.

**Example 3: Identification of the regions on the $M_{110}$ subunit of protein phosphatase 1M that interact with the $M_{21}$ subunit and with myosin**

Abbreviations:- $PP1_M$, myofibril-associated form of protein phosphatase 1; PP1c, catalytic subunit of protein phosphatase-1; $M_{110}$ and $M_{21}$, 110 kDa and 21 kDa regulatory subunits of $PP1_M$; MBP, maltose-binding protein; GST, glutathione-S-transferase.

## SUMMARY

We have previously isolated a form of protein phosphatase-1 ($PP1_M$) from avian smooth muscle myofibrils which is composed of the catalytic subunit of PP1 (PP1c) bound to an M-complex consisting of 110 kDa ($M_{110}$) and 21 kDa ($M_{21}$) subunits. The interaction of PP1c with an N-terminal region of the $M_{110}$ subunit enhances the dephosphorylation of myosin and suppresses the dephosphorylation of other substrates [Alessi, D.R., MacDougall, L.K., Sola, M.M., Ikebe, M. and Cohen, P. (1992) *Eur. J. Biochem* **210**, 1023-1035;

Chen, Y.H., Chen, M.X., Alessi, D.R., Campbell, D.G., Shanahan, C., Cohen, P. and Cohen, P.T.W. (1994) *FEBS Lett* 356, 51-56; Johnson, D.F., Moorhead, G., Caudwell, F.B., Cohen, P., Chen, Y.H., Chen, M.X. and Cohen, P.T.W. (1996) *Eur. J. Biochem.* 239, 317-325]. In this Example we establish that $PP1_M$ accounts for nearly all the myosin phosphatase activity in myofibrils, that the $M_{110}$ and $M_{21}$ subunits are present at similar concentrations in the myofibrillar fraction and that these subunits are entirely bound to PP1. We demonstrate that the $M_{21}$ subunit does not interact with PP1c, but with the C-terminal 72 residues of the $M_{110}$ subunit, a region which is 43% identical to residues 87-161 of the $M_{21}$ subunit. A fragment of the $M_{21}$ subunit, $M_{21}$-(M1-L146), lacking the C-terminal leucine zipper, also bound to the $M_{110}$ subunit, but two other fragments $M_{21}$-(M1-E110) and $M_{21}$-(E110-K186) did not. The $M_{110}$ and $M_{21}$ subunits were both found to be myosin-binding proteins. The C-terminal 291 residues of the $M_{110}$ subunit, but not the C-terminal 72 residues, bound to myosin, but the N-terminal fragments $M_{110}$-(M1-E309) and $M_{110}$-(M1-S477) did not. Thus the region of the $M_{110}$ subunit which stimulates the dephosphorylation of myosin by PP1c is distinct from the region which targets $PP1_M$ to myosin. Remarkably, each myosin dimer was capable of binding about 20 moles of $M_{21}$ subunit and many of the $M_{21}$-binding sites were located in the myosin "rod domain". The potential significance of this observation is discussed.

## Introduction

Protein phosphatase-1 (PP1), one of the major serine/threonine-specific protein phosphatases in eukaryotic cells, is regulated by targetting subunits that direct it to particular subcellular loci, modify its substrate specificity and confer the ability to be regulated by extracellular signals (reviewed in [1, 2]). A significant proportion of the PP1 in vertebrate muscle extracts is associated with myofibrils and has enhanced activity towards the P-light chain of myosin and

reduced activity towards other substrates, such as glycogen phosphorylase [3, 4]. When isolated from avian (chicken gizzard) [4, 5] or mammalian (pig bladder) [6] smooth muscle, this form of PP1 ($PP1_M$) was found to be composed of three subunits, namely the catalytic subunit of PP1 (PP1c) and two other proteins with molecular masses of 110 kDa and 21 kDa, termed the $M_{110}$ and $M_{21}$ subunits, respectively [4, 5]. The $M_{110}$ subunit is complexed to both PP1c and the $M_{21}$ subunit [4], and is the component which modulates the substrate specificity of PP1c because selective removal of the $M_{21}$ subunit from $PP1_M$ does not affect the rate at which either myosin or glycogen phosphorylase are dephosphorylated [7].

The $M_{110}$ subunit has been cloned from rat aorta [5], chicken gizzard [8] and rat kidney [9] cDNA libraries. The N-terminus of the $M_{110}$ subunit contains seven ankyrin repeats (residues 39-296 of the rat aorta protein), while alternative splicing in rat uterus [5] gives rise to two different C-termini (Fig 17A), termed Rat1 and Rat2. The C-terminus of Rat1 is virtually identical to the C-terminus of the $M_{110}$ subunit from chicken gizzard (Fig 17A). The sequence of the $M_{21}$ subunit from chicken gizzard is structurally related to the C-terminal region of the $M_{110}$ subunit, the most striking similarities occurring from residues 76-141 of the $M_{21}$ subunit and residues 921-984 of the chicken gizzard $M_{110}$ subunit (54% identity, Fig 17B). However, the C-terminal 53 residues of the $M_{21}$ subunit from chicken gizzard are strikingly similar (83% identity) to the C-terminal 53 residues of the rat aorta sequence, both terminating in a leucine zipper (Fig 17B, [5]).

Residues 1-309 of the $M_{110}$ subunit from rat aorta, $M_{110}$-(M1-E309), mimic the intact $M_{110}$ subunit in stimulating the dephosphorylation of myosin and in suppressing the dephosphorylation of glycogen phosphorylase by PP1c, but a slightly shorter construct $M_{110}$-(D39-E309) (which still contains the seven ankyrin repeats) is unable to modulate the specificity of PP1c [7]. This

observation led to the finding that the N-terminal 38 residues, $M_{110}$-(M1-F38), bind to PP1c and enhance the dephosphorylation of myosin. However, $M_{110}$-(M1-F38) does not suppress the dephosphorylation of glycogen phosphorylase, suggesting that the ankyrin repeats either contain a second PP1c-binding site or prevent glycogen phosphorylase from binding to the active site of PP1c, perhaps by steric hindrance [7].

A 13 residue peptide $G_M$-(G63-N75) from the subunit ($G_M$) which targets PP1c to glycogen and the sarcoplasmic reticulum in striated muscle, has been co-crystallised with PP1c and the structure of the complex solved to 3Å resolution [2]. These studies showed that a hexapeptide sequence in $G_M$-(G63-N75) (Arg-Arg-Val-Ser-Phe-Ala) (SEQ ID No 3) binds to a small hydrophobic groove on the surface of PP1c forming a $\beta$-sheet which runs parallel to another $\beta$-sheet in PP1c. Moreover, inspection of other mammalian PP1c-binding proteins reveals that almost all contain an Arg/Lys-Val/Ile-Xaa-Phe motif that is likely to be critical for interaction with PP1c [2]. For example, a Lys-Val-Lys-Phe (SEQ ID No 5) motif is present between residues 35 and 38 of the $M_{110}$ subunit and the deletion of residues 36-38 from $M_{110}$-(M1-F38) prevents this peptide from stimulating the dephosphorylation of myosin, and from disrupting the interaction of PP1c with other targetting subunits [2].

The finding that a region near the N-terminus of the $M_{110}$ subunit binds to PP1c and modulates its specificity raised the question of which region on the $M_{110}$ subunit interacted with the $M_{21}$ subunit, and how the $PP1_M$ complex is targeted to the myofibrils. In this Example we identify regions near the C-terminus of the $M_{110}$ subunit that interact with the $M_{21}$ subunit and with myosin, and demonstrate that the $M_{21}$ subunit is also a myosin-binding protein. These findings indicate that the domain of the $M_{110}$ subunit which enhances the dephosphorylation of the myosin P-light chain is distinct from the region which targets PP1c to the contractile apparatus.

## MATERIALS AND METHODS

### Materials

$PP1_M$ [4] and the dephosphorylated form of myosin [10] were isolated from chicken gizzard, and the rod-domain and light meromyosin were obtained by subdigestion of chicken gizzard myosin with papain and chymotrypsin, respectively [11]. $PP1_G$ was purified from rabbit skeletal muscle by Dr G. Moorhead in this laboratory [12] and PP1c dissociated from the glycogen-binding subunit by incubation for 2 h in 2 M LiBr and then purified by gel-filtration on a 30 x 1 cm column of Superose 12 (Pharmacia, Milton Keynes, UK) in the presence of LiBr (0.5 M). All other chemicals were from BDH Chemicals (Poole, UK) or Sigma (Poole, UK).

*Construction of vectors for the expression of fragments of the $M_{110}$ subunit from rat aorta (rat2 sequence in Fig 17A) as glutathione-S-transferase (GST) fusion proteins in E. coli.*

A construct pGEX-$M_{110}$-(M1-E309) for the expression of GST-$M_{110}$-(M1-E309) from rat aorta was produced as described previously [7]. A construct for the expression of GST-$M_{110}$-(M1-S477) was prepared by subcloning a *Xho*I-*Hind*III fragment (encoding L24-S477) of pKS-$M_{110}$-(M1-S477) described in [5] into the same sites of pGEX-$M_{110}$-(M1-E309). The resulting construct expressed a GST-$M_{110}$-(M1-S477) fusion protein with the additional amino acids SAANSISSLIHRD* (SEQ ID No 27) after S477. An expression construct for GST-$M_{110}$-(M377-K976) was produced by deleting a *Nco*I-*Nco*I fragment of the construct pGEX-$M_{110}$-(L24-K976) [7].

*Construction of vectors for the expression of C-terminal fragments of the $M_{110}$ subunit from chicken gizzard (Ch1 sequence in Fig 17A, [5]) as maltose binding*

*protein (MBP) fusion proteins in E. coli.*

A pT7.7 vector for the expression of the C-terminal 291 residues of the $M_{110}$ subunit from chicken gizzard, pT7-$M_{110}$-(R714-I1004) was described previously [7]. A construct for the expression of MBP-$M_{110}$-(R714-I1004) was produced by cloning an *Nde*I-*Bam*HI fragment of pT7-$M_{110}$-(R714-I1004) into the pMAL-HA vector (New England Biolabs). Removal of a *Hin*dIII-*Hin*dIII restriction fragment from pMBP-$M_{110}$-(R714-I1004) allowed expression of MBP-$M_{110}$-(R714-L934) with the sequence GTGRRFTTS (SEQ ID No 28) added to its C-terminus. Removal of a *Nde*I-*Hin*dIII restriction fragment from pMBP-$M_{110}$-(R714-I1004), followed by filling in the overhanging ends and religating them, allowed expression of MBP-$M_{110}$-(K933-I1004).

*Construction of vectors for the expression in E. coli. of the $M_{21}$ subunit from chicken gizzard [5], with and without the C-terminal leucine zipper domain.*

A pT7.7 vector for the expression of the entire coding region (M1-K186) of the $M_{21}$ subunit was described previously [7]. The leucine zipper motif of the $M_{21}$ subunit was deleted by removing a *Sac*I-*Bam*HI restriction fragment from pT7.7 $M_{21}$, filling in the overhanging ends and religating them. The construct expressed $M_{21}$-(M1-R144) with an extra I and L after residue 144. The $M_{21}$-(M1-R144) protein was insoluble when expressed and was purified as described for the expressed $M_{21}$ subunit [7].

*Construction of vectors for the expression of the $M_{21}$ subunit from chicken gizzard [5] and fragments of the $M_{21}$ subunit as glutathione-S-transferase (GST) fusion proteins in E. coli.*

A construct expressing GST-$M_{21}$ was produced by inserting a *Nde*I-*Hin*dIII fragment of pT7.7 $M_{21}$ encoding M1-K186 into the same sites of the pGEX

vector modified to include an *Nde*I site. A construct expressing GST-$M_{21}$-(M1-E110) plus an additional Ala residue at the C-terminus was constructed by deleting a *Xho*I-*Hin*dIII fragment of pGEX-$M_{21}$, filling in the overhanging ends and religating them. In order to express GST-$M_{21}$-(E110-K186), a *Nde*I-*Xho*I restriction fragment of pGEX-$M_{21}$ was deleted and the overhanging ends filled in and religated.

*Expression of proteins in E. coli.*

This was carried out essentially as described in [7], except that, after freezing the cells at -80°C and thawing, the lysates were not treated with DNAase but sonicated for 4 min on ice (ensuring that the temperature remained below 4°C) until the suspension was no longer viscous. The soluble GST-fusion proteins and MBP-fusion proteins were purified from the supernatant by affinity chromatography on glutathione-Sepharose (Sigma) and amylose resin (New England Biolabs), respectively, according to the instructions of the manufacturers. After expression in *E. coli* $M_{110}$-(R714-I1004) was the major soluble protein and all experiments with this fragment were performed using the bacterial extracts.

The chicken gizzard $M_{21}$ subunit was isolated from *E. coli* extracts as described [7]. $M_{21}$ subunit lacking the leucine zipper domain, $M_{21}$-(M1-L146), like the $M_{21}$ subunit itself, was obtained in inclusion bodies and therefore recovered in the pellet obtained after centrifugation of the bacterial lysates for 30 min at 28 000 x g. The inclusion bodies were washed three times in 50 mM Tris/HCl pH 7.5, 0.1M NaCl, 10 mM EDTA, 0.1% (by vol) 2-mercaptoethanol, 1 mM benzamidine, 0.2 mM phenylmethylsulphonyl fluoride and 0.5% (by mass) Triton X-100, then resuspended in 50 mM Tris/HCl pH 7.5, 1 mM EDTA, 1 mM EGTA, 0.03% (by mass) Brij-35, 0.1% (by vol) 2-mercaptoethanol. An aliquot (containing 3 mg protein) was made 0.5% (by vol) in trifluoroacetic

acid, sonicated, centrifuged for 2 min at 13,000 x g and the supernatant (containing the solubilised $M_{21}$ subunit) loaded on to a Vydac C18 column (Separations Group, Hesperia, CA, USA) equilibrated in 0.1% (by vol) trifluoroacetic acid. The column was developed with a linear acetonitrile gradient at a flow rate of 1.0 ml / min with an increase in acetonitrile concentration of 1% per min. Homogeneous $M_{21}$ subunit, which eluted at 42% acetonitrile, and $M_{21}$-(M1-L146) which eluted at 40% acetonitrile were dried in a vacuum concentrator redissolved in water, redried and then dissolved in 50 mM Tris/HCl pH 7.5, 0.1 mM EGTA, 0.03% (by mass) Brij-35, 0.1% (by vol) 2-mercaptoethanol.

*Removal of GST and MBP tags from fusion proteins.*

GST-$M_{110}$-(1-477) was cleaved with thrombin and the proteinase removed using benzamidine agarose [7]. GST-$M_{21}$-(E110-K186) (1mg / ml) was cleaved by incubation for 1 h at 30°C with 10 $\mu$g/ml thrombin, while GST-$M_{21}$-(M1-E110) (1mg / ml) was cleaved by incubation for 3 h at 30°C with 1 $\mu$g/ml thrombin, because it was more susceptible to degradation by thrombin. MBP-$M_{110}$(K933-I1004) (1 mg / ml) was cleaved by incubation for 8 h at 23°C with Factor Xa (10 $\mu$g/ml). Other conditions and removal of Factor Xa were carried out as described for thrombin [7].

*Preparation of phosphorylated myosin P-light chain and phosphatase assays.*

$^{32}$P-labelled myosin P-light chains containing 1.0 mol phosphate per mol subunit was prepared by phosphorylation with smooth muscle myosin light chain kinase [4]. The dephosphorylation of myosin P-light chain (1 $\mu$M) was carried out as in [4] and one unit of activity (U) was that amount which catalysed the release of 1 $\mu$mole of phosphate in one min. When assaying $PP1_M$ in immunoprecipitates from the myofibrillar extracts, the tubes were

shaken continuously and 3 nM okadaic acid was included to inhibit any PP2A present.

*Immunoprecipitation of $PP1_M$ from myofibrillar extracts.*

Antibodies raised against the $PP1_M$ holoenzyme (1 $\mu$g), which recognise both the $M_{110}$ and $M_{21}$ subunits, but not PP1c, affinity purified antibodies specific for either the $M_{110}$ subunit or $M_{21}$ subunit (5 $\mu$g) [7], and control IgG (5 $\mu$g) were conjugated separately to 10 $\mu$l of pelleted protein G-Sepharose. After incubation for 30 min at 4°C, the Protein G-Sepharose-antibody conjugate was washed three times with 50 mM Tris/HCl pH 7.5, 0.1 mM EGTA, 0.03% (by mass) Brij-35, 0.3M NaCl, 0.1% (by vol) 2-mercaptoethanol before addition of a 100 $\mu$l of myofibrillar extract (prepared as in [4]) which had been diluted 10-fold in 50 mM Tris/HCl pH 7.5, 0.1 mM EGTA, 0.1% (by vol) 2-mercaptoethanol, 0.2 mM phenylmethylsulphonyl fluoride, 1 mM benzamidine, 10 $\mu$g/ml leupeptin containing 1 mg/ml bovine serum albumin. After incubation for 1 h at 4°C, with shaking, a 10 $\mu$l aliquot of the suspension was removed to measure the total activity. The remaining 90 $\mu$l was centrifuged for 1 min at 13,000 x g, the supernatant was removed, and the pellet washed twice in dilution buffer containing 0.2 M NaCl and 0.03% (by mass) Brij-35 (but no bovine serum albumin), once in dilution buffer and then resuspended in 90 $\mu$l of dilution buffer. Myosin P-light chain phosphatase activity was then measured in the supernatant and the resuspended pellet at a further 30-fold final dilution.

*Myosin binding assays.* Myosin (0.5 mg / ml, 1 $\mu$M in terms of myosin heavy chains) in 10 mM Hepes pH 7.5, 50 mM KCl, 5 mM MgCl2, 0.1% (by vol) 2-mercaptoethanol, was mixed with $PP1_M$, $M_{21}$ subunit, or fragments of the $M_{110}$ and $M_{21}$ subunits, at the concentrations indicated in figure legends. After incubation for 15 min at 0°C, the solutions were centrifuged for 2 min at

13,000 x g, the supernatants removed, and the pellets washed twice in 10 mM Hepes pH 7.5, 50 mM KCl, 5 mM MgCl2, 0.1% (by vol) 2-mercaptoethanol before resuspension in 50 mM Tris-HCl pH 7.5, 0.1 mM EGTA, 0.03% (by mass) Brij 35, 0.6 M NaCl, 0.1% (by vol) 2-mercaptoethanol. Aliquots of the supernatant, the resuspended pellet and the suspension before centrifugation were either assayed for myosin P-light chain phosphatase activity or denatured in SDS and analysed by SDS/polyacrylamide gel electrophoresis.

*Preparation of a complex between GST-$M_{21}$ and $M_{110}$-(R714-I1004).*

GST-$M_{21}$ (10 $\mu$g) was mixed with 80 $\mu$l of bacterial extract expressing $M_{110}$-(R714-I1004). After incubation for 15 min at ambient temperature the solution was added to 20 $\mu$l (packed volume) of glutathione-Sepharose equilibrated in 50 mM Tris HCl pH 7.5, 0.1 mM EGTA, 0.03% (by mass) Brij 35, 0.1% (by vol) 2-mercaptoethanol, 0.2 mM phenylmethylsulphonyl fluoride, 1 mM benzamidine and 0.15 M NaCl. After incubation for 30 min at 4°C with shaking, the Sepharose was washed three times in the same buffer before eluting the complex with buffer containing 20 mM glutathione pH 8.0.

*Other procedures.*

Proteins were labelled with digoxigenin and Far Western analyses carried out as described [4], except that the digoxigenin-labelled probe was used at a concentration of 0.2 $\mu$g/ml instead of 2 $\mu$g/ml. SDS/polyacrylamide gel electrophoresis was carried out on 7.5-15% gels according to Laemmli [13] and on 16.5% gels according to Schagger and von Jagow [14]. Protein was estimated according to Bradford [15].

**Results**

*$PP1_M$ accounts for nearly all the myosin phosphatase activity in extracts prepared from chicken gizzard myofibrils.*

80-90% of the myosin phosphatase activity present in chicken gizzard homogenates is recovered in the myofibrils [4]. In the present study, we used antibodies that recognise the $M_{110}$ and/or the $M_{21}$ subunits of chicken gizzard $PP1_M$ [7] to immunoprecipitate the myosin P-light chain phosphatase activity from the myofibrillar extracts. About 90% of the activity was immunoprecipitated by antibodies raised against the $PP1_M$ holoenzyme (Fig 18A) which recognise both the $M_{110}$ and $M_{21}$ subunits in immunoblotting experiments, but not PP1c. Similarly, about 80% of the myosin P-light chain phosphatase activity in the myofibrillar extracts was immunoprecipitated by either the anti-$M_{110}$ antibody or by the anti-$M_{21}$ antibody (Fig 18A). Thus, most of the myosin P-light chain phosphatase activity in myofibrillar extracts is catalysed by PP1c present as a complex containing both the $M_{110}$ and the $M_{21}$ subunits.

Immunoblotting experiments demonstrated that the ratio $M_{110}$:$M_{21}$ in myofibrillar extracts was identical to the ratio of these subunits in purified $PP1_M$ (Fig 18B), which is 1:1 [4]. These immunoblotting experiments also demonstrated that $PP1_M$ comprises 0.1% of the protein in the myofibrillar extract (see legend to Fig 18B), identical to the proportion estimated from the fold-purification needed to obtain pure $PP1_M$ from this fraction (see Table 1 in Ref 4). These experiments imply that $PP1_M$ accounts for virtually all the myosin phosphatase activity associated with myofibrils, and that neither the $M_{110}$ nor the $M_{21}$ subunit is present in a significant molar excess over PP1c in the myofibrils.

*Identification of a region on the $M_{110}$ subunit that binds to the $M_{21}$ subunit.*

$PP1_M$ and several fragments of the $M_{110}$ subunit, were subjected to SDS/polyacrylamide gel electrophoresis (Fig 19A) and, after transfer to nitrocellulose, the blots were probed with digoxigenin-labelled $M_{21}$ subunit (Fig 19B). These experiments showed that the $M_{21}$ subunit recognised the full length $M_{110}$ subunit (Fig 19B, track 1), $M_{110}$-(R714-I1004) (Fig 19B, tracks 2 and 3) and $M_{110}$-(K933-I1004) (Fig 19B, track 5), but not $M_{110}$-(R714-L934) (Fig 19B, track 4), $M_{110}$-(M1-E309) (Fig 19B, track 7) or $M_{110}$-(M1-S477) (Fig 19B, track 8). Thus, the $M_{21}$ subunit binds to the C-terminal 72 residues of the $M_{110}$ subunit. The specificity of this interaction was indicated by the observation that digoxigenin-labelled $M_{21}$ subunit recognised only $M_{110}$-(R714-I1004) and no other protein in the *E. coli* extract (track 2 in Figs 19A and 19B), nor did it recognise the MBP or GST tags, PP1c (Figs 19A and 19B) or any of the molecular mass markers (data not shown).

Consistent with the results in Fig 19, digoxigenin-labelled MBP-$M_{110}$-(R714-I1004) (data not shown) and MBP-$M_{110}$-(K933-I1004) (Fig 20B), but not digoxigenin-labelled MBP-$M_{110}$-(R714-L934) (data not shown), recognised the full length $M_{21}$ subunit and $M_{21}$(M1-L146) in Far Western blotting experiments.

*The region of the $M_{21}$ subunit that interacts with the $M_{110}$ subunit.*

Digoxigenin-labelled $M_{21}$-(M1-L146) recognised the same fragments of the $M_{110}$ subunit as the full length $M_{21}$ protein (Fig 19C), demonstrating that the C-terminal leucine zipper of the $M_{21}$ subunit is not required for interaction with the $M_{110}$ subunit. However, neither digoxigenin-labelled GST-$M_{21}$-(M1-E110) nor digoxigenin-labelled GST-$M_{21}$-(E110-K186) recognised $M_{110}$-(K933-I1004) in Far Western blotting experiments (data not shown). Consistent with these findings, digoxigenin-labelled $M_{110}$-(K933-I1004) recognised the full length $M_{21}$

protein and $M_{21}$-(M1-L146), but not $M_{21}$-(M1-E110) or $M_{21}$-(E110-K186) in Far Western blotting experiments (Figs 20A and B). However, digoxigenin-labelled $M_{110}$-(K933-I1004) did recognise a proteolytic fragment of the $M_{21}$ subunit with an apparent molecular mass only slightly larger than $M_{21}$-(M1-E110) (Fig 20B, track 2 and compare tracks 2 and 4 in Fig 20A). These results are considered further under Discussion.

*The isolated $M_{21}$ subunit dimerizes and the region involved in dimerization is identical to that which interacts with the $M_{110}$ subunit.*

Although the $M_{110}$ subunit binds to both PP1c and the $M_{21}$ subunit [4], and removal of the $M_{21}$ subunit does not alter the specificity of the $PP1_M$ complex [7], an interaction between the $M_{21}$ subunit and PP1c had not been excluded. In order to examine this point, PP1c and the $M_{21}$ subunit were mixed together and subjected to gel filtration on Superose 12. The $M_{21}$ subunit eluted just before the 37 kDa PP1c protein, demonstrating that they do not form a high affinity complex and suggesting that the isolated $M_{21}$ subunit dimerizes (data not shown). These results were supported by the finding that digoxigenin-labelled full length $M_{21}$ subunit recognised the $M_{21}$ subunit as well as the $M_{110}$ subunit, but not PP1c, in Far Western blotting experiments (Fig 21, track 1). Similar results were obtained with $M_{21}$-(M1-L146) (Fig 21, track 2). Digoxigenin-labelled $M_{21}$ subunit, like digoxigenin-labelled $M_{110}$-(K933-I1004), recognised a fragment of the $M_{21}$ subunit that migrated slightly more slowly than $M_{21}$-(M1-E110), but did not recognise $M_{21}$-(M1-E110) or $M_{21}$-(E110-K186) (Tracks 2, 4 and 5 in Figs 20B and 20C).

*Identification of a region on the $M_{110}$ subunit that binds to myosin.*

When $PP1_M$ (30 nM) was mixed with chicken gizzard myosin (1 $\mu$M) and centrifuged to pellet the myosin, 85% of the myosin P-light chain phosphatase

was recovered in the pellet (Figs 22 and 23A). In contrast, neither PP1c (Fig 22) nor bovine serum albumin (data not shown) bound to myosin under these conditions. After removal of the $M_{21}$ subunit from $PP1_M$ [7], the $M_{110}$-PP1c complex ($PP1_M(\Delta M_{21})$ still pelleted with myosin in a similar manner to $PP1_M$ itself (Fig 22), indicating that the $M_{110}$ subunit is a myosin-binding protein.

In order to identify the myosin-binding domain(s), several fragments of the $M_{110}$ subunit were expressed and purified from *E. coli* extracts and their binding to myosin was studied. GST-$M_{110}$-(M1-S477), like GST-$M_{110}$-(M1-E309) [7], stimulated the PP1c-catalysed dephosphorylation of the myosin P-light chain and inhibited the dephosphorylation of glycogen phosphorylase in a similar manner to the full length $M_{110}$ subunit (data not shown). However, neither GST-$M_{110}$-(M1-S477) nor GST-$M_{110}$-(M1-E309) bound to myosin (data not shown), even after removal of the GST-tag from GST-$M_{110}$-(M1-S477) (Fig 23A).

A fragment comprising GST-$M_{110}$-(M377-K976) from rat aorta migrated as multiple bands on SDS/polyacrylamide gels after purification on glutathione-Sepharose (Fig 23A), indicating cleavage at multiple sites within the $M_{110}$ subunit. Only the largest fragment, with an apparent molecular mass corresponding to undegraded GST-$M_{110}$-(M377-K976) bound to myosin (Fig 23A), suggesting that the myosin binding site(s) was located towards the C-terminus of the $M_{110}$ subunit. Consistent with this finding, $M_{110}$-(R714-I1004) from chicken gizzard also bound to myosin (Fig 23B). However, $M_{110}$-(K933-I1004), which bound to the $M_{21}$ subunit (Fig 20B), did not bind to myosin in these experiments (Fig 23B).

*The $M_{21}$ subunit, and a complex between $M_{21}$ and $M_{110}$-(R714-I1004) bind to myosin.*

After purification on glutathione-Sepharose, GST-$M_{21}$ migrated as four protein staining bands (track 1 in Fig 20A), the two species of highest apparent molecular mass being recognised by the anti-$M_{21}$ antibody (Fig 23B). The apparent molecular mass of the slowest migrating band (47 kDa) corresponds to undegraded GST-$M_{21}$ and this species bound to myosin (Fig 23B). The next most slowly migrating band had an apparent molecular mass of 38 kDa, slightly less than that of GST-$M_{21}$-(M1-E110) (data not shown) indicating that it corresponds to GST fused to about the first 100 residues of the $M_{21}$ subunit; this fragment hardly bound to myosin (Fig 23B).

Bacterial extracts expressing $M_{110}$-(R714-I1004) were mixed with GST-$M_{21}$ and the resulting complex was purified on glutathione-Sepharose. This complex bound quantitatively to myosin (Fig 23B). In contrast, the GST-$M_{21}$ fragment of apparent molecular mass 38 kDa was not complexed to $M_{110}$-(R714-I1004) and did not bind to myosin (Fig 23B). The C-terminal fragment of the $M_{21}$ subunit, $M_{21}$-(E110-K186) also did not bind to myosin under these conditions (data not shown).

*Multiple binding sites for the $M_{21}$ subunit on the myosin molecule.*

The molar ratio myosin:$PP1_M$ in chicken gizzard is about 80:1 *in vivo* [4] and the myosin binding experiments described above were therefore carried out using a large (ten fold) molar excess of myosin over either the $M_{21}$ or the $M_{110}$ subunit. However, further experiments carried out with the $M_{21}$ subunit in excess revealed that, remarkably, 20 or more moles of $M_{21}$ subunit could be bound to each myosin dimer (Fig 24A). Many of the binding sites were located in the region of myosin involved in filament formation, because the $M_{21}$

subunit was pelleted with the myosin "rod" domain even when the molar ratio $M_{21}$: myosin dimer was 10:1 (Fig 24B). A shorter portion of the rod, termed light meromyosin, also bound the $M_{21}$ subunit avidly. However, a fragment of the $M_{21}$ subunit lacking the first 15 residues from the N-terminus, which was a contaminant in this preparation, did not bind to light meromyosin (Fig 24B), although it bound to the longer myosin rod (Fig 24B). The $M_{21}$ subunit lacking the C-terminal leucine zipper, $M_{21}$-(M1-L146), bound to both myosin and the rod domain, but fewer moles of $M_{21}$-(M1-L146) could be bound and this C-terminally truncated species did not bind to light meromyosin under the conditions studied (Fig 24C).

*Multiple forms of the $M_{110}$ subunit*

Comparison of two different clones encoding the $M_{110}$ subunit from chicken gizzard revealed a 123 bp (41 amino acid) deletion/insertion after Asn-511 (Fig 17, [8]). Since the rat aorta sequence [5] showed considerable variation from the chicken sequences in this region, compared to the high degree of sequence similarity throughout most of the rest of the molecule (Fig 17), it seemed probable that forms of the rat $M_{110}$ subunit also existed that varied in this middle section of the protein. PCR of the "variable region" of several rat aorta clones gave fragments of either 608 bp or 776 bp. Direct sequencing of these fragments showed an in frame insertion of 168bp (56 amino acids) after Ser-552 (Fig. 1); i.e. a slightly different position from the deletion reported for the chicken gizzard $M_{110}$ subunit (Fig 17). Furthermore, a different 62 amino acid deletion/insertion in this section is apparent by comparison of the rat aorta sequences with that of the $M_{110}$ protein from rat kidney (Fig. 1) [9]. While it is likely that most of these variations arise by alternative splicing of the mRNA, Southern blotting of rat genomic DNA revealed the presence of two closely related genes (data not shown).

*Discussion*

The contraction of smooth muscle is triggered by phosphorylation of the P-light chain of myosin catalysed by myosin light chain kinase. However, the identity of the myosin P-light chain phosphatase remained unclear for many years. In 1992 we reported that 80-90% of the myosin phosphatase activity in chicken gizzard homogenates was associated with myofibrils and purified a myosin phosphatase to homogeneity from this fraction [4]. This enzyme, termed $PP1_M$, was found to be composed of the $\beta$-isoform of PP1c (termed the $\delta$-isoform in [16]) and an "M-complex" consisting of two other subunits [4] whose molecular masses were 21 kDa ($M_{21}$) [5] and 110 kDa ($M_{110}$) [5, 8], respectively. Further evidence that a form of PP1 was the major myosin phosphatase in smooth muscle was indicated by the finding that tautomycin (a much more potent inhibitor of PP1 than PP2A [17]) stimulated the contraction of permeabilised mammalian smooth muscle fibres at much lower concentrations than okadaic acid [18] (a much more potent inhibitor of PP2A than PP1 [19]).

Two further pieces of evidence presented in this Example establish that $PP1_M$ accounts for most, if not all, of the myosin phosphatase activity associated with chicken gizzard myofibrils, reinforcing the view that it is likely to be the major myosin P-light chain phosphatase *in vivo*. Firstly, nearly all the myosin P-light chain phosphatase activity was immunoprecipitated by antibodies that recognise either the $M_{110}$ or the $M_{21}$ subunit specifically (Fig 18A). Secondly, $PP1_M$ was found to represent 0.1% of the protein in the myofibrillar extracts whether its concentration was calculated from the increase in specific activity needed for purification to homogeneity [4] or from immunoblotting experiments with the anti-$M_{110}$ and anti-$M_{21}$ antibodies (Fig 18B). Had another enzyme been the major myosin phosphatase in the myofibrillar extracts the enrichment estimated by immunoblotting with anti-$M_{110}$ and anti-$M_{21}$ antibodies would have been

much higher.

The experiments presented in Fig 18 also demonstrate that the $M_{110}$ and $M_{21}$ subunits are not present in myofibrillar extracts in a significant molar excess over PP1c and that all the $M_{110}$ subunits are complexed to $M_{21}$ subunit and vice versa. The $M_{21}$ subunit was found to bind to the C-terminal 72 residues of the chicken gizzard $M_{110}$ subunit (Figs 19 and 25), a region whose amino acid sequence is 43% identical to residues 87-161 of the $M_{21}$ subunit (Fig 17B). The C-terminal leucine zipper of the $M_{21}$ subunit (residues 145-186) is not required for interaction with the $M_{110}$ subunit, and the site on the $M_{21}$ subunit which interacts with the $M_{110}$ subunit lies within about the N-terminal 120 residues (Fig 20B). Interestingly, the same region is essential for the dimerisation of the $M_{21}$ subunit (compare Figs 20B and 20C), suggesting that the region(s) involved in interaction is probably located between residues 60 and 120 of the $M_{21}$ subunit and 906-965 of the $M_{110}$ subunit from chicken gizzard; i.e. the regions with greatest amino acid identity between these two proteins (Fig 17). More digoxigenin-labelled $M_{21}$ subunit bound to the $M_{110}$ subunit than to the $M_{21}$ subunit in Far Western blotting experiments (Fig 21), consistent with the observation that $M_{110}/M_{21}$ heterodimers form *in vivo*, but not $M_{21}/M_{21}$ homodimers. The finding that the C-terminus of the $M_{110}$ subunit interacts with the $M_{21}$ subunit explains why preparations of $PP1_M$ comprising PP1c complexed to N-terminal fragments of the $M_{110}$ subunit do not contain the $M_{21}$ subunit [8, 20].

$PP1_M$ binds to the dephosphorylated form of myosin and our data demonstrate that the $M_{110}$ subunit (Fig 22) and the $M_{21}$ subunit (Fig 23B and Fig 24) are both myosin-binding proteins. The C-terminal 600 residues of the $M_{110}$ subunit from rat aorta, $M_{110}$-(M377-K976) (Fig 23A) and the C-terminal 291 residues of the $M_{110}$ subunit from chicken gizzard, $M_{110}$-(R714-I1004), bound to myosin, but the C-terminal 72 residues of the $M_{110}$ subunit, $M_{110}$-(K933-1004), did not

(Fig 23B), indicating that a myosin-binding domain is likely to be situated in the $M_{110}$ subunit just N-terminal to the $M_{21}$-binding domain (Fig 25). In contrast, two N-terminal fragments of the $M_{110}$ subunit $M_{110}$-(M1-S477) (Fig 23A) and $M_{110}$-(M1-E309) (data not shown) did not bind to myosin under the conditions studied. Since $M_{110}$-(M1-E309) [7] and $M_{110}$-(M1-S477) (data not shown) stimulate the dephosphorylation of myosin and inhibit the dephosphorylation of glycogen phosphorylase by PP1c, and in a similar manner to full length $M_{110}$ subunit, these results show that the region of the $M_{110}$ subunit which stimulates the dephosphorylation of the myosin P-light chain is distinct from that which binds the dephosphorylated form of myosin and thereby targets $PP1_M$ to the contractile apparatus.

Digestion of chicken gizzard $PP1_M$ with chymotrypsin cleaves the $M_{110}$ subunit to a fragment with an apparent molecular mass of 58 kDa and a form of PP1, termed here $PP1_M$*, can then be isolated by gel-filtration which appears to comprise just the 58 kDa fragment and PP1c in a 1:1 molar ratio [8]. The 58 kDa fragment, like the $M_{110}$ subunit, has a blocked N-terminus and seven tryptic peptides isolated were located between residues 286 and 467, suggesting that the 58 kDa fragment corresponds to the N-terminal portion of the $M_{110}$ subunit [8]. $PP1_M$* was reported to bind to myosin, albeit less effectively than $PP1_M$ [8], suggesting the presence of a myosin-binding domain within the 58 kDa fragment. This result is in apparent conflict with the present study, because the fragment $M_{110}$-(M1-S477), which also migrates on SDS/polyacrylamide gels with an apparent molecular mass of 58 kDa, did not bind to dephosphorylated myosin under conditions where 80-90% of the $PP1_M$ and $M_{110}$-(R714-I1004) was pelleted with myosin (Fig 23A). One possible explanation for this discrepancy is that $PP1_M$* also contains small myosin-binding fragments from the C-terminus of the $M_{110}$ subunit which still interact with the N-terminal 58 kDa fragment, but are too small to be detected by SDS/polyacrylamide gel electrophoresis. In a separate study heavy meromyosin

(50 $\mu$g) was found to bind partially to 2 mg of $M_{110}$-(1-633) coupled to Affigel 15, at very low ionic strength but not at 150-200 mM NaCl [21]. The significance of this observation is unclear because of the extremely high concentration of the $M_{110}$-(1-633) used in these experiments. The average intracellular concentration of $PP1_M$ in chicken gizzard is about 1 $\mu$M, 100-fold lower than the concentration of myosin. In the present study, we analysed the binding of the $M_{110}$ subunit and its subfragments (30-100 nM) to myosin (1 $\mu$M) using low concentrations of these proteins to try and ensure that only high affinity binding sites were identified.

The isolated $M_{21}$ subunit also bound to myosin and up to 20 moles of $M_{21}$ subunit could be bound to each myosin dimer (Fig 24). These observations indicate that each myosin molecule contains multiple binding sites for the $M_{21}$ subunit, many of which are located within the "rod domain" (Figs 24B and 24C). *In vivo*, the molar ratio $PP1_M$: myosin is about 1:80 and yet, during muscle relaxation, all the myosin P-light chains can be dephosphorylated by $PP1_M$ within seconds. This implies that $PP1_M$ must be highly mobile within the myofibrils and move extremely rapidly from one myosin molecule to another. The "off rates" for binding of $PP1_M$ to myosin must therefore be very fast as well as the "on rates". It is tempting to speculate that the presence of multiple binding sites on myosin for the $M_{21}$ subunit (and perhaps for the $M_{110}$ subunit as well) allows $PP1_M$ to "slide" rapidly from one myosin molecule to another.

## Example 4: Design of small molecules to modulate the properties of PP1

Table A is a print-out of the atomic coordinates of the protein phosphatase-1 peptide coordinates as deduced in Example 2. The format is Protein Data Bank. The structure of the protein phosphatase-1 catalytic subunit (PP1c) in complex with a 13-residue peptide ($G_M$ peptide) corresponding to a site of interaction between PP1c and the glycogen targeting subunit provides a frame-

work for the rational design of small molecules to modulate the functions and properties of PP1 *in vivo*. Knowledge of the structural nature of the interactions between the $G_M$ peptide and PP1c allows the design of inhibitors that mimic these interactions. These inhibitors may be designed for increased potency, cell permeability and with improved pharmokinetic properties.

Computer graphics systems may be used to design such inhibitors in conjunction with computer graphics modelling software such as SYBIL available from: Tripos Inc, 16995 S Hanley Road, St Louis, Missouri 63144-2913, USA and LUDI available from: Molecular Simulations Inc, 9685 Scranton Road, San Diego, CA 92121-3752, USA, and in conjunction with the atomic coordinates shown in Table A.

**Example 5: Effect of peptide derived from p53BP2 binding site to PP1 *in vivo***

The function of p53BP2 is ascertained by examining the *in vivo* effect of peptides based on the sequence of the p53BP2 binding site to PP1. This may be done by reference to the consensus peptide sequence described in the previous Examples and by reference to the crystal structure in Example 2. The peptide is introduced into cultured cells using penetratin available from Appligene. Other importins may also be used. Alternatively cDNA specifying p53BP2 proteins mutant in the p53BP2 binding site to PP1 are transfected in cultured cells. The effect of these agents on the cell cycle and apoptosis are assessed by a number of methods, for example WAF1 ELISA and Nuclear Matrix Protein ELISA assays (Amersham).

The effect of the p53BP2 peptide is to modulate the interaction between PP1 and p53BP2 *in vivo* and affect cell regulation and apoptosis. The p53BP2 peptide may also be micro-injected into the cell.

## Table A

| | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|
| ATOM | 1 | N | LYS | 6 | -10.263 | 46.372 | 91.126 | 1.00 | 53.07 | 0 |
| ATOM | 3 | CA | LYS | 6 | -9.182 | 46.177 | 90.159 | 1.00 | 53.07 | 0 |
| ATOM | 4 | CB | LYS | 6 | -9.220 | 47.277 | 89.092 | 1.00 | 45.20 | 0 |
| ATOM | 5 | CG | LYS | 6 | -10.284 | 47.095 | 88.015 | 1.00 | 45.20 | 0 |
| ATOM | 6 | CD | LYS | 6 | -9.809 | 46.200 | 86.868 | 1.00 | 45.20 | 0 |
| ATOM | 7 | CE | LYS | 6 | -8.832 | 46.919 | 85.927 | 1.00 | 45.20 | 0 |
| ATOM | 8 | NZ | LYS | 6 | -7.498 | 47.216 | 86.540 | 1.00 | 45.20 | 0 |
| ATOM | 12 | C | LYS | 6 | -7.814 | 46.179 | 90.835 | 1.00 | 53.07 | 0 |
| ATOM | 13 | O | LYS | 6 | -6.854 | 45.624 | 90.303 | 1.00 | 45.20 | 0 |
| ATOM | 14 | N | LEU | 7 | -7.746 | 46.816 | 92.005 | 1.00 | 42.33 | 0 |
| ATOM | 16 | CA | LEU | 7 | -6.527 | 46.941 | 92.800 | 1.00 | 43.14 | 0 |
| ATOM | 17 | CB | LEU | 7 | -6.840 | 47.599 | 94.141 | 1.00 | 24.45 | 0 |
| ATOM | 18 | CG | LEU | 7 | -5.670 | 47.782 | 95.106 | 1.00 | 18.34 | 0 |
| ATOM | 19 | CD1 | LEU | 7 | -4.775 | 48.881 | 94.589 | 1.00 | 25.09 | 0 |
| ATOM | 20 | CD2 | LEU | 7 | -6.186 | 48.121 | 96.496 | 1.00 | 22.21 | 0 |
| ATOM | 21 | C | LEU | 7 | -5.892 | 45.594 | 93.063 | 1.00 | 42.81 | 0 |
| ATOM | 22 | O | LEU | 7 | -6.497 | 44.723 | 93.675 | 1.00 | 23.55 | 0 |
| ATOM | 23 | N | ASN | 8 | -4.656 | 45.424 | 92.627 | 1.00 | 17.03 | 0 |
| ATOM | 25 | CA | ASN | 8 | -4.000 | 44.156 | 92.846 | 1.00 | 11.65 | 0 |
| ATOM | 26 | CB | ASN | 8 | -3.204 | 43.744 | 91.610 | 1.00 | 18.54 | 0 |
| ATOM | 27 | CG | ASN | 8 | -3.486 | 42.312 | 91.193 | 1.00 | 15.30 | 0 |
| ATOM | 28 | OD1 | ASN | 8 | -4.643 | 41.903 | 91.068 | 1.00 | 14.53 | 0 |
| ATOM | 29 | ND2 | ASN | 8 | -2.429 | 41.538 | 90.993 | 1.00 | 7.61 | 0 |
| ATOM | 32 | C | ASN | 8 | -3.110 | 44.207 | 94.079 | 1.00 | 11.35 | 0 |
| ATOM | 33 | O | ASN | 8 | -1.906 | 44.515 | 93.985 | 1.00 | 12.23 | 0 |
| ATOM | 34 | N | ILE | 9 | -3.716 | 43.900 | 95.232 | 1.00 | 12.56 | 0 |
| ATOM | 36 | CA | ILE | 9 | -3.018 | 43.894 | 96.523 | 1.00 | 14.41 | 0 |
| ATOM | 37 | CB | ILE | 9 | -3.955 | 43.439 | 97.690 | 1.00 | 2.00 | 0 |
| ATOM | 38 | CG2 | ILE | 9 | -3.155 | 42.828 | 98.812 | 1.00 | 2.00 | 0 |
| ATOM | 39 | CG1 | ILE | 9 | -4.742 | 44.634 | 98.244 | 1.00 | 2.00 | 0 |
| ATOM | 40 | CD1 | ILE | 9 | -3.865 | 45.837 | 98.581 | 1.00 | 2.00 | 0 |
| ATOM | 41 | C | ILE | 9 | -1.796 | 42.996 | 96.501 | 1.00 | 10.07 | 0 |
| ATOM | 42 | O | ILE | 9 | -0.759 | 43.351 | 97.045 | 1.00 | 2.00 | 0 |
| ATOM | 43 | N | ASP | 10 | -1.916 | 41.845 | 95.849 | 1.00 | 2.00 | 0 |
| ATOM | 45 | CA | ASP | 10 | -0.822 | 40.887 | 95.782 | 1.00 | 2.00 | 0 |
| ATOM | 46 | CB | ASP | 10 | -1.336 | 39.562 | 95.208 | 1.00 | 45.77 | 0 |
| ATOM | 47 | CG | ASP | 10 | -2.234 | 38.801 | 96.191 | 1.00 | 46.34 | 0 |
| ATOM | 48 | OD1 | ASP | 10 | -3.054 | 39.444 | 96.879 | 1.00 | 50.94 | 0 |
| ATOM | 49 | OD2 | ASP | 10 | -2.123 | 37.558 | 96.281 | 1.00 | 55.84 | 0 |
| ATOM | 50 | C | ASP | 10 | 0.426 | 41.369 | 95.036 | 1.00 | 2.00 | 0 |
| ATOM | 51 | O | ASP | 10 | 1.540 | 41.181 | 95.516 | 1.00 | 43.44 | 0 |
| ATOM | 52 | N | SER | 11 | 0.245 | 41.993 | 93.874 | 1.00 | 2.00 | 0 |
| ATOM | 54 | CA | SER | 11 | 1.387 | 42.494 | 93.112 | 1.00 | 2.00 | 0 |
| ATOM | 55 | CB | SER | 11 | 0.987 | 42.834 | 91.678 | 1.00 | 24.54 | 0 |
| ATOM | 56 | OG | SER | 11 | -0.025 | 43.819 | 91.653 | 1.00 | 26.40 | 0 |
| ATOM | 58 | C | SER | 11 | 1.964 | 43.727 | 93.804 | 1.00 | 2.00 | 0 |
| ATOM | 59 | O | SER | 11 | 3.168 | 44.010 | 93.702 | 1.00 | 23.86 | 0 |
| ATOM | 60 | N | ILE | 12 | 1.099 | 44.467 | 94.493 | 1.00 | 19.26 | 0 |
| ATOM | 62 | CA | ILE | 12 | 1.536 | 45.641 | 95.226 | 1.00 | 19.26 | 0 |
| ATOM | 63 | CB | ILE | 12 | 0.345 | 46.351 | 95.878 | 1.00 | 2.00 | 0 |
| ATOM | 64 | CG2 | ILE | 12 | 0.831 | 47.364 | 96.909 | 1.00 | 2.00 | 0 |
| ATOM | 65 | CG1 | ILE | 12 | -0.499 | 46.986 | 94.775 | 1.00 | 2.00 | 0 |
| ATOM | 66 | CD1 | ILE | 12 | -1.722 | 47.687 | 95.245 | 1.00 | 2.00 | 0 |
| ATOM | 67 | C | ILE | 12 | 2.501 | 45.112 | 96.275 | 1.00 | 19.26 | 0 |
| ATOM | 68 | O | ILE | 12 | 3.684 | 45.445 | 96.264 | 1.00 | 2.00 | 0 |
| ATOM | 69 | N | ILE | 13 | 1.987 | 44.246 | 97.141 | 1.00 | 2.00 | 0 |
| ATOM | 71 | CA | ILE | 13 | 2.764 | 43.605 | 98.199 | 1.00 | 2.00 | 0 |
| ATOM | 72 | CB | ILE | 13 | 1.899 | 42.504 | 98.897 | 1.00 | 2.00 | 0 |
| ATOM | 73 | CG2 | ILE | 13 | 2.747 | 41.645 | 99.810 | 1.00 | 2.00 | 0 |
| ATOM | 74 | CG1 | ILE | 13 | 0.764 | 43.154 | 99.691 | 1.00 | 2.00 | 0 |
| ATOM | 75 | CD1 | ILE | 13 | -0.213 | 42.167 | 100.331 | 1.00 | 2.00 | 0 |
| ATOM | 76 | C | ILE | 13 | 4.039 | 42.960 | 97.602 | 1.00 | 2.00 | 0 |
| ATOM | 77 | O | ILE | 13 | 5.142 | 43.099 | 98.158 | 1.00 | 2.00 | 0 |
| ATOM | 78 | N | GLN | 14 | 3.864 | 42.278 | 96.462 | 1.00 | 2.00 | 0 |
| ATOM | 80 | CA | GLN | 14 | 4.937 | 41.582 | 95.740 | 1.00 | 2.00 | 0 |
| ATOM | 81 | CB | GLN | 14 | 4.415 | 41.065 | 94.391 | 1.00 | 21.13 | 0 |
| ATOM | 82 | CG | GLN | 14 | 5.467 | 40.470 | 93.454 | 1.00 | 32.43 | 0 |
| ATOM | 83 | CD | GLN | 14 | 5.655 | 41.284 | 92.171 | 1.00 | 28.89 | 0 |

| | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|
| ATOM | 84 | OE1 | GLN | 14 | 4.726 | 41.428 | 91.363 | 1.00 | 30.84 | 0 |
| ATOM | 85 | NE2 | GLN | 14 | 6.861 | 41.818 | 91.977 | 1.00 | 29.15 | 0 |
| ATOM | 88 | C | GLN | 14 | 6.088 | 42.519 | 95.515 | 1.00 | 2.00 | 0 |
| ATOM | 89 | O | GLN | 14 | 7.206 | 42.249 | 95.934 | 1.00 | 24.80 | 0 |
| ATOM | 90 | N | ARG | 15 | 5.789 | 43.625 | 94.848 | 1.00 | 15.16 | 0 |
| ATOM | 92 | CA | ARG | 15 | 6.776 | 44.638 | 94.552 | 1.00 | 15.16 | 0 |
| ATOM | 93 | CB | ARG | 15 | 6.122 | 45.812 | 93.846 | 1.00 | 8.83 | 0 |
| ATOM | 94 | CG | ARG | 15 | 6.530 | 45.981 | 92.388 | 1.00 | 8.83 | 0 |
| ATOM | 95 | CD | ARG | 15 | 5.543 | 46.882 | 91.684 | 1.00 | 8.83 | 0 |
| ATOM | 96 | NE | ARG | 15 | 4.195 | 46.322 | 91.761 | 1.00 | 8.83 | 0 |
| ATOM | 98 | CZ | ARG | 15 | 3.094 | 46.998 | 91.465 | 1.00 | 8.83 | 0 |
| ATOM | 99 | NH1 | ARG | 15 | 3.178 | 48.261 | 91.073 | 1.00 | 9.33 | 0 |
| ATOM | 102 | NH2 | ARG | 15 | 1.907 | 46.413 | 91.567 | 1.00 | 8.83 | 0 |
| ATOM | 105 | C | ARG | 15 | 7.405 | 45.106 | 95.841 | 1.00 | 15.16 | 0 |
| ATOM | 106 | O | ARG | 15 | 8.622 | 45.124 | 95.952 | 1.00 | 13.09 | 0 |
| ATOM | 107 | N | LEU | 16 | 6.575 | 45.462 | 96.820 | 1.00 | 2.00 | 0 |
| ATOM | 109 | CA | LEU | 16 | 7.049 | 45.924 | 98.124 | 1.00 | 2.00 | 0 |
| ATOM | 110 | CB | LEU | 16 | 5.853 | 46.215 | 99.033 | 1.00 | 2.00 | 0 |
| ATOM | 111 | CG | LEU | 16 | 4.982 | 47.420 | 98.662 | 1.00 | 2.00 | 0 |
| ATOM | 112 | CD1 | LEU | 16 | 3.630 | 47.302 | 99.324 | 1.00 | 2.00 | 0 |
| ATOM | 113 | CD2 | LEU | 16 | 5.664 | 48.707 | 99.056 | 1.00 | 2.00 | 0 |
| ATOM | 114 | C | LEU | 16 | 8.014 | 44.942 | 98.809 | 1.00 | 2.00 | 0 |
| ATOM | 115 | O | LEU | 16 | 9.031 | 45.354 | 99.361 | 1.00 | 2.00 | 0 |
| ATOM | 116 | N | LEU | 17 | 7.712 | 43.650 | 98.770 | 1.00 | 12.70 | 0 |
| ATOM | 118 | CA | LEU | 17 | 8.590 | 42.652 | 99.395 | 1.00 | 4.33 | 0 |
| ATOM | 119 | CB | LEU | 17 | 7.812 | 41.387 | 99.780 | 1.00 | 4.50 | 0 |
| ATOM | 120 | CG | LEU | 17 | 6.740 | 41.515 | 100.838 | 1.00 | 4.52 | 0 |
| ATOM | 121 | CD1 | LEU | 17 | 6.338 | 40.159 | 101.302 | 1.00 | 11.14 | 0 |
| ATOM | 122 | CD2 | LEU | 17 | 7.285 | 42.318 | 101.997 | 1.00 | 6.93 | 0 |
| ATOM | 123 | C | LEU | 17 | 9.796 | 42.225 | 98.548 | 1.00 | 7.39 | 0 |
| ATOM | 124 | O | LEU | 17 | 10.751 | 41.652 | 99.086 | 1.00 | 15.30 | 0 |
| ATOM | 125 | N | GLU | 18 | 9.758 | 42.492 | 97.238 | 1.00 | 65.13 | 0 |
| ATOM | 127 | CA | GLU | 18 | 10.847 | 42.104 | 96.329 | 1.00 | 70.48 | 0 |
| ATOM | 128 | CB | GLU | 18 | 10.505 | 42.471 | 94.883 | 1.00 | 89.02 | 0 |
| ATOM | 129 | CG | GLU | 18 | 10.769 | 43.929 | 94.547 | 1.00 | 97.06 | 0 |
| ATOM | 130 | CD | GLU | 18 | 10.677 | 44.239 | 93.069 | 1.00 | 39.46 | 0 |
| ATOM | 131 | OE1 | GLU | 18 | 11.030 | 43.351 | 92.256 | 1.00 | 39.46 | 0 |
| ATOM | 132 | OE2 | GLU | 18 | 10.265 | 45.375 | 92.727 | 1.00 | 39.46 | 0 |
| ATOM | 133 | C | GLU | 18 | 12.199 | 42.724 | 96.687 | 1.00 | 70.82 | 0 |
| ATOM | 134 | O | GLU | 18 | 13.244 | 42.249 | 96.240 | 1.00 | 88.34 | 0 |
| ATOM | 135 | N | VAL | 19 | 12.172 | 43.793 | 97.480 | 1.00 | 28.97 | 0 |
| ATOM | 137 | CA | VAL | 19 | 13.394 | 44.470 | 97.891 | 1.00 | 28.97 | 0 |
| ATOM | 138 | CB | VAL | 19 | 13.139 | 45.968 | 98.207 | 1.00 | 6.66 | 0 |
| ATOM | 139 | CG1 | VAL | 19 | 12.746 | 46.702 | 96.942 | 1.00 | 6.86 | 0 |
| ATOM | 140 | CG2 | VAL | 19 | 12.044 | 46.117 | 99.231 | 1.00 | 4.03 | 0 |
| ATOM | 141 | C | VAL | 19 | 14.079 | 43.805 | 99.081 | 1.00 | 28.97 | 0 |
| ATOM | 142 | O | VAL | 19 | 15.134 | 44.258 | 99.514 | 1.00 | 13.23 | 0 |
| ATOM | 143 | N | ARG | 20 | 13.490 | 42.736 | 99.615 | 1.00 | 2.00 | 0 |
| ATOM | 145 | CA | ARG | 20 | 14.093 | 42.016 | 100.748 | 1.00 | 2.00 | 0 |
| ATOM | 146 | CB | ARG | 20 | 13.242 | 40.812 | 101.142 | 1.00 | 17.66 | 0 |
| ATOM | 147 | CG | ARG | 20 | 12.043 | 41.138 | 101.990 | 1.00 | 16.46 | 0 |
| ATOM | 148 | CD | ARG | 20 | 11.192 | 39.899 | 102.195 | 1.00 | 21.30 | 0 |
| ATOM | 149 | NE | ARG | 20 | 12.006 | 38.733 | 102.532 | 1.00 | 18.45 | 0 |
| ATOM | 151 | CZ | ARG | 20 | 11.559 | 37.481 | 102.546 | 1.00 | 23.19 | 0 |
| ATOM | 152 | NH1 | ARG | 20 | 10.288 | 37.232 | 102.249 | 1.00 | 28.11 | 0 |
| ATOM | 155 | NH2 | ARG | 20 | 12.383 | 36.477 | 102.836 | 1.00 | 21.96 | 0 |
| ATOM | 158 | C | ARG | 20 | 15.480 | 41.521 | 100.333 | 1.00 | 2.00 | 0 |
| ATOM | 159 | O | ARG | 20 | 15.609 | 40.778 | 99.353 | 1.00 | 20.52 | 0 |
| ATOM | 160 | N | GLY | 21 | 16.514 | 41.956 | 101.047 | 1.00 | 61.97 | 0 |
| ATOM | 162 | CA | GLY | 21 | 17.863 | 41.527 | 100.718 | 1.00 | 65.49 | 0 |
| ATOM | 163 | C | GLY | 21 | 18.702 | 42.522 | 99.930 | 1.00 | 66.05 | 0 |
| ATOM | 164 | O | GLY | 21 | 19.933 | 42.409 | 99.889 | 1.00 | 13.74 | 0 |
| ATOM | 165 | N | SER | 22 | 18.055 | 43.490 | 99.290 | 1.00 | 19.66 | 0 |
| ATOM | 167 | CA | SER | 22 | 18.790 | 44.491 | 98.523 | 1.00 | 17.08 | 0 |
| ATOM | 168 | CB | SER | 22 | 17.874 | 45.159 | 97.481 | 1.00 | 26.61 | 0 |
| ATOM | 169 | OG | SER | 22 | 16.821 | 45.908 | 98.074 | 1.00 | 32.17 | 0 |
| ATOM | 171 | C | SER | 22 | 19.371 | 45.538 | 99.466 | 1.00 | 17.54 | 0 |
| ATOM | 172 | O | SER | 22 | 19.047 | 45.558 | 100.657 | 1.00 | 21.05 | 0 |

| | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|
| ATOM | 173 | N | LYS | 23 | 20.222 | 46.409 | 98.935 | 1.00 | 53.24 | 0 |
| ATOM | 175 | CA | LYS | 23 | 20.828 | 47.458 | 99.740 | 1.00 | 49.50 | 0 |
| ATOM | 176 | CB | LYS | 23 | 21.565 | 48.471 | 98.852 | 1.00 | 94.25 | 0 |
| ATOM | 177 | CG | LYS | 23 | 20.639 | 49.422 | 98.085 | 1.00 | 59.71 | 0 |
| ATOM | 178 | CD | LYS | 23 | 21.341 | 50.716 | 97.688 | 1.00 | 94.25 | 0 |
| ATOM | 179 | CE | LYS | 23 | 20.346 | 51.775 | 97.214 | 1.00 | 59.77 | 0 |
| ATOM | 180 | NZ | LYS | 23 | 19.448 | 52.240 | 98.306 | 1.00 | 59.94 | 0 |
| ATOM | 184 | C | LYS | 23 | 19.739 | 48.190 | 100.528 | 1.00 | 49.47 | 0 |
| ATOM | 185 | O | LYS | 23 | 18.659 | 48.488 | 99.998 | 1.00 | 59.94 | 0 |
| ATOM | 186 | N | PRO | 24 | 19.990 | 48.458 | 101.813 | 1.00 | 37.72 | 0 |
| ATOM | 187 | CD | PRO | 24 | 21.185 | 48.148 | 102.614 | 1.00 | 2.00 | 0 |
| ATOM | 188 | CA | PRO | 24 | 18.987 | 49.165 | 102.613 | 1.00 | 36.73 | 0 |
| ATOM | 189 | CB | PRO | 24 | 19.618 | 49.217 | 104.004 | 1.00 | 2.00 | 0 |
| ATOM | 190 | CG | PRO | 24 | 21.109 | 49.208 | 103.704 | 1.00 | 2.00 | 0 |
| ATOM | 191 | C | PRO | 24 | 18.798 | 50.551 | 102.019 | 1.00 | 33.26 | 0 |
| ATOM | 192 | O | PRO | 24 | 19.752 | 51.325 | 101.938 | 1.00 | 2.00 | 0 |
| ATOM | 193 | N | GLY | 25 | 17.579 | 50.835 | 101.575 | 1.00 | 22.79 | 0 |
| ATOM | 195 | CA | GLY | 25 | 17.275 | 52.119 | 100.981 | 1.00 | 22.84 | 0 |
| ATOM | 196 | C | GLY | 25 | 16.653 | 51.904 | 99.624 | 1.00 | 18.00 | 0 |
| ATOM | 197 | O | GLY | 25 | 16.098 | 52.827 | 99.037 | 1.00 | 28.24 | 0 |
| ATOM | 198 | N | LYS | 26 | 16.750 | 50.679 | 99.116 | 1.00 | 2.00 | 0 |
| ATOM | 200 | CA | LYS | 26 | 16.174 | 50.351 | 97.817 | 1.00 | 2.00 | 0 |
| ATOM | 201 | CB | LYS | 26 | 16.469 | 48.892 | 97.458 | 1.00 | 45.45 | 0 |
| ATOM | 202 | CG | LYS | 26 | 15.931 | 48.437 | 96.110 | 1.00 | 55.13 | 0 |
| ATOM | 203 | CD | LYS | 26 | 16.209 | 49.435 | 94.979 | 1.00 | 59.31 | 0 |
| ATOM | 204 | CE | LYS | 26 | 17.694 | 49.644 | 94.691 | 1.00 | 60.93 | 0 |
| ATOM | 205 | NZ | LYS | 26 | 17.883 | 50.619 | 93.569 | 1.00 | 68.30 | 0 |
| ATOM | 209 | C | LYS | 26 | 14.674 | 50.624 | 97.856 | 1.00 | 2.00 | 0 |
| ATOM | 210 | O | LYS | 26 | 13.916 | 49.964 | 98.566 | 1.00 | 42.74 | 0 |
| ATOM | 211 | N | ASN | 27 | 14.278 | 51.648 | 97.111 | 1.00 | 2.00 | 0 |
| ATOM | 213 | CA | ASN | 27 | 12.894 | 52.086 | 97.027 | 1.00 | 2.00 | 0 |
| ATOM | 214 | CB | ASN | 27 | 12.836 | 53.526 | 96.517 | 1.00 | 50.37 | 0 |
| ATOM | 215 | CG | ASN | 27 | 13.257 | 54.525 | 97.563 | 1.00 | 56.29 | 0 |
| ATOM | 216 | OD1 | ASN | 27 | 12.929 | 54.381 | 98.740 | 1.00 | 61.45 | 0 |
| ATOM | 217 | ND2 | ASN | 27 | 13.982 | 55.551 | 97.142 | 1.00 | 59.50 | 0 |
| ATOM | 220 | C | ASN | 27 | 11.964 | 51.219 | 96.183 | 1.00 | 2.00 | 0 |
| ATOM | 221 | O | ASN | 27 | 12.384 | 50.256 | 95.540 | 1.00 | 54.11 | 0 |
| ATOM | 222 | N | VAL | 28 | 10.689 | 51.590 | 96.209 | 1.00 | 12.34 | 0 |
| ATOM | 224 | CA | VAL | 28 | 9.646 | 50.910 | 95.473 | 1.00 | 12.71 | 0 |
| ATOM | 225 | CB | VAL | 28 | 9.126 | 49.693 | 96.283 | 1.00 | 2.00 | 0 |
| ATOM | 226 | CG1 | VAL | 28 | 8.777 | 50.111 | 97.684 | 1.00 | 2.00 | 0 |
| ATOM | 227 | CG2 | VAL | 28 | 7.932 | 49.053 | 95.599 | 1.00 | 2.00 | 0 |
| ATOM | 228 | C | VAL | 28 | 8.549 | 51.935 | 95.145 | 1.00 | 19.22 | 0 |
| ATOM | 229 | O | VAL | 28 | 7.757 | 52.363 | 96.000 | 1.00 | 2.00 | 0 |
| ATOM | 230 | N | GLN | 29 | 8.548 | 52.372 | 93.892 | 1.00 | 26.36 | 0 |
| ATOM | 232 | CA | GLN | 29 | 7.586 | 53.365 | 93.424 | 1.00 | 27.97 | 0 |
| ATOM | 233 | CB | GLN | 29 | 8.203 | 54.239 | 92.325 | 1.00 | 11.00 | 0 |
| ATOM | 234 | CG | GLN | 29 | 7.479 | 55.543 | 92.080 | 1.00 | 8.47 | 0 |
| ATOM | 235 | CD | GLN | 29 | 7.684 | 56.541 | 93.201 | 1.00 | 11.72 | 0 |
| ATOM | 236 | OE1 | GLN | 29 | 7.097 | 57.619 | 93.198 | 1.00 | 13.39 | 0 |
| ATOM | 237 | NE2 | GLN | 29 | 8.525 | 56.195 | 94.159 | 1.00 | 12.03 | 0 |
| ATOM | 240 | C | GLN | 29 | 6.347 | 52.688 | 92.887 | 1.00 | 27.73 | 0 |
| ATOM | 241 | O | GLN | 29 | 6.401 | 51.934 | 91.926 | 1.00 | 8.22 | 0 |
| ATOM | 242 | N | LEU | 30 | 5.229 | 52.941 | 93.531 | 1.00 | 2.00 | 0 |
| ATOM | 244 | CA | LEU | 30 | 3.978 | 52.359 | 93.087 | 1.00 | 2.00 | 0 |
| ATOM | 245 | CB | LEU | 30 | 3.157 | 51.859 | 94.279 | 1.00 | 18.06 | 0 |
| ATOM | 246 | CG | LEU | 30 | 3.381 | 50.416 | 94.729 | 1.00 | 18.06 | 0 |
| ATOM | 247 | CD1 | LEU | 30 | 4.857 | 50.152 | 94.928 | 1.00 | 18.06 | 0 |
| ATOM | 248 | CD2 | LEU | 30 | 2.603 | 50.171 | 96.009 | 1.00 | 18.06 | 0 |
| ATOM | 249 | C | LEU | 30 | 3.223 | 53.441 | 92.348 | 1.00 | 2.00 | 0 |
| ATOM | 250 | O | LEU | 30 | 3.363 | 54.621 | 92.664 | 1.00 | 18.06 | 0 |
| ATOM | 251 | N | GLN | 31 | 2.441 | 53.050 | 91.355 | 1.00 | 75.78 | 0 |
| ATOM | 253 | CA | GLN | 31 | 1.679 | 54.026 | 90.599 | 1.00 | 80.15 | 0 |
| ATOM | 254 | CB | GLN | 31 | 0.782 | 53.336 | 89.593 | 1.00 | 2.00 | 0 |
| ATOM | 255 | CG | GLN | 31 | 1.448 | 52.204 | 88.883 | 1.00 | 2.00 | 0 |
| ATOM | 256 | CD | GLN | 31 | 0.498 | 51.469 | 87.976 | 1.00 | 2.00 | 0 |
| ATOM | 257 | OE1 | GLN | 31 | 0.933 | 50.694 | 87.122 | 1.00 | 2.00 | 0 |
| ATOM | 258 | NE2 | GLN | 31 | -0.809 | 51.698 | 88.150 | 1.00 | 2.00 | 0 |

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|---|---|---|---|---|---|---|---|---|---|---|
| ATOM | 261 | C | GLN | 31 | 0.819 | 54.783 | 91.585 | 1.00 | 79.69 | 0 |
| ATOM | 262 | O | GLN | 31 | 0.276 | 54.187 | 92.512 | 1.00 | 2.00 | 0 |
| ATOM | 263 | N | GLU | 32 | 0.716 | 56.091 | 91.380 | 1.00 | 2.00 | 0 |
| ATOM | 265 | CA | GLU | 32 | -0.074 | 56.979 | 92.228 | 1.00 | 2.00 | 0 |
| ATOM | 266 | CB | GLU | 32 | -0.236 | 58.333 | 91.523 | 1.00 | 57.69 | 0 |
| ATOM | 267 | CG | GLU | 32 | -1.206 | 59.320 | 92.181 | 1.00 | 62.36 | 0 |
| ATOM | 268 | CD | GLU | 32 | -1.652 | 60.426 | 91.226 | 1.00 | 60.46 | 0 |
| ATOM | 269 | OE1 | GLU | 32 | -2.596 | 61.176 | 91.570 | 1.00 | 59.61 | 0 |
| ATOM | 270 | OE2 | GLU | 32 | -1.059 | 60.543 | 90.128 | 1.00 | 62.85 | 0 |
| ATOM | 271 | C | GLU | 32 | -1.449 | 56.370 | 92.539 | 1.00 | 2.00 | 0 |
| ATOM | 272 | O | GLU | 32 | -1.875 | 56.341 | 93.695 | 1.00 | 53.86 | 0 |
| ATOM | 273 | N | ASN | 33 | -2.127 | 55.865 | 91.517 | 1.00 | 6.25 | 0 |
| ATOM | 275 | CA | ASN | 33 | -3.445 | 55.278 | 91.714 | 1.00 | 7.45 | 0 |
| ATOM | 276 | CB | ASN | 33 | -4.134 | 55.026 | 90.364 | 1.00 | 30.19 | 0 |
| ATOM | 277 | CG | ASN | 33 | -3.291 | 54.199 | 89.412 | 1.00 | 30.49 | 0 |
| ATOM | 278 | OD1 | ASN | 33 | -2.592 | 53.261 | 89.810 | 1.00 | 32.73 | 0 |
| ATOM | 279 | ND2 | ASN | 33 | -3.349 | 54.551 | 88.141 | 1.00 | 33.00 | 0 |
| ATOM | 282 | C | ASN | 33 | -3.448 | 54.002 | 92.565 | 1.00 | 10.76 | 0 |
| ATOM | 283 | O | ASN | 33 | -4.466 | 53.670 | 93.182 | 1.00 | 23.15 | 0 |
| ATOM | 284 | N | GLU | 34 | -2.322 | 53.292 | 92.598 | 1.00 | 27.56 | 0 |
| ATOM | 286 | CA | GLU | 34 | -2.217 | 52.081 | 93.402 | 1.00 | 24.54 | 0 |
| ATOM | 287 | CB | GLU | 34 | -1.005 | 51.251 | 92.985 | 1.00 | 23.44 | 0 |
| ATOM | 288 | CG | GLU | 34 | -1.203 | 50.479 | 91.698 | 1.00 | 22.75 | 0 |
| ATOM | 289 | CD | GLU | 34 | -0.120 | 49.438 | 91.479 | 1.00 | 28.72 | 0 |
| ATOM | 290 | OE1 | GLU | 34 | -0.443 | 48.226 | 91.460 | 1.00 | 34.33 | 0 |
| ATOM | 291 | OE2 | GLU | 34 | 1.055 | 49.834 | 91.330 | 1.00 | 31.11 | 0 |
| ATOM | 292 | C | GLU | 34 | -2.106 | 52.470 | 94.871 | 1.00 | 25.10 | 0 |
| ATOM | 293 | O | GLU | 34 | -2.797 | 51.923 | 95.716 | 1.00 | 19.23 | 0 |
| ATOM | 294 | N | ILE | 35 | -1.244 | 53.430 | 95.172 | 1.00 | 14.94 | 0 |
| ATOM | 296 | CA | ILE | 35 | -1.083 | 53.889 | 96.541 | 1.00 | 28.22 | 0 |
| ATOM | 297 | CB | ILE | 35 | 0.045 | 54.888 | 96.632 | 1.00 | 2.00 | 0 |
| ATOM | 298 | CG2 | ILE | 35 | 0.013 | 55.607 | 97.961 | 1.00 | 2.00 | 0 |
| ATOM | 299 | CG1 | ILE | 35 | 1.354 | 54.154 | 96.395 | 1.00 | 2.00 | 0 |
| ATOM | 300 | CD1 | ILE | 35 | 2.554 | 55.045 | 96.414 | 1.00 | 2.00 | 0 |
| ATOM | 301 | C | ILE | 35 | -2.368 | 54.536 | 97.034 | 1.00 | 13.21 | 0 |
| ATOM | 302 | O | ILE | 35 | -2.794 | 54.302 | 98.172 | 1.00 | 2.00 | 0 |
| ATOM | 303 | N | ARG | 36 | -2.985 | 55.340 | 96.171 | 1.00 | 2.00 | 0 |
| ATOM | 305 | CA | ARG | 36 | -4.237 | 56.015 | 96.506 | 1.00 | 2.00 | 0 |
| ATOM | 306 | CB | ARG | 36 | -4.578 | 57.082 | 95.446 | 1.00 | 8.06 | 0 |
| ATOM | 307 | CG | ARG | 36 | -5.725 | 56.703 | 94.502 | 1.00 | 14.08 | 0 |
| ATOM | 308 | CD | ARG | 36 | -6.059 | 57.824 | 93.555 | 1.00 | 20.55 | 0 |
| ATOM | 309 | NE | ARG | 36 | -6.465 | 59.029 | 94.267 | 1.00 | 14.43 | 0 |
| ATOM | 311 | CZ | ARG | 36 | -7.726 | 59.383 | 94.491 | 1.00 | 22.93 | 0 |
| ATOM | 312 | NH1 | ARG | 36 | -8.729 | 58.618 | 94.064 | 1.00 | 22.80 | 0 |
| ATOM | 315 | NH2 | ARG | 36 | -7.987 | 60.518 | 95.134 | 1.00 | 19.87 | 0 |
| ATOM | 318 | C | ARG | 36 | -5.394 | 55.005 | 96.657 | 1.00 | 2.00 | 0 |
| ATOM | 319 | O | ARG | 36 | -6.415 | 55.305 | 97.279 | 1.00 | 2.00 | 0 |
| ATOM | 320 | N | GLY | 37 | -5.240 | 53.828 | 96.059 | 1.00 | 2.00 | 0 |
| ATOM | 322 | CA | GLY | 37 | -6.264 | 52.814 | 96.177 | 1.00 | 2.00 | 0 |
| ATOM | 323 | C | GLY | 37 | -6.118 | 52.251 | 97.575 | 1.00 | 2.00 | 0 |
| ATOM | 324 | O | GLY | 37 | -7.106 | 52.030 | 98.289 | 1.00 | 2.00 | 0 |
| ATOM | 325 | N | LEU | 38 | -4.864 | 52.039 | 97.975 | 1.00 | 8.88 | 0 |
| ATOM | 327 | CA | LEU | 38 | -4.558 | 51.515 | 99.288 | 1.00 | 8.88 | 0 |
| ATOM | 328 | CB | LEU | 38 | -3.061 | 51.550 | 99.559 | 1.00 | 2.00 | 0 |
| ATOM | 329 | CG | LEU | 38 | -2.202 | 50.559 | 98.784 | 1.00 | 2.00 | 0 |
| ATOM | 330 | CD1 | LEU | 38 | -0.765 | 50.804 | 99.171 | 1.00 | 2.00 | 0 |
| ATOM | 331 | CD2 | LEU | 38 | -2.614 | 49.106 | 99.063 | 1.00 | 2.00 | 0 |
| ATOM | 332 | C | LEU | 38 | -5.278 | 52.406 | 100.258 | 1.00 | 8.88 | 0 |
| ATOM | 333 | O | LEU | 38 | -6.130 | 51.928 | 101.002 | 1.00 | 2.00 | 0 |
| ATOM | 334 | N | CYS | 39 | -4.976 | 53.705 | 100.216 | 1.00 | 2.00 | 0 |
| ATOM | 336 | CA | CYS | 39 | -5.613 | 54.690 | 101.099 | 1.00 | 2.00 | 0 |
| ATOM | 337 | CB | CYS | 39 | -5.339 | 56.096 | 100.607 | 1.00 | 2.00 | 0 |
| ATOM | 338 | SG | CYS | 39 | -3.719 | 56.686 | 100.830 | 1.00 | 2.00 | 0 |
| ATOM | 339 | C | CYS | 39 | -7.140 | 54.555 | 101.201 | 1.00 | 2.00 | 0 |
| ATOM | 340 | O | CYS | 39 | -7.708 | 54.580 | 102.296 | 1.00 | 2.00 | 0 |
| ATOM | 341 | N | LEU | 40 | -7.793 | 54.412 | 100.053 | 1.00 | 2.00 | 0 |
| ATOM | 343 | CA | LEU | 40 | -9.233 | 54.330 | 99.999 | 1.00 | 2.00 | 0 |
| ATOM | 344 | CB | LEU | 40 | -9.735 | 54.704 | 98.599 | 1.00 | 2.00 | 0 |

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|---|---|---|---|---|---|---|---|---|---|
| ATOM | 345 | CG | LEU | 40 | -10.127 | 56.184 | 98.419 | 1.00 | 2.00 | 0 |
| ATOM | 346 | CD1 | LEU | 40 | -9.020 | 57.095 | 98.939 | 1.00 | 2.00 | 0 |
| ATOM | 347 | CD2 | LEU | 40 | -10.401 | 56.484 | 96.960 | 1.00 | 2.00 | 0 |
| ATOM | 348 | C | LEU | 40 | -9.817 | 53.014 | 100.426 | 1.00 | 2.00 | 0 |
| ATOM | 349 | O | LEU | 40 | -10.853 | 52.987 | 101.071 | 1.00 | 2.00 | 0 |
| ATOM | 350 | N | LYS | 41 | -9.174 | 51.916 | 100.081 | 1.00 | 7.31 | 0 |
| ATOM | 352 | CA | LYS | 41 | -9.721 | 50.630 | 100.468 | 1.00 | 7.31 | 0 |
| ATOM | 353 | CB | LYS | 41 | -9.123 | 49.517 | 99.598 | 1.00 | 2.00 | 0 |
| ATOM | 354 | CG | LYS | 41 | -9.685 | 48.157 | 99.884 | 1.00 | 2.00 | 0 |
| ATOM | 355 | CD | LYS | 41 | -11.188 | 48.216 | 99.923 | 1.00 | 2.00 | 0 |
| ATOM | 356 | CE | LYS | 41 | -11.746 | 46.968 | 100.560 | 1.00 | 2.00 | 0 |
| ATOM | 357 | NZ | LYS | 41 | -11.198 | 45.721 | 99.910 | 1.00 | 2.00 | 0 |
| ATOM | 361 | C | LYS | 41 | -9.475 | 50.376 | 101.963 | 1.00 | 7.31 | 0 |
| ATOM | 362 | O | LYS | 41 | -10.375 | 49.934 | 102.674 | 1.00 | 2.00 | 0 |
| ATOM | 363 | N | SER | 42 | -8.266 | 50.666 | 102.440 | 1.00 | 3.34 | 0 |
| ATOM | 365 | CA | SER | 42 | -7.935 | 50.477 | 103.844 | 1.00 | 3.34 | 0 |
| ATOM | 366 | CB | SER | 42 | -6.496 | 50.854 | 104.094 | 1.00 | 2.00 | 0 |
| ATOM | 367 | OG | SER | 42 | -6.315 | 52.215 | 103.766 | 1.00 | 2.00 | 0 |
| ATOM | 369 | C | SER | 42 | -8.844 | 51.398 | 104.650 | 1.00 | 7.34 | 0 |
| ATOM | 370 | O | SER | 42 | -9.504 | 50.955 | 105.600 | 1.00 | 2.00 | 0 |
| ATOM | 371 | N | ARG | 43 | -8.906 | 52.671 | 104.247 | 1.00 | 2.00 | 0 |
| ATOM | 373 | CA | ARG | 43 | -9.746 | 53.650 | 104.928 | 1.00 | 2.00 | 0 |
| ATOM | 374 | CB | ARG | 43 | -9.856 | 54.946 | 104.135 | 1.00 | 2.00 | 0 |
| ATOM | 375 | CG | ARG | 43 | -10.530 | 56.063 | 104.917 | 1.00 | 2.00 | 0 |
| ATOM | 376 | CD | ARG | 43 | -11.541 | 56.826 | 104.097 | 1.00 | 2.00 | 0 |
| ATOM | 377 | NE | ARG | 43 | -11.803 | 58.137 | 104.679 | 1.00 | 2.00 | 0 |
| ATOM | 379 | CZ | ARG | 43 | -13.010 | 58.603 | 105.005 | 1.00 | 2.00 | 0 |
| ATOM | 380 | NH1 | ARG | 43 | -14.112 | 57.877 | 104.826 | 1.00 | 2.00 | 0 |
| ATOM | 383 | NH2 | ARG | 43 | -13.120 | 59.827 | 105.502 | 1.00 | 2.00 | 0 |
| ATOM | 386 | C | ARG | 43 | -11.136 | 53.103 | 105.104 | 1.00 | 2.00 | 0 |
| ATOM | 387 | O | ARG | 43 | -11.800 | 53.385 | 106.083 | 1.00 | 2.00 | 0 |
| ATOM | 388 | N | GLU | 44 | -11.574 | 52.321 | 104.130 | 1.00 | 19.11 | 0 |
| ATOM | 390 | CA | GLU | 44 | -12.901 | 51.727 | 104.146 | 1.00 | 19.41 | 0 |
| ATOM | 391 | CB | GLU | 44 | -13.179 | 51.107 | 102.776 | 1.00 | 23.41 | 0 |
| ATOM | 392 | CG | GLU | 44 | -14.599 | 50.695 | 102.542 | 1.00 | 34.12 | 0 |
| ATOM | 393 | CD | GLU | 44 | -14.711 | 49.574 | 101.532 | 1.00 | 38.72 | 0 |
| ATOM | 394 | OE1 | GLU | 44 | -15.634 | 49.626 | 100.699 | 1.00 | 43.51 | 0 |
| ATOM | 395 | OE2 | GLU | 44 | -13.886 | 48.639 | 101.576 | 1.00 | 35.90 | 0 |
| ATOM | 396 | C | GLU | 44 | -12.987 | 50.674 | 105.260 | 1.00 | 20.56 | 0 |
| ATOM | 397 | O | GLU | 44 | -13.967 | 50.622 | 106.007 | 1.00 | 24.61 | 0 |
| ATOM | 398 | N | ILE | 45 | -11.945 | 49.857 | 105.379 | 1.00 | 8.30 | 0 |
| ATOM | 400 | CA | ILE | 45 | -11.896 | 48.811 | 106.384 | 1.00 | 8.30 | 0 |
| ATOM | 401 | CB | ILE | 45 | -10.720 | 47.876 | 106.133 | 1.00 | 2.00 | 0 |
| ATOM | 402 | CG2 | ILE | 45 | -10.795 | 46.678 | 107.049 | 1.00 | 2.00 | 0 |
| ATOM | 403 | CG1 | ILE | 45 | -10.774 | 47.382 | 104.698 | 1.00 | 2.00 | 0 |
| ATOM | 404 | CD1 | ILE | 45 | -9.559 | 46.593 | 104.285 | 1.00 | 2.00 | 0 |
| ATOM | 405 | C | ILE | 45 | -11.775 | 49.401 | 107.784 | 1.00 | 8.30 | 0 |
| ATOM | 406 | O | ILE | 45 | -12.249 | 48.819 | 108.756 | 1.00 | 2.00 | 0 |
| ATOM | 407 | N | PHE | 46 | -11.134 | 50.550 | 107.905 | 1.00 | 2.00 | 0 |
| ATOM | 409 | CA | PHE | 46 | -11.013 | 51.154 | 109.214 | 1.00 | 2.00 | 0 |
| ATOM | 410 | CB | PHE | 46 | -10.076 | 52.352 | 109.176 | 1.00 | 2.00 | 0 |
| ATOM | 411 | CG | PHE | 46 | -8.665 | 51.992 | 108.843 | 1.00 | 2.00 | 0 |
| ATOM | 412 | CD1 | PHE | 46 | -7.829 | 52.906 | 108.223 | 1.00 | 2.00 | 0 |
| ATOM | 413 | CD2 | PHE | 46 | -8.168 | 50.726 | 109.151 | 1.00 | 2.00 | 0 |
| ATOM | 414 | CE1 | PHE | 46 | -6.516 | 52.558 | 107.915 | 1.00 | 2.00 | 0 |
| ATOM | 415 | CE2 | PHE | 46 | -6.859 | 50.375 | 108.845 | 1.00 | 2.00 | 0 |
| ATOM | 416 | CZ | PHE | 46 | -6.027 | 51.289 | 108.227 | 1.00 | 2.00 | 0 |
| ATOM | 417 | C | PHE | 46 | -12.396 | 51.561 | 109.686 | 1.00 | 2.00 | 0 |
| ATOM | 418 | O | PHE | 46 | -12.840 | 51.109 | 110.731 | 1.00 | 2.00 | 0 |
| ATOM | 419 | N | LEU | 47 | -13.106 | 52.358 | 108.896 | 1.00 | 2.00 | 0 |
| ATOM | 421 | CA | LEU | 47 | -14.441 | 52.807 | 109.277 | 1.00 | 2.00 | 0 |
| ATOM | 422 | CB | LEU | 47 | -15.043 | 53.705 | 108.190 | 1.00 | 2.00 | 0 |
| ATOM | 423 | CG | LEU | 47 | -14.641 | 55.181 | 108.110 | 1.00 | 2.00 | 0 |
| ATOM | 424 | CD1 | LEU | 47 | -14.094 | 55.641 | 109.462 | 1.00 | 2.00 | 0 |
| ATOM | 425 | CD2 | LEU | 47 | -13.619 | 55.397 | 107.030 | 1.00 | 2.00 | 0 |
| ATOM | 426 | C | LEU | 47 | -15.424 | 51.677 | 109.578 | 1.00 | 2.00 | 0 |
| ATOM | 427 | O | LEU | 47 | -16.432 | 51.905 | 110.243 | 1.00 | 2.00 | 0 |
| ATOM | 428 | N | SER | 48 | -15.145 | 50.469 | 109.091 | 1.00 | 2.00 | 0 |

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|---|---|---|---|---|---|---|---|---|---|
| ATOM | 430 | CA | SER | 48 | -16.037 | 49.339 | 109.305 | 1.00 | 2.00 | 0 |
| ATOM | 431 | CB | SER | 48 | -16.121 | 48.483 | 108.039 | 1.00 | 23.35 | 0 |
| ATOM | 432 | OG | SER | 48 | -14.844 | 48.045 | 107.622 | 1.00 | 30.63 | 0 |
| ATOM | 434 | C | SER | 48 | -15.624 | 48.473 | 110.482 | 1.00 | 2.00 | 0 |
| ATOM | 435 | O | SER | 48 | -16.184 | 47.390 | 110.700 | 1.00 | 28.70 | 0 |
| ATOM | 436 | N | GLN | 49 | -14.627 | 48.922 | 111.225 | 1.00 | 61.72 | 0 |
| ATOM | 438 | CA | GLN | 49 | -14.175 | 48.193 | 112.394 | 1.00 | 63.25 | 0 |
| ATOM | 439 | CB | GLN | 49 | -12.763 | 47.645 | 112.173 | 1.00 | 13.32 | 0 |
| ATOM | 440 | CG | GLN | 49 | -12.668 | 46.511 | 111.146 | 1.00 | 7.00 | 0 |
| ATOM | 441 | CD | GLN | 49 | -11.246 | 45.952 | 110.995 | 1.00 | 8.88 | 0 |
| ATOM | 442 | OE1 | GLN | 49 | -10.251 | 46.640 | 111.258 | 1.00 | 9.23 | 0 |
| ATOM | 443 | NE2 | GLN | 49 | -11.151 | 44.700 | 110.573 | 1.00 | 7.45 | 0 |
| ATOM | 446 | C | GLN | 49 | -14.210 | 49.205 | 113.540 | 1.00 | 63.04 | 0 |
| ATOM | 447 | O | GLN | 49 | -13.864 | 50.373 | 113.357 | 1.00 | 14.61 | 0 |
| ATOM | 448 | N | PRO | 50 | -14.645 | 48.778 | 114.734 | 1.00 | 34.58 | 0 |
| ATOM | 449 | CD | PRO | 50 | -14.967 | 47.399 | 115.118 | 1.00 | 4.85 | 0 |
| ATOM | 450 | CA | PRO | 50 | -14.728 | 49.657 | 115.901 | 1.00 | 34.58 | 0 |
| ATOM | 451 | CB | PRO | 50 | -15.037 | 48.678 | 117.032 | 1.00 | 2.00 | 0 |
| ATOM | 452 | CG | PRO | 50 | -14.496 | 47.365 | 116.531 | 1.00 | 2.00 | 0 |
| ATOM | 453 | C | PRO | 50 | -13.459 | 50.468 | 116.164 | 1.00 | 34.58 | 0 |
| ATOM | 454 | O | PRO | 50 | -12.356 | 50.002 | 115.884 | 1.00 | 2.95 | 0 |
| ATOM | 455 | N | ILE | 51 | -13.626 | 51.673 | 116.708 | 1.00 | 2.00 | 0 |
| ATOM | 457 | CA | ILE | 51 | -12.499 | 52.550 | 117.015 | 1.00 | 2.00 | 0 |
| ATOM | 458 | CB | ILE | 51 | -13.001 | 53.975 | 117.318 | 1.00 | 2.00 | 0 |
| ATOM | 459 | CG2 | ILE | 51 | -13.642 | 54.035 | 118.673 | 1.00 | 2.00 | 0 |
| ATOM | 460 | CG1 | ILE | 51 | -11.850 | 54.958 | 117.295 | 1.00 | 2.00 | 0 |
| ATOM | 461 | CD1 | ILE | 51 | -12.328 | 56.370 | 117.351 | 1.00 | 2.00 | 0 |
| ATOM | 462 | C | ILE | 51 | -11.650 | 51.996 | 118.172 | 1.00 | 2.00 | 0 |
| ATOM | 463 | O | ILE | 51 | -10.456 | 52.303 | 118.283 | 1.00 | 2.00 | 0 |
| ATOM | 464 | N | LEU | 52 | -12.284 | 51.187 | 119.028 | 1.00 | 2.00 | 0 |
| ATOM | 466 | CA | LEU | 52 | -11.622 | 50.522 | 120.159 | 1.00 | 2.00 | 0 |
| ATOM | 467 | CB | LEU | 52 | -12.391 | 50.746 | 121.473 | 1.00 | 2.00 | 0 |
| ATOM | 468 | CG | LEU | 52 | -11.655 | 50.518 | 122.808 | 1.00 | 2.00 | 0 |
| ATOM | 469 | CD1 | LEU | 52 | -12.559 | 50.899 | 123.944 | 1.00 | 2.00 | 0 |
| ATOM | 470 | CD2 | LEU | 52 | -11.233 | 49.085 | 122.973 | 1.00 | 2.00 | 0 |
| ATOM | 471 | C | LEU | 52 | -11.660 | 49.033 | 119.770 | 1.00 | 2.00 | 0 |
| ATOM | 472 | O | LEU | 52 | -12.652 | 48.331 | 120.006 | 1.00 | 2.00 | 0 |
| ATOM | 473 | N | LEU | 53 | -10.584 | 48.576 | 119.136 | 1.00 | 2.00 | 0 |
| ATOM | 475 | CA | LEU | 53 | -10.464 | 47.204 | 118.667 | 1.00 | 2.00 | 0 |
| ATOM | 476 | CB | LEU | 53 | -9.066 | 46.982 | 118.069 | 1.00 | 2.00 | 0 |
| ATOM | 477 | CG | LEU | 53 | -8.802 | 47.038 | 116.555 | 1.00 | 2.00 | 0 |
| ATOM | 478 | CD1 | LEU | 53 | -9.835 | 47.889 | 115.810 | 1.00 | 2.00 | 0 |
| ATOM | 479 | CD2 | LEU | 53 | -7.401 | 47.550 | 116.353 | 1.00 | 2.00 | 0 |
| ATOM | 480 | C | LEU | 53 | -10.686 | 46.230 | 119.792 | 1.00 | 2.00 | 0 |
| ATOM | 481 | O | LEU | 53 | -10.365 | 46.522 | 120.937 | 1.00 | 2.00 | 0 |
| ATOM | 482 | N | GLU | 54 | -11.251 | 45.076 | 119.472 | 1.00 | 19.77 | 0 |
| ATOM | 484 | CA | GLU | 54 | -11.465 | 44.049 | 120.474 | 1.00 | 20.13 | 0 |
| ATOM | 485 | CB | GLU | 54 | -12.955 | 43.809 | 120.714 | 1.00 | 56.32 | 0 |
| ATOM | 486 | CG | GLU | 54 | -13.244 | 43.362 | 122.135 | 1.00 | 66.19 | 0 |
| ATOM | 487 | CD | GLU | 54 | -14.668 | 42.873 | 122.346 | 1.00 | 69.64 | 0 |
| ATOM | 488 | OE1 | GLU | 54 | -15.613 | 43.627 | 122.024 | 1.00 | 78.06 | 0 |
| ATOM | 489 | OE2 | GLU | 54 | -14.839 | 41.734 | 122.848 | 1.00 | 73.27 | 0 |
| ATOM | 490 | C | GLU | 54 | -10.798 | 42.820 | 119.882 | 1.00 | 19.77 | 0 |
| ATOM | 491 | O | GLU | 54 | -11.451 | 41.949 | 119.313 | 1.00 | 48.57 | 0 |
| ATOM | 492 | N | LEU | 55 | -9.473 | 42.800 | 119.974 | 1.00 | 2.00 | 0 |
| ATOM | 494 | CA | LEU | 55 | -8.666 | 41.712 | 119.452 | 1.00 | 2.00 | 0 |
| ATOM | 495 | CB | LEU | 55 | -7.245 | 42.188 | 119.176 | 1.00 | 2.00 | 0 |
| ATOM | 496 | CG | LEU | 55 | -7.148 | 43.458 | 118.336 | 1.00 | 2.00 | 0 |
| ATOM | 497 | CD1 | LEU | 55 | -5.695 | 43.728 | 117.961 | 1.00 | 2.00 | 0 |
| ATOM | 498 | CD2 | LEU | 55 | -8.024 | 43.298 | 117.108 | 1.00 | 2.00 | 0 |
| ATOM | 499 | C | LEU | 55 | -8.624 | 40.586 | 120.456 | 1.00 | 2.00 | 0 |
| ATOM | 500 | O | LEU | 55 | -8.724 | 40.807 | 121.664 | 1.00 | 10.45 | 0 |
| ATOM | 501 | N | GLU | 56 | -8.448 | 39.374 | 119.961 | 1.00 | 2.00 | 0 |
| ATOM | 503 | CA | GLU | 56 | -8.407 | 38.224 | 120.826 | 1.00 | 2.00 | 0 |
| ATOM | 504 | CB | GLU | 56 | -9.741 | 37.467 | 120.729 | 1.00 | 18.79 | 0 |
| ATOM | 505 | CG | GLU | 56 | -10.989 | 38.283 | 121.171 | 1.00 | 30.34 | 0 |
| ATOM | 506 | CD | GLU | 56 | -11.012 | 38.677 | 122.658 | 1.00 | 42.94 | 0 |
| ATOM | 507 | OE1 | GLU | 56 | -11.188 | 37.789 | 123.526 | 1.00 | 44.70 | 0 |

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|---|---|---|---|---|---|---|---|---|---|---|
| ATOM | 508 | OE2 | GLU | 56 | -10.872 | 39.882 | 122.955 | 1.00 | 47.48 | 0 |
| ATOM | 509 | C | GLU | 56 | -7.244 | 37.343 | 120.393 | 1.00 | 2.00 | 0 |
| ATOM | 510 | O | GLU | 56 | -6.292 | 37.839 | 119.800 | 1.00 | 3.40 | 0 |
| ATOM | 511 | N | ALA | 57 | -7.312 | 36.062 | 120.765 | 1.00 | 65.90 | 0 |
| ATOM | 513 | CA | ALA | 57 | -6.336 | 35.026 | 120.405 | 1.00 | 62.88 | 0 |
| ATOM | 514 | CB | ALA | 57 | -6.750 | 34.434 | 119.039 | 1.00 | 26.61 | 0 |
| ATOM | 515 | C | ALA | 57 | -4.867 | 35.474 | 120.387 | 1.00 | 68.03 | 0 |
| ATOM | 516 | O | ALA | 57 | -4.543 | 36.519 | 120.932 | 1.00 | 14.05 | 0 |
| ATOM | 517 | N | PRO | 58 | -3.951 | 34.632 | 119.857 | 1.00 | 2.00 | 0 |
| ATOM | 518 | CD | PRO | 58 | -4.109 | 33.203 | 119.533 | 1.00 | 9.23 | 0 |
| ATOM | 519 | CA | PRO | 58 | -2.526 | 34.988 | 119.782 | 1.00 | 2.00 | 0 |
| ATOM | 520 | CB | PRO | 58 | -1.852 | 33.645 | 119.501 | 1.00 | 9.23 | 0 |
| ATOM | 521 | CG | PRO | 58 | -2.881 | 32.926 | 118.711 | 1.00 | 9.49 | 0 |
| ATOM | 522 | C | PRO | 58 | -2.176 | 36.002 | 118.672 | 1.00 | 2.00 | 0 |
| ATOM | 523 | O | PRO | 58 | -2.688 | 35.901 | 117.540 | 1.00 | 12.29 | 0 |
| ATOM | 524 | N | LEU | 59 | -1.284 | 36.947 | 118.975 | 1.00 | 17.05 | 0 |
| ATOM | 526 | CA | LEU | 59 | -0.856 | 37.944 | 117.989 | 1.00 | 17.05 | 0 |
| ATOM | 527 | CB | LEU | 59 | -1.862 | 39.100 | 117.895 | 1.00 | 2.00 | 0 |
| ATOM | 528 | CG | LEU | 59 | -1.842 | 40.166 | 118.993 | 1.00 | 2.00 | 0 |
| ATOM | 529 | CD1 | LEU | 59 | -2.880 | 41.252 | 118.706 | 1.00 | 2.00 | 0 |
| ATOM | 530 | CD2 | LEU | 59 | -2.117 | 39.498 | 120.339 | 1.00 | 2.00 | 0 |
| ATOM | 531 | C | LEU | 59 | 0.510 | 38.501 | 118.351 | 1.00 | 17.05 | 0 |
| ATOM | 532 | O | LEU | 59 | 1.030 | 38.229 | 119.429 | 1.00 | 2.00 | 0 |
| ATOM | 533 | N | LYS | 60 | 1.103 | 39.259 | 117.438 | 1.00 | 21.64 | 0 |
| ATOM | 535 | CA | LYS | 60 | 2.399 | 39.872 | 117.688 | 1.00 | 21.64 | 0 |
| ATOM | 536 | CB | LYS | 60 | 3.358 | 39.655 | 116.513 | 1.00 | 10.44 | 0 |
| ATOM | 537 | CG | LYS | 60 | 3.185 | 38.327 | 115.768 | 1.00 | 11.70 | 0 |
| ATOM | 538 | CD | LYS | 60 | 3.556 | 37.101 | 116.608 | 1.00 | 12.19 | 0 |
| ATOM | 539 | CE | LYS | 60 | 5.034 | 36.783 | 116.544 | 1.00 | 8.37 | 0 |
| ATOM | 540 | NZ | LYS | 60 | 5.824 | 37.927 | 117.066 | 1.00 | 8.37 | 0 |
| ATOM | 544 | C | LYS | 60 | 2.063 | 41.353 | 117.804 | 1.00 | 21.64 | 0 |
| ATOM | 545 | O | LYS | 60 | 1.142 | 41.832 | 117.128 | 1.00 | 13.47 | 0 |
| ATOM | 546 | N | ILE | 61 | 2.757 | 42.072 | 118.680 | 1.00 | 20.60 | 0 |
| ATOM | 548 | CA | ILE | 61 | 2.499 | 43.496 | 118.822 | 1.00 | 22.32 | 0 |
| ATOM | 549 | CB | ILE | 61 | 2.032 | 43.859 | 120.240 | 1.00 | 2.00 | 0 |
| ATOM | 550 | CG2 | ILE | 61 | 1.485 | 45.288 | 120.239 | 1.00 | 2.00 | 0 |
| ATOM | 551 | CG1 | ILE | 61 | 0.940 | 42.881 | 120.702 | 1.00 | 2.00 | 0 |
| ATOM | 552 | CD1 | ILE | 61 | 0.019 | 43.422 | 121.783 | 1.00 | 2.00 | 0 |
| ATOM | 553 | C | ILE | 61 | 3.791 | 44.220 | 118.494 | 1.00 | 23.52 | 0 |
| ATOM | 554 | O | ILE | 61 | 4.862 | 43.752 | 118.868 | 1.00 | 2.00 | 0 |
| ATOM | 555 | N | CYS | 62 | 3.698 | 45.341 | 117.787 | 1.00 | 2.00 | 0 |
| ATOM | 557 | CA | CYS | 62 | 4.874 | 46.095 | 117.393 | 1.00 | 2.00 | 0 |
| ATOM | 558 | CB | CYS | 62 | 5.147 | 45.925 | 115.895 | 1.00 | 11.47 | 0 |
| ATOM | 559 | SG | CYS | 62 | 5.439 | 44.252 | 115.266 | 1.00 | 11.47 | 0 |
| ATOM | 560 | C | CYS | 62 | 4.607 | 47.560 | 117.658 | 1.00 | 2.00 | 0 |
| ATOM | 561 | O | CYS | 62 | 3.451 | 47.957 | 117.751 | 1.00 | 11.47 | 0 |
| ATOM | 562 | N | GLY | 63 | 5.662 | 48.367 | 117.739 | 1.00 | 2.00 | 0 |
| ATOM | 564 | CA | GLY | 63 | 5.507 | 49.789 | 117.971 | 1.00 | 2.00 | 0 |
| ATOM | 565 | C | GLY | 63 | 6.548 | 50.610 | 117.222 | 1.00 | 2.00 | 0 |
| ATOM | 566 | O | GLY | 63 | 7.624 | 50.109 | 116.897 | 1.00 | 11.39 | 0 |
| ATOM | 567 | N | ASP | 64 | 6.216 | 51.870 | 116.959 | 1.00 | 2.00 | 0 |
| ATOM | 569 | CA | ASP | 64 | 7.068 | 52.834 | 116.255 | 1.00 | 3.88 | 0 |
| ATOM | 570 | CB | ASP | 64 | 7.805 | 53.721 | 117.245 | 1.00 | 6.62 | 0 |
| ATOM | 571 | CG | ASP | 64 | 6.873 | 54.589 | 118.025 | 1.00 | 6.62 | 0 |
| ATOM | 572 | OD1 | ASP | 64 | 5.996 | 54.019 | 118.708 | 1.00 | 12.70 | 0 |
| ATOM | 573 | OD2 | ASP | 64 | 7.003 | 55.829 | 117.946 | 1.00 | 12.70 | 0 |
| ATOM | 574 | C | ASP | 64 | 8.064 | 52.362 | 115.221 | 1.00 | 14.37 | 0 |
| ATOM | 575 | O | ASP | 64 | 9.221 | 52.080 | 115.557 | 1.00 | 8.57 | 0 |
| ATOM | 576 | N | ILE | 65 | 7.619 | 52.326 | 113.963 | 1.00 | 5.19 | 0 |
| ATOM | 578 | CA | ILE | 65 | 8.471 | 51.924 | 112.849 | 1.00 | 3.07 | 0 |
| ATOM | 579 | CB | ILE | 65 | 7.663 | 51.310 | 111.672 | 1.00 | 2.00 | 0 |
| ATOM | 580 | CG2 | ILE | 65 | 8.609 | 50.903 | 110.535 | 1.00 | 2.00 | 0 |
| ATOM | 581 | CG1 | ILE | 65 | 6.871 | 50.095 | 112.151 | 1.00 | 2.00 | 0 |
| ATOM | 582 | CD1 | ILE | 65 | 7.723 | 49.023 | 112.763 | 1.00 | 2.00 | 0 |
| ATOM | 583 | C | ILE | 65 | 9.185 | 53.177 | 112.357 | 1.00 | 2.24 | 0 |
| ATOM | 584 | O | ILE | 65 | 10.379 | 53.148 | 112.101 | 1.00 | 2.00 | 0 |
| ATOM | 585 | N | HIS | 66 | 8.451 | 54.276 | 112.235 | 1.00 | 2.00 | 0 |
| ATOM | 587 | CA | HIS | 66 | 9.022 | 55.536 | 111.776 | 1.00 | 2.00 | 0 |

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|---|---|---|---|---|---|---|---|---|---|---|
| ATOM | 588 | C | HIS | 66 | 9.847 | 55.525 | 110.502 | 1.00 | 2.00 | 0 |
| ATOM | 589 | O | HIS | 66 | 11.042 | 55.818 | 110.539 | 1.00 | 12.38 | 0 |
| ATOM | 590 | CB | HIS | 66 | 9.846 | 56.182 | 112.881 | 1.00 | 8.25 | 0 |
| ATOM | 591 | CG | HIS | 66 | 9.040 | 57.046 | 113.782 | 1.00 | 8.25 | 0 |
| ATOM | 592 | ND1 | HIS | 66 | 8.104 | 57.949 | 113.337 | 1.00 | 8.25 | 0 |
| ATOM | 594 | CD2 | HIS | 66 | 9.001 | 57.109 | 115.133 | 1.00 | 8.25 | 0 |
| ATOM | 595 | NE2 | HIS | 66 | 8.042 | 58.043 | 115.526 | 1.00 | 8.25 | 0 |
| ATOM | 596 | CE1 | HIS | 66 | 7.536 | 58.516 | 114.399 | 1.00 | 8.25 | 0 |
| ATOM | 597 | N | GLY | 67 | 9.197 | 55.195 | 109.385 | 1.00 | 11.52 | 0 |
| ATOM | 599 | CA | GLY | 67 | 9.835 | 55.174 | 108.078 | 1.00 | 11.52 | 0 |
| ATOM | 600 | C | GLY | 67 | 11.029 | 54.266 | 107.868 | 1.00 | 11.52 | 0 |
| ATOM | 601 | O | GLY | 67 | 11.782 | 54.462 | 106.915 | 1.00 | 81.94 | 0 |
| ATOM | 602 | N | GLN | 68 | 11.214 | 53.272 | 108.730 | 1.00 | 18.96 | 0 |
| ATOM | 604 | CA | GLN | 68 | 12.353 | 52.364 | 108.602 | 1.00 | 20.32 | 0 |
| ATOM | 605 | CB | GLN | 68 | 13.007 | 52.139 | 109.957 | 1.00 | 6.39 | 0 |
| ATOM | 606 | CG | GLN | 68 | 13.261 | 53.407 | 110.711 | 1.00 | 4.06 | 0 |
| ATOM | 607 | CD | GLN | 68 | 14.315 | 53.239 | 111.757 | 1.00 | 7.01 | 0 |
| ATOM | 608 | OE1 | GLN | 68 | 15.013 | 54.197 | 112.111 | 1.00 | 8.21 | 0 |
| ATOM | 609 | NE2 | GLN | 68 | 14.453 | 52.020 | 112.270 | 1.00 | 5.84 | 0 |
| ATOM | 612 | C | GLN | 68 | 11.916 | 51.039 | 108.010 | 1.00 | 18.72 | 0 |
| ATOM | 613 | O | GLN | 68 | 12.018 | 49.975 | 108.634 | 1.00 | 10.73 | 0 |
| ATOM | 614 | N | TYR | 69 | 11.450 | 51.119 | 106.777 | 1.00 | 5.70 | 0 |
| ATOM | 616 | CA | TYR | 69 | 10.959 | 49.970 | 106.054 | 1.00 | 5.52 | 0 |
| ATOM | 617 | CB | TYR | 69 | 10.807 | 50.313 | 104.587 | 1.00 | 2.00 | 0 |
| ATOM | 618 | CG | TYR | 69 | 9.988 | 49.322 | 103.841 | 1.00 | 2.00 | 0 |
| ATOM | 619 | CD1 | TYR | 69 | 8.658 | 49.099 | 104.187 | 1.00 | 2.00 | 0 |
| ATOM | 620 | CE1 | TYR | 69 | 7.873 | 48.194 | 103.477 | 1.00 | 2.00 | 0 |
| ATOM | 621 | CD2 | TYR | 69 | 10.526 | 48.611 | 102.762 | 1.00 | 2.00 | 0 |
| ATOM | 622 | CE2 | TYR | 69 | 9.751 | 47.701 | 102.038 | 1.00 | 2.00 | 0 |
| ATOM | 623 | CZ | TYR | 69 | 8.431 | 47.506 | 102.408 | 1.00 | 2.00 | 0 |
| ATOM | 624 | OH | TYR | 69 | 7.656 | 46.632 | 101.715 | 1.00 | 2.00 | 0 |
| ATOM | 626 | C | TYR | 69 | 11.815 | 48.730 | 106.188 | 1.00 | 8.52 | 0 |
| ATOM | 627 | O | TYR | 69 | 11.284 | 47.641 | 106.393 | 1.00 | 2.00 | 0 |
| ATOM | 628 | N | TYR | 70 | 13.132 | 48.877 | 106.093 | 1.00 | 2.00 | 0 |
| ATOM | 630 | CA | TYR | 70 | 13.992 | 47.703 | 106.186 | 1.00 | 2.00 | 0 |
| ATOM | 631 | CB | TYR | 70 | 15.420 | 48.031 | 105.741 | 1.00 | 64.80 | 0 |
| ATOM | 632 | CG | TYR | 70 | 15.533 | 47.964 | 104.231 | 1.00 | 70.91 | 0 |
| ATOM | 633 | CD1 | TYR | 70 | 15.026 | 48.993 | 103.431 | 1.00 | 73.06 | 0 |
| ATOM | 634 | CE1 | TYR | 70 | 15.082 | 48.924 | 102.041 | 1.00 | 68.38 | 0 |
| ATOM | 635 | CD2 | TYR | 70 | 16.107 | 46.857 | 103.597 | 1.00 | 73.86 | 0 |
| ATOM | 636 | CE2 | TYR | 70 | 16.171 | 46.780 | 102.200 | 1.00 | 70.94 | 0 |
| ATOM | 637 | CZ | TYR | 70 | 15.654 | 47.820 | 101.433 | 1.00 | 72.52 | 0 |
| ATOM | 638 | OH | TYR | 70 | 15.712 | 47.779 | 100.062 | 1.00 | 70.35 | 0 |
| ATOM | 640 | C | TYR | 70 | 13.943 | 47.007 | 107.538 | 1.00 | 2.00 | 0 |
| ATOM | 641 | O | TYR | 70 | 13.967 | 45.771 | 107.610 | 1.00 | 64.08 | 0 |
| ATOM | 642 | N | ASP | 71 | 13.821 | 47.789 | 108.608 | 1.00 | 7.87 | 0 |
| ATOM | 644 | CA | ASP | 71 | 13.728 | 47.203 | 109.927 | 1.00 | 6.73 | 0 |
| ATOM | 645 | CB | ASP | 71 | 14.030 | 48.242 | 110.998 | 1.00 | 14.88 | 0 |
| ATOM | 646 | CG | ASP | 71 | 15.514 | 48.600 | 111.054 | 1.00 | 25.87 | 0 |
| ATOM | 647 | OD1 | ASP | 71 | 15.826 | 49.778 | 111.293 | 1.00 | 24.58 | 0 |
| ATOM | 648 | OD2 | ASP | 71 | 16.375 | 47.714 | 110.861 | 1.00 | 21.52 | 0 |
| ATOM | 649 | C | ASP | 71 | 12.331 | 46.622 | 110.051 | 1.00 | 6.73 | 0 |
| ATOM | 650 | O | ASP | 71 | 12.116 | 45.697 | 110.826 | 1.00 | 14.14 | 0 |
| ATOM | 651 | N | LEU | 72 | 11.399 | 47.148 | 109.250 | 1.00 | 2.00 | 0 |
| ATOM | 653 | CA | LEU | 72 | 10.015 | 46.654 | 109.208 | 1.00 | 2.00 | 0 |
| ATOM | 654 | CB | LEU | 72 | 9.094 | 47.613 | 108.456 | 1.00 | 2.00 | 0 |
| ATOM | 655 | CG | LEU | 72 | 7.771 | 46.946 | 108.067 | 1.00 | 2.00 | 0 |
| ATOM | 656 | CD1 | LEU | 72 | 7.025 | 46.562 | 109.342 | 1.00 | 2.00 | 0 |
| ATOM | 657 | CD2 | LEU | 72 | 6.935 | 47.867 | 107.208 | 1.00 | 2.00 | 0 |
| ATOM | 658 | C | LEU | 72 | 10.014 | 45.320 | 108.476 | 1.00 | 2.00 | 0 |
| ATOM | 659 | O | LEU | 72 | 9.259 | 44.401 | 108.814 | 1.00 | 2.00 | 0 |
| ATOM | 660 | N | LEU | 73 | 10.848 | 45.231 | 107.449 | 1.00 | 44.35 | 0 |
| ATOM | 662 | CA | LEU | 73 | 10.968 | 44.005 | 106.693 | 1.00 | 42.59 | 0 |
| ATOM | 663 | CB | LEU | 73 | 11.846 | 44.218 | 105.460 | 1.00 | 2.00 | 0 |
| ATOM | 664 | CG | LEU | 73 | 11.248 | 44.759 | 104.160 | 1.00 | 2.00 | 0 |
| ATOM | 665 | CD1 | LEU | 73 | 12.324 | 44.728 | 103.101 | 1.00 | 2.00 | 0 |
| ATOM | 666 | CD2 | LEU | 73 | 10.052 | 43.920 | 103.725 | 1.00 | 2.00 | 0 |
| ATOM | 667 | C | LEU | 73 | 11.603 | 42.978 | 107.629 | 1.00 | 42.42 | 0 |

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|---|---|---|---|---|---|---|---|---|---|---|
| ATOM | 668 | O | LEU | 73 | 11.059 | 41.890 | 107.817 | 1.00 | 2.00 | 0 |
| ATOM | 669 | N | ARG | 74 | 12.729 | 43.354 | 108.241 | 1.00 | 2.00 | 0 |
| ATOM | 671 | CA | ARG | 74 | 13.462 | 42.494 | 109.179 | 1.00 | 2.00 | 0 |
| ATOM | 672 | CB | ARG | 74 | 14.591 | 43.285 | 109.840 | 1.00 | 31.22 | 0 |
| ATOM | 673 | CG | ARG | 74 | 15.809 | 43.478 | 108.958 | 1.00 | 31.18 | 0 |
| ATOM | 674 | CD | ARG | 74 | 16.944 | 44.146 | 109.710 | 1.00 | 37.63 | 0 |
| ATOM | 675 | NE | ARG | 74 | 17.250 | 43.459 | 110.960 | 1.00 | 37.44 | 0 |
| ATOM | 677 | CZ | ARG | 74 | 17.210 | 44.041 | 112.157 | 1.00 | 41.10 | 0 |
| ATOM | 678 | NH1 | ARG | 74 | 16.888 | 45.327 | 112.265 | 1.00 | 39.99 | 0 |
| ATOM | 681 | NH2 | ARG | 74 | 17.476 | 43.339 | 113.254 | 1.00 | 39.22 | 0 |
| ATOM | 684 | C | ARG | 74 | 12.569 | 41.896 | 110.259 | 1.00 | 2.00 | 0 |
| ATOM | 685 | O | ARG | 74 | 12.621 | 40.703 | 110.544 | 1.00 | 29.18 | 0 |
| ATOM | 686 | N | LEU | 75 | 11.747 | 42.742 | 110.853 | 1.00 | 2.00 | 0 |
| ATOM | 688 | CA | LEU | 75 | 10.818 | 42.331 | 111.901 | 1.00 | 2.00 | 0 |
| ATOM | 689 | CB | LEU | 75 | 10.069 | 43.580 | 112.407 | 1.00 | 3.53 | 0 |
| ATOM | 690 | CG | LEU | 75 | 8.704 | 43.654 | 113.091 | 1.00 | 3.53 | 0 |
| ATOM | 691 | CD1 | LEU | 75 | 8.554 | 45.074 | 113.606 | 1.00 | 3.53 | 0 |
| ATOM | 692 | CD2 | LEU | 75 | 7.561 | 43.337 | 112.138 | 1.00 | 3.53 | 0 |
| ATOM | 693 | C | LEU | 75 | 9.850 | 41.279 | 111.384 | 1.00 | 2.00 | 0 |
| ATOM | 694 | O | LEU | 75 | 9.594 | 40.284 | 112.043 | 1.00 | 3.53 | 0 |
| ATOM | 695 | N | PHE | 76 | 9.325 | 41.514 | 110.190 | 1.00 | 2.00 | 0 |
| ATOM | 697 | CA | PHE | 76 | 8.382 | 40.604 | 109.573 | 1.00 | 2.00 | 0 |
| ATOM | 698 | CB | PHE | 76 | 7.883 | 41.173 | 108.255 | 1.00 | 2.00 | 0 |
| ATOM | 699 | CG | PHE | 76 | 6.626 | 41.966 | 108.382 | 1.00 | 2.00 | 0 |
| ATOM | 700 | CD1 | PHE | 76 | 6.447 | 43.124 | 107.642 | 1.00 | 2.00 | 0 |
| ATOM | 701 | CD2 | PHE | 76 | 5.616 | 41.550 | 109.240 | 1.00 | 2.00 | 0 |
| ATOM | 702 | CE1 | PHE | 76 | 5.277 | 43.852 | 107.753 | 1.00 | 2.00 | 0 |
| ATOM | 703 | CE2 | PHE | 76 | 4.447 | 42.270 | 109.358 | 1.00 | 2.00 | 0 |
| ATOM | 704 | CZ | PHE | 76 | 4.272 | 43.423 | 108.615 | 1.00 | 2.00 | 0 |
| ATOM | 705 | C | PHE | 76 | 9.016 | 39.271 | 109.322 | 1.00 | 2.00 | 0 |
| ATOM | 706 | O | PHE | 76 | 8.339 | 38.260 | 109.363 | 1.00 | 2.00 | 0 |
| ATOM | 707 | N | GLU | 77 | 10.316 | 39.283 | 109.043 | 1.00 | 2.00 | 0 |
| ATOM | 709 | CA | GLU | 77 | 11.080 | 38.065 | 108.789 | 1.00 | 2.00 | 0 |
| ATOM | 710 | CB | GLU | 77 | 12.436 | 38.409 | 108.191 | 1.00 | 84.85 | 0 |
| ATOM | 711 | CG | GLU | 77 | 12.331 | 39.117 | 106.861 | 1.00 | 89.26 | 0 |
| ATOM | 712 | CD | GLU | 77 | 13.651 | 39.690 | 106.391 | 1.00 | 98.60 | 0 |
| ATOM | 713 | OE1 | GLU | 77 | 13.627 | 40.493 | 105.434 | 1.00 | 98.04 | 0 |
| ATOM | 714 | OE2 | GLU | 77 | 14.709 | 39.345 | 106.973 | 1.00 | 0.97 | 0 |
| ATOM | 715 | C | GLU | 77 | 11.262 | 37.316 | 110.100 | 1.00 | 2.00 | 0 |
| ATOM | 716 | O | GLU | 77 | 11.469 | 36.103 | 110.099 | 1.00 | 80.75 | 0 |
| ATOM | 717 | N | TYR | 78 | 11.182 | 38.045 | 111.216 | 1.00 | 15.29 | 0 |
| ATOM | 719 | CA | TYR | 78 | 11.325 | 37.449 | 112.538 | 1.00 | 15.29 | 0 |
| ATOM | 720 | CB | TYR | 78 | 11.945 | 38.455 | 113.514 | 1.00 | 67.13 | 0 |
| ATOM | 721 | CG | TYR | 78 | 12.459 | 37.828 | 114.796 | 1.00 | 69.14 | 0 |
| ATOM | 722 | CD1 | TYR | 78 | 11.822 | 36.717 | 115.368 | 1.00 | 76.95 | 0 |
| ATOM | 723 | CE1 | TYR | 78 | 12.278 | 36.142 | 116.548 | 1.00 | 77.96 | 0 |
| ATOM | 724 | CD2 | TYR | 78 | 13.577 | 38.346 | 115.446 | 1.00 | 75.81 | 0 |
| ATOM | 725 | CE2 | TYR | 78 | 14.044 | 37.775 | 116.698 | 1.00 | 77.77 | 0 |
| ATOM | 726 | CZ | TYR | 78 | 13.387 | 36.673 | 117.181 | 1.00 | 77.18 | 0 |
| ATOM | 727 | OH | TYR | 78 | 13.826 | 36.115 | 118.365 | 1.00 | 87.14 | 0 |
| ATOM | 729 | C | TYR | 78 | 9.967 | 36.964 | 113.053 | 1.00 | 15.29 | 0 |
| ATOM | 730 | O | TYR | 78 | 9.811 | 35.796 | 113.403 | 1.00 | 62.78 | 0 |
| ATOM | 731 | N | GLY | 79 | 8.992 | 37.863 | 113.117 | 1.00 | 2.00 | 0 |
| ATOM | 733 | CA | GLY | 79 | 7.675 | 37.485 | 113.582 | 1.00 | 2.00 | 0 |
| ATOM | 734 | C | GLY | 79 | 6.977 | 36.532 | 112.629 | 1.00 | 2.00 | 0 |
| ATOM | 735 | O | GLY | 79 | 6.226 | 35.649 | 113.052 | 1.00 | 34.11 | 0 |
| ATOM | 736 | N | GLY | 80 | 7.237 | 36.699 | 111.338 | 1.00 | 49.23 | 0 |
| ATOM | 738 | CA | GLY | 80 | 6.601 | 35.870 | 110.330 | 1.00 | 48.34 | 0 |
| ATOM | 739 | C | GLY | 80 | 5.699 | 36.782 | 109.520 | 1.00 | 47.91 | 0 |
| ATOM | 740 | O | GLY | 80 | 4.955 | 37.572 | 110.097 | 1.00 | 15.83 | 0 |
| ATOM | 741 | N | PHE | 81 | 5.759 | 36.692 | 108.193 | 1.00 | 2.00 | 0 |
| ATOM | 743 | CA | PHE | 81 | 4.948 | 37.558 | 107.343 | 1.00 | 2.00 | 0 |
| ATOM | 744 | CB | PHE | 81 | 5.386 | 37.403 | 105.880 | 1.00 | 2.00 | 0 |
| ATOM | 745 | CG | PHE | 81 | 6.673 | 38.134 | 105.556 | 1.00 | 2.00 | 0 |
| ATOM | 746 | CD1 | PHE | 81 | 7.899 | 37.506 | 105.685 | 1.00 | 2.00 | 0 |
| ATOM | 747 | CD2 | PHE | 81 | 6.652 | 39.467 | 105.139 | 1.00 | 2.00 | 0 |
| ATOM | 748 | CE1 | PHE | 81 | 9.082 | 38.193 | 105.405 | 1.00 | 2.00 | 0 |
| ATOM | 749 | CE2 | PHE | 81 | 7.829 | 40.154 | 104.859 | 1.00 | 2.00 | 0 |

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|---|---|---|---|---|---|---|---|---|---|---|
| ATOM | 750 | CZ | PHE | 81 | 9.044 | 39.517 | 104.992 | 1.00 | 2.00 | 0 |
| ATOM | 751 | C | PHE | 81 | 3.428 | 37.380 | 107.548 | 1.00 | 2.00 | 0 |
| ATOM | 752 | O | PHE | 81 | 2.918 | 36.257 | 107.636 | 1.00 | 2.00 | 0 |
| ATOM | 753 | N | PRO | 82 | 2.694 | 38.505 | 107.618 | 1.00 | 2.00 | 0 |
| ATOM | 754 | CD | PRO | 82 | 3.317 | 39.807 | 107.337 | 1.00 | 21.23 | 0 |
| ATOM | 755 | CA | PRO | 82 | 1.261 | 38.702 | 107.820 | 1.00 | 2.00 | 0 |
| ATOM | 756 | CB | PRO | 82 | 0.996 | 39.979 | 107.079 | 1.00 | 20.78 | 0 |
| ATOM | 757 | CG | PRO | 82 | 2.144 | 40.765 | 107.502 | 1.00 | 22.98 | 0 |
| ATOM | 758 | C | PRO | 82 | 0.273 | 37.623 | 107.490 | 1.00 | 2.00 | 0 |
| ATOM | 759 | O | PRO | 82 | -0.761 | 37.529 | 108.161 | 1.00 | 36.87 | 0 |
| ATOM | 760 | N | PRO | 83 | 0.501 | 36.841 | 106.423 | 1.00 | 27.66 | 0 |
| ATOM | 761 | CD | PRO | 83 | 1.439 | 36.880 | 105.290 | 1.00 | 2.85 | 0 |
| ATOM | 762 | CA | PRO | 83 | -0.514 | 35.812 | 106.201 | 1.00 | 30.55 | 0 |
| ATOM | 763 | CB | PRO | 83 | 0.089 | 34.958 | 105.083 | 1.00 | 5.44 | 0 |
| ATOM | 764 | CG | PRO | 83 | 1.550 | 35.427 | 104.971 | 1.00 | 10.08 | 0 |
| ATOM | 765 | C | PRO | 83 | -0.791 | 34.990 | 107.460 | 1.00 | 24.53 | 0 |
| ATOM | 766 | O | PRO | 83 | -1.947 | 34.863 | 107.882 | 1.00 | 5.06 | 0 |
| ATOM | 767 | N | GLU | 84 | 0.284 | 34.504 | 108.080 | 1.00 | 63.06 | 0 |
| ATOM | 769 | CA | GLU | 84 | 0.190 | 33.665 | 109.268 | 1.00 | 65.66 | 0 |
| ATOM | 770 | CB | GLU | 84 | 1.448 | 32.797 | 109.382 | 1.00 | 61.87 | 0 |
| ATOM | 771 | CG | GLU | 84 | 1.194 | 31.402 | 109.979 | 1.00 | 75.07 | 0 |
| ATOM | 772 | CD | GLU | 84 | 0.401 | 30.452 | 109.056 | 1.00 | 79.88 | 0 |
| ATOM | 773 | OE1 | GLU | 84 | 1.015 | 29.508 | 108.504 | 1.00 | 76.25 | 0 |
| ATOM | 774 | OE2 | GLU | 84 | -0.832 | 30.635 | 108.891 | 1.00 | 74.31 | 0 |
| ATOM | 775 | C | GLU | 84 | -0.066 | 34.394 | 110.588 | 1.00 | 66.47 | 0 |
| ATOM | 776 | O | GLU | 84 | -1.194 | 34.406 | 111.085 | 1.00 | 61.22 | 0 |
| ATOM | 777 | N | SER | 85 | 0.984 | 34.978 | 111.161 | 1.00 | 66.52 | 0 |
| ATOM | 779 | CA | SER | 85 | 0.882 | 35.691 | 112.431 | 1.00 | 64.76 | 0 |
| ATOM | 780 | CB | SER | 85 | 2.266 | 36.145 | 112.900 | 1.00 | 2.00 | 0 |
| ATOM | 781 | OG | SER | 85 | 3.198 | 35.078 | 112.871 | 1.00 | 2.00 | 0 |
| ATOM | 783 | C | SER | 85 | -0.013 | 36.917 | 112.349 | 1.00 | 62.83 | 0 |
| ATOM | 784 | O | SER | 85 | -0.005 | 37.633 | 111.341 | 1.00 | 2.00 | 0 |
| ATOM | 785 | N | ASN | 86 | -0.785 | 37.146 | 113.412 | 1.00 | 2.00 | 0 |
| ATOM | 787 | CA | ASN | 86 | -1.647 | 38.321 | 113.490 | 1.00 | 2.00 | 0 |
| ATOM | 788 | CB | ASN | 86 | -2.747 | 38.123 | 114.520 | 1.00 | 2.00 | 0 |
| ATOM | 789 | CG | ASN | 86 | -3.887 | 37.283 | 113.994 | 1.00 | 10.84 | 0 |
| ATOM | 790 | OD1 | ASN | 86 | -3.763 | 36.629 | 112.957 | 1.00 | 12.15 | 0 |
| ATOM | 791 | ND2 | ASN | 86 | -5.017 | 37.300 | 114.705 | 1.00 | 6.45 | 0 |
| ATOM | 794 | C | ASN | 86 | -0.742 | 39.467 | 113.912 | 1.00 | 2.00 | 0 |
| ATOM | 795 | O | ASN | 86 | 0.363 | 39.229 | 114.423 | 1.00 | 2.00 | 0 |
| ATOM | 796 | N | TYR | 87 | -1.183 | 40.703 | 113.723 | 1.00 | 2.00 | 0 |
| ATOM | 798 | CA | TYR | 87 | -0.337 | 41.830 | 114.081 | 1.00 | 2.00 | 0 |
| ATOM | 799 | CB | TYR | 87 | 0.529 | 42.253 | 112.870 | 1.00 | 2.00 | 0 |
| ATOM | 800 | CG | TYR | 87 | 1.802 | 41.448 | 112.684 | 1.00 | 2.00 | 0 |
| ATOM | 801 | CD1 | TYR | 87 | 1.879 | 40.421 | 111.749 | 1.00 | 2.00 | 0 |
| ATOM | 802 | CE1 | TYR | 87 | 3.039 | 39.689 | 111.598 | 1.00 | 2.00 | 0 |
| ATOM | 803 | CD2 | TYR | 87 | 2.930 | 41.714 | 113.458 | 1.00 | 2.00 | 0 |
| ATOM | 804 | CE2 | TYR | 87 | 4.080 | 40.991 | 113.313 | 1.00 | 2.00 | 0 |
| ATOM | 805 | CZ | TYR | 87 | 4.127 | 39.986 | 112.384 | 1.00 | 2.00 | 0 |
| ATOM | 806 | OH | TYR | 87 | 5.280 | 39.281 | 112.259 | 1.00 | 2.00 | 0 |
| ATOM | 808 | C | TYR | 87 | -1.104 | 43.029 | 114.588 | 1.00 | 2.00 | 0 |
| ATOM | 809 | O | TYR | 87 | -2.264 | 43.238 | 114.216 | 1.00 | 2.00 | 0 |
| ATOM | 810 | N | LEU | 88 | -0.440 | 43.810 | 115.435 | 1.00 | 2.00 | 0 |
| ATOM | 812 | CA | LEU | 88 | -1.015 | 45.026 | 115.987 | 1.00 | 2.00 | 0 |
| ATOM | 813 | CB | LEU | 88 | -1.615 | 44.766 | 117.375 | 1.00 | 2.00 | 0 |
| ATOM | 814 | CG | LEU | 88 | -2.364 | 45.917 | 118.062 | 1.00 | 2.00 | 0 |
| ATOM | 815 | CD1 | LEU | 88 | -3.657 | 46.225 | 117.348 | 1.00 | 2.00 | 0 |
| ATOM | 816 | CD2 | LEU | 88 | -2.675 | 45.551 | 119.493 | 1.00 | 2.00 | 0 |
| ATOM | 817 | C | LEU | 88 | 0.119 | 46.034 | 116.084 | 1.00 | 2.00 | 0 |
| ATOM | 818 | O | LEU | 88 | 1.082 | 45.814 | 116.814 | 1.00 | 2.00 | 0 |
| ATOM | 819 | N | PHE | 89 | 0.061 | 47.108 | 115.309 | 1.00 | 2.00 | 0 |
| ATOM | 821 | CA | PHE | 89 | 1.114 | 48.117 | 115.393 | 1.00 | 2.00 | 0 |
| ATOM | 822 | CB | PHE | 89 | 1.567 | 48.599 | 114.004 | 1.00 | 2.00 | 0 |
| ATOM | 823 | CG | PHE | 89 | 2.305 | 47.563 | 113.221 | 1.00 | 2.00 | 0 |
| ATOM | 824 | CD1 | PHE | 89 | 1.617 | 46.543 | 112.578 | 1.00 | 2.00 | 0 |
| ATOM | 825 | CD2 | PHE | 89 | 3.683 | 47.581 | 113.159 | 1.00 | 2.00 | 0 |
| ATOM | 826 | CE1 | PHE | 89 | 2.284 | 45.547 | 111.885 | 1.00 | 2.00 | 0 |
| ATOM | 827 | CE2 | PHE | 89 | 4.379 | 46.586 | 112.464 | 1.00 | 2.00 | 0 |

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|---|---|---|---|---|---|---|---|---|---|---|
| ATOM | 828 | CZ | PHE | 89 | 3.673 | 45.565 | 111.826 | 1.00 | 2.00 | 0 |
| ATOM | 829 | C | PHE | 89 | 0.495 | 49.250 | 116.197 | 1.00 | 2.00 | 0 |
| ATOM | 830 | O | PHE | 89 | -0.664 | 49.615 | 115.985 | 1.00 | 2.00 | 0 |
| ATOM | 831 | N | LEU | 90 | 1.271 | 49.797 | 117.124 | 1.00 | 4.99 | 0 |
| ATOM | 833 | CA | LEU | 90 | 0.810 | 50.856 | 118.014 | 1.00 | 4.99 | 0 |
| ATOM | 834 | CB | LEU | 90 | 1.519 | 50.702 | 119.370 | 1.00 | 2.00 | 0 |
| ATOM | 835 | CG | LEU | 90 | 1.516 | 49.291 | 119.991 | 1.00 | 2.00 | 0 |
| ATOM | 836 | CD1 | LEU | 90 | 2.488 | 49.246 | 121.147 | 1.00 | 2.00 | 0 |
| ATOM | 837 | CD2 | LEU | 90 | 0.111 | 48.870 | 120.402 | 1.00 | 2.00 | 0 |
| ATOM | 838 | C | LEU | 90 | 1.000 | 52.275 | 117.463 | 1.00 | 4.99 | 0 |
| ATOM | 839 | O | LEU | 90 | 1.382 | 53.196 | 118.200 | 1.00 | 2.00 | 0 |
| ATOM | 840 | N | GLY | 91 | 0.734 | 52.459 | 116.175 | 1.00 | 14.03 | 0 |
| ATOM | 842 | CA | GLY | 91 | 0.884 | 53.774 | 115.588 | 1.00 | 14.03 | 0 |
| ATOM | 843 | C | GLY | 91 | 2.307 | 54.139 | 115.209 | 1.00 | 14.03 | 0 |
| ATOM | 844 | O | GLY | 91 | 3.220 | 53.312 | 115.267 | 1.00 | 32.27 | 0 |
| ATOM | 845 | N | ASP | 92 | 2.471 | 55.400 | 114.820 | 1.00 | 2.00 | 0 |
| ATOM | 847 | CA | ASP | 92 | 3.736 | 55.978 | 114.382 | 1.00 | 2.00 | 0 |
| ATOM | 848 | CB | ASP | 92 | 4.670 | 56.170 | 115.576 | 1.00 | 2.00 | 0 |
| ATOM | 849 | CG | ASP | 92 | 4.185 | 57.239 | 116.525 | 1.00 | 2.00 | 0 |
| ATOM | 850 | OD1 | ASP | 92 | 3.449 | 58.145 | 116.063 | 1.00 | 2.00 | 0 |
| ATOM | 851 | OD2 | ASP | 92 | 4.541 | 57.177 | 117.725 | 1.00 | 2.00 | 0 |
| ATOM | 852 | C | ASP | 92 | 4.427 | 55.205 | 113.259 | 1.00 | 2.00 | 0 |
| ATOM | 853 | O | ASP | 92 | 5.515 | 54.631 | 113.422 | 1.00 | 2.00 | 0 |
| ATOM | 854 | N | TYR | 93 | 3.792 | 55.234 | 112.096 | 1.00 | 2.00 | 0 |
| ATOM | 856 | CA | TYR | 93 | 4.301 | 54.523 | 110.938 | 1.00 | 2.00 | 0 |
| ATOM | 857 | CB | TYR | 93 | 3.149 | 53.907 | 110.171 | 1.00 | 2.00 | 0 |
| ATOM | 858 | CG | TYR | 93 | 2.122 | 53.226 | 111.029 | 1.00 | 2.00 | 0 |
| ATOM | 859 | CD1 | TYR | 93 | 0.875 | 53.801 | 111.227 | 1.00 | 2.00 | 0 |
| ATOM | 860 | CE1 | TYR | 93 | -0.086 | 53.176 | 112.004 | 1.00 | 2.00 | 0 |
| ATOM | 861 | CD2 | TYR | 93 | 2.390 | 52.002 | 111.628 | 1.00 | 2.00 | 0 |
| ATOM | 862 | CE2 | TYR | 93 | 1.445 | 51.362 | 112.405 | 1.00 | 2.00 | 0 |
| ATOM | 863 | CZ | TYR | 93 | 0.204 | 51.951 | 112.593 | 1.00 | 2.00 | 0 |
| ATOM | 864 | OH | TYR | 93 | -0.736 | 51.315 | 113.379 | 1.00 | 2.00 | 0 |
| ATOM | 866 | C | TYR | 93 | 5.088 | 55.399 | 109.992 | 1.00 | 2.00 | 0 |
| ATOM | 867 | O | TYR | 93 | 5.998 | 54.922 | 109.335 | 1.00 | 2.00 | 0 |
| ATOM | 868 | N | VAL | 94 | 4.718 | 56.667 | 109.904 | 1.00 | 2.00 | 0 |
| ATOM | 870 | CA | VAL | 94 | 5.380 | 57.607 | 109.004 | 1.00 | 2.00 | 0 |
| ATOM | 871 | CB | VAL | 94 | 4.322 | 58.340 | 108.112 | 1.00 | 2.00 | 0 |
| ATOM | 872 | CG1 | VAL | 94 | 3.365 | 57.315 | 107.523 | 1.00 | 2.00 | 0 |
| ATOM | 873 | CG2 | VAL | 94 | 3.551 | 59.396 | 108.903 | 1.00 | 2.00 | 0 |
| ATOM | 874 | C | VAL | 94 | 6.253 | 58.614 | 109.780 | 1.00 | 2.00 | 0 |
| ATOM | 875 | O | VAL | 94 | 6.447 | 58.457 | 110.985 | 1.00 | 2.00 | 0 |
| ATOM | 876 | N | ASP | 95 | 6.774 | 59.629 | 109.094 | 1.00 | 8.40 | 0 |
| ATOM | 878 | CA | ASP | 95 | 7.641 | 60.648 | 109.689 | 1.00 | 2.00 | 0 |
| ATOM | 879 | CB | ASP | 95 | 6.967 | 61.356 | 110.868 | 1.00 | 39.32 | 0 |
| ATOM | 880 | CG | ASP | 95 | 5.975 | 62.433 | 110.449 | 1.00 | 45.35 | 0 |
| ATOM | 881 | OD1 | ASP | 95 | 6.227 | 63.167 | 109.471 | 1.00 | 44.75 | 0 |
| ATOM | 882 | OD2 | ASP | 95 | 4.937 | 62.561 | 111.127 | 1.00 | 53.79 | 0 |
| ATOM | 883 | C | ASP | 95 | 8.975 | 60.074 | 110.155 | 1.00 | 2.71 | 0 |
| ATOM | 884 | O | ASP | 95 | 9.092 | 58.877 | 110.421 | 1.00 | 37.69 | 0 |
| ATOM | 885 | N | ARG | 96 | 9.972 | 60.949 | 110.252 | 1.00 | 21.97 | 0 |
| ATOM | 887 | CA | ARG | 96 | 11.322 | 60.589 | 110.685 | 1.00 | 27.39 | 0 |
| ATOM | 888 | CB | ARG | 96 | 11.285 | 59.989 | 112.099 | 1.00 | 18.63 | 0 |
| ATOM | 889 | CG | ARG | 96 | 12.037 | 60.816 | 113.128 | 1.00 | 24.81 | 0 |
| ATOM | 890 | CD | ARG | 96 | 11.255 | 62.052 | 113.581 | 1.00 | 32.64 | 0 |
| ATOM | 891 | NE | ARG | 96 | 10.551 | 61.833 | 114.850 | 1.00 | 39.46 | 0 |
| ATOM | 893 | CZ | ARG | 96 | 9.890 | 62.774 | 115.525 | 1.00 | 39.86 | 0 |
| ATOM | 894 | NH1 | ARG | 96 | 9.824 | 64.018 | 115.066 | 1.00 | 40.95 | 0 |
| ATOM | 897 | NH2 | ARG | 96 | 9.290 | 62.471 | 116.670 | 1.00 | 44.56 | 0 |
| ATOM | 900 | C | ARG | 96 | 12.109 | 59.659 | 109.732 | 1.00 | 24.24 | 0 |
| ATOM | 901 | O | ARG | 96 | 13.114 | 60.072 | 109.135 | 1.00 | 13.09 | 0 |
| ATOM | 902 | N | GLY | 97 | 11.668 | 58.411 | 109.592 | 1.00 | 19.94 | 0 |
| ATOM | 904 | CA | GLY | 97 | 12.359 | 57.480 | 108.716 | 1.00 | 20.45 | 0 |
| ATOM | 905 | C | GLY | 97 | 12.412 | 57.920 | 107.269 | 1.00 | 23.76 | 0 |
| ATOM | 906 | O | GLY | 97 | 11.516 | 58.617 | 106.773 | 1.00 | 84.64 | 0 |
| ATOM | 907 | N | LYS | 98 | 13.460 | 57.469 | 106.584 | 1.00 | 47.57 | 0 |
| ATOM | 909 | CA | LYS | 98 | 13.698 | 57.806 | 105.182 | 1.00 | 46.79 | 0 |
| ATOM | 910 | CB | LYS | 98 | 15.147 | 57.462 | 104.832 | 1.00 | 31.45 | 0 |

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|---|---|---|---|---|---|---|---|---|---|---|
| ATOM | 911 | CG | LYS | 98 | 16.169 | 58.397 | 105.487 | 1.00 | 30.73 | 0 |
| ATOM | 912 | CD | LYS | 98 | 17.606 | 58.061 | 105.087 | 1.00 | 32.79 | 0 |
| ATOM | 913 | CE | LYS | 98 | 18.605 | 59.089 | 105.627 | 1.00 | 30.08 | 0 |
| ATOM | 914 | NZ | LYS | 98 | 20.036 | 58.743 | 105.315 | 1.00 | 31.54 | 0 |
| ATOM | 918 | C | LYS | 98 | 12.741 | 57.196 | 104.146 | 1.00 | 44.78 | 0 |
| ATOM | 919 | O | LYS | 98 | 12.613 | 57.707 | 103.040 | 1.00 | 31.43 | 0 |
| ATOM | 920 | N | GLN | 99 | 12.059 | 56.120 | 104.517 | 1.00 | 2.00 | 0 |
| ATOM | 922 | CA | GLN | 99 | 11.132 | 55.430 | 103.639 | 1.00 | 2.00 | 0 |
| ATOM | 923 | CB | GLN | 99 | 11.654 | 54.023 | 103.337 | 1.00 | 11.21 | 0 |
| ATOM | 924 | CG | GLN | 99 | 12.945 | 53.993 | 102.552 | 1.00 | 6.66 | 0 |
| ATOM | 925 | CD | GLN | 99 | 13.361 | 52.586 | 102.177 | 1.00 | 11.01 | 0 |
| ATOM | 926 | OE1 | GLN | 99 | 13.802 | 51.805 | 103.031 | 1.00 | 10.44 | 0 |
| ATOM | 927 | NE2 | GLN | 99 | 13.229 | 52.247 | 100.895 | 1.00 | 8.18 | 0 |
| ATOM | 930 | C | GLN | 99 | 9.741 | 55.328 | 104.245 | 1.00 | 2.00 | 0 |
| ATOM | 931 | O | GLN | 99 | 9.177 | 54.238 | 104.317 | 1.00 | 6.66 | 0 |
| ATOM | 932 | N | SER | 100 | 9.178 | 56.460 | 104.657 | 1.00 | 24.01 | 0 |
| ATOM | 934 | CA | SER | 100 | 7.839 | 56.475 | 105.257 | 1.00 | 24.01 | 0 |
| ATOM | 935 | CB | SER | 100 | 7.481 | 57.897 | 105.739 | 1.00 | 2.00 | 0 |
| ATOM | 936 | OG | SER | 100 | 8.479 | 58.490 | 106.556 | 1.00 | 2.00 | 0 |
| ATOM | 938 | C | SER | 100 | 6.749 | 55.987 | 104.272 | 1.00 | 24.01 | 0 |
| ATOM | 939 | O | SER | 100 | 5.703 | 55.463 | 104.680 | 1.00 | 2.00 | 0 |
| ATOM | 940 | N | LEU | 101 | 7.015 | 56.153 | 102.977 | 1.00 | 27.83 | 0 |
| ATOM | 942 | CA | LEU | 101 | 6.084 | 55.786 | 101.913 | 1.00 | 27.83 | 0 |
| ATOM | 943 | CB | LEU | 101 | 6.551 | 56.416 | 100.599 | 1.00 | 3.66 | 0 |
| ATOM | 944 | CG | LEU | 101 | 5.593 | 57.224 | 99.721 | 1.00 | 3.66 | 0 |
| ATOM | 945 | CD1 | LEU | 101 | 4.209 | 56.591 | 99.749 | 1.00 | 3.66 | 0 |
| ATOM | 946 | CD2 | LEU | 101 | 5.532 | 58.653 | 100.208 | 1.00 | 3.66 | 0 |
| ATOM | 947 | C | LEU | 101 | 5.852 | 54.284 | 101.689 | 1.00 | 27.83 | 0 |
| ATOM | 948 | O | LEU | 101 | 4.731 | 53.851 | 101.467 | 1.00 | 3.66 | 0 |
| ATOM | 949 | N | GLU | 102 | 6.901 | 53.480 | 101.725 | 1.00 | 2.00 | 0 |
| ATOM | 951 | CA | GLU | 102 | 6.713 | 52.055 | 101.490 | 1.00 | 2.00 | 0 |
| ATOM | 952 | CB | GLU | 102 | 7.976 | 51.470 | 100.870 | 1.00 | 13.98 | 0 |
| ATOM | 953 | CG | GLU | 102 | 9.211 | 52.208 | 101.294 | 1.00 | 13.98 | 0 |
| ATOM | 954 | CD | GLU | 102 | 10.116 | 52.539 | 100.136 | 1.00 | 13.98 | 0 |
| ATOM | 955 | OE1 | GLU | 102 | 10.181 | 53.727 | 99.737 | 1.00 | 13.98 | 0 |
| ATOM | 956 | OE2 | GLU | 102 | 10.772 | 51.599 | 99.643 | 1.00 | 13.98 | 0 |
| ATOM | 957 | C | GLU | 102 | 6.307 | 51.324 | 102.763 | 1.00 | 2.00 | 0 |
| ATOM | 958 | O | GLU | 102 | 5.686 | 50.263 | 102.729 | 1.00 | 13.98 | 0 |
| ATOM | 959 | N | THR | 103 | 6.664 | 51.901 | 103.897 | 1.00 | 2.00 | 0 |
| ATOM | 961 | CA | THR | 103 | 6.293 | 51.330 | 105.173 | 1.00 | 2.00 | 0 |
| ATOM | 962 | CB | THR | 103 | 6.923 | 52.098 | 106.309 | 1.00 | 2.00 | 0 |
| ATOM | 963 | OG1 | THR | 103 | 8.313 | 52.297 | 106.028 | 1.00 | 2.00 | 0 |
| ATOM | 965 | CG2 | THR | 103 | 6.758 | 51.329 | 107.599 | 1.00 | 2.00 | 0 |
| ATOM | 966 | C | THR | 103 | 4.775 | 51.440 | 105.296 | 1.00 | 2.00 | 0 |
| ATOM | 967 | O | THR | 103 | 4.081 | 50.428 | 105.394 | 1.00 | 2.00 | 0 |
| ATOM | 968 | N | ILE | 104 | 4.256 | 52.667 | 105.257 | 1.00 | 2.00 | 0 |
| ATOM | 970 | CA | ILE | 104 | 2.824 | 52.873 | 105.363 | 1.00 | 2.00 | 0 |
| ATOM | 971 | CB | ILE | 104 | 2.486 | 54.389 | 105.300 | 1.00 | 12.72 | 0 |
| ATOM | 972 | CG2 | ILE | 104 | 2.856 | 54.965 | 103.956 | 1.00 | 12.35 | 0 |
| ATOM | 973 | CG1 | ILE | 104 | 0.996 | 54.618 | 105.548 | 1.00 | 13.84 | 0 |
| ATOM | 974 | CD1 | ILE | 104 | 0.459 | 53.940 | 106.787 | 1.00 | 12.35 | 0 |
| ATOM | 975 | C | ILE | 104 | 2.074 | 52.062 | 104.294 | 1.00 | 2.00 | 0 |
| ATOM | 976 | O | ILE | 104 | 0.975 | 51.581 | 104.544 | 1.00 | 18.28 | 0 |
| ATOM | 977 | N | CYS | 105 | 2.690 | 51.868 | 103.127 | 1.00 | 23.45 | 0 |
| ATOM | 979 | CA | CYS | 105 | 2.080 | 51.092 | 102.042 | 1.00 | 21.74 | 0 |
| ATOM | 980 | CB | CYS | 105 | 2.722 | 51.458 | 100.708 | 1.00 | 20.76 | 0 |
| ATOM | 981 | SG | CYS | 105 | 2.010 | 52.958 | 99.957 | 1.00 | 18.03 | 0 |
| ATOM | 982 | C | CYS | 105 | 2.061 | 49.563 | 102.214 | 1.00 | 17.08 | 0 |
| ATOM | 983 | O | CYS | 105 | 1.114 | 48.915 | 101.781 | 1.00 | 20.76 | 0 |
| ATOM | 984 | N | LEU | 106 | 3.089 | 48.982 | 102.833 | 1.00 | 2.00 | 0 |
| ATOM | 986 | CA | LEU | 106 | 3.124 | 47.526 | 103.073 | 1.00 | 2.00 | 0 |
| ATOM | 987 | CB | LEU | 106 | 4.519 | 47.042 | 103.495 | 1.00 | 2.00 | 0 |
| ATOM | 988 | CG | LEU | 106 | 4.680 | 45.544 | 103.802 | 1.00 | 2.00 | 0 |
| ATOM | 989 | CD1 | LEU | 106 | 4.200 | 44.694 | 102.639 | 1.00 | 2.00 | 0 |
| ATOM | 990 | CD2 | LEU | 106 | 6.133 | 45.247 | 104.053 | 1.00 | 2.00 | 0 |
| ATOM | 991 | C | LEU | 106 | 2.154 | 47.179 | 104.178 | 1.00 | 2.00 | 0 |
| ATOM | 992 | O | LEU | 106 | 1.589 | 46.088 | 104.192 | 1.00 | 2.00 | 0 |
| ATOM | 993 | N | LEU | 107 | 1.992 | 48.107 | 105.116 | 1.00 | 2.00 | 0 |

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|---|---|---|---|---|---|---|---|---|---|---|
| ATOM | 995 | CA | LEU | 107 | 1.078 | 47.922 | 106.226 | 1.00 | 2.00 | 0 |
| ATOM | 996 | CB | LEU | 107 | 1.347 | 48.967 | 107.319 | 1.00 | 2.00 | 0 |
| ATOM | 997 | CG | LEU | 107 | 2.761 | 48.857 | 107.911 | 1.00 | 2.00 | 0 |
| ATOM | 998 | CD1 | LEU | 107 | 3.106 | 50.016 | 108.815 | 1.00 | 2.00 | 0 |
| ATOM | 999 | CD2 | LEU | 107 | 2.868 | 47.535 | 108.638 | 1.00 | 2.00 | 0 |
| ATOM | 1000 | C | LEU | 107 | -0.339 | 48.035 | 105.683 | 1.00 | 2.00 | 0 |
| ATOM | 1001 | O | LEU | 107 | -1.153 | 47.125 | 105.873 | 1.00 | 2.00 | 0 |
| ATOM | 1002 | N | LEU | 108 | -0.623 | 49.126 | 104.971 | 1.00 | 2.00 | 0 |
| ATOM | 1004 | CA | LEU | 108 | -1.953 | 49.340 | 104.394 | 1.00 | 2.00 | 0 |
| ATOM | 1005 | CB | LEU | 108 | -2.020 | 50.666 | 103.637 | 1.00 | 2.00 | 0 |
| ATOM | 1006 | CG | LEU | 108 | -2.103 | 51.925 | 104.499 | 1.00 | 2.00 | 0 |
| ATOM | 1007 | CD1 | LEU | 108 | -2.244 | 53.164 | 103.618 | 1.00 | 2.00 | 0 |
| ATOM | 1008 | CD2 | LEU | 108 | -3.281 | 51.792 | 105.433 | 1.00 | 2.00 | 0 |
| ATOM | 1009 | C | LEU | 108 | -2.352 | 48.206 | 103.455 | 1.00 | 2.00 | 0 |
| ATOM | 1010 | O | LEU | 108 | -3.533 | 47.846 | 103.369 | 1.00 | 2.00 | 0 |
| ATOM | 1011 | N | ALA | 109 | -1.366 | 47.643 | 102.762 | 1.00 | 2.00 | 0 |
| ATOM | 1013 | CA | ALA | 109 | -1.608 | 46.539 | 101.839 | 1.00 | 2.00 | 0 |
| ATOM | 1014 | CB | ALA | 109 | -0.336 | 46.209 | 101.087 | 1.00 | 33.06 | 0 |
| ATOM | 1015 | C | ALA | 109 | -2.091 | 45.316 | 102.605 | 1.00 | 2.00 | 0 |
| ATOM | 1016 | O | ALA | 109 | -3.146 | 44.746 | 102.305 | 1.00 | 24.92 | 0 |
| ATOM | 1017 | N | TYR | 110 | -1.311 | 44.929 | 103.609 | 1.00 | 5.11 | 0 |
| ATOM | 1019 | CA | TYR | 110 | -1.625 | 43.781 | 104.452 | 1.00 | 2.00 | 0 |
| ATOM | 1020 | CB | TYR | 110 | -0.495 | 43.564 | 105.438 | 1.00 | 2.00 | 0 |
| ATOM | 1021 | CG | TYR | 110 | 0.674 | 42.771 | 104.922 | 1.00 | 2.00 | 0 |
| ATOM | 1022 | CD1 | TYR | 110 | 1.966 | 43.235 | 105.092 | 1.00 | 2.00 | 0 |
| ATOM | 1023 | CE1 | TYR | 110 | 3.053 | 42.474 | 104.706 | 1.00 | 2.00 | 0 |
| ATOM | 1024 | CD2 | TYR | 110 | 0.494 | 41.517 | 104.340 | 1.00 | 2.00 | 0 |
| ATOM | 1025 | CE2 | TYR | 110 | 1.578 | 40.743 | 103.950 | 1.00 | 2.00 | 0 |
| ATOM | 1026 | CZ | TYR | 110 | 2.859 | 41.230 | 104.139 | 1.00 | 2.00 | 0 |
| ATOM | 1027 | OH | TYR | 110 | 3.963 | 40.483 | 103.779 | 1.00 | 2.00 | 0 |
| ATOM | 1029 | C | TYR | 110 | -2.948 | 43.940 | 105.215 | 1.00 | 2.00 | 0 |
| ATOM | 1030 | O | TYR | 110 | -3.663 | 42.961 | 105.441 | 1.00 | 2.00 | 0 |
| ATOM | 1031 | N | LYS | 111 | -3.265 | 45.168 | 105.618 | 1.00 | 2.00 | 0 |
| ATOM | 1033 | CA | LYS | 111 | -4.508 | 45.430 | 106.333 | 1.00 | 2.00 | 0 |
| ATOM | 1034 | CB | LYS | 111 | -4.619 | 46.904 | 106.708 | 1.00 | 2.00 | 0 |
| ATOM | 1035 | CG | LYS | 111 | -5.942 | 47.262 | 107.393 | 1.00 | 2.00 | 0 |
| ATOM | 1036 | CD | LYS | 111 | -6.085 | 46.501 | 108.685 | 1.00 | 2.00 | 0 |
| ATOM | 1037 | CE | LYS | 111 | -7.410 | 46.743 | 109.354 | 1.00 | 2.00 | 0 |
| ATOM | 1038 | NZ | LYS | 111 | -7.643 | 45.735 | 110.428 | 1.00 | 2.00 | 0 |
| ATOM | 1042 | C | LYS | 111 | -5.698 | 45.051 | 105.465 | 1.00 | 2.00 | 0 |
| ATOM | 1043 | O | LYS | 111 | -6.655 | 44.431 | 105.951 | 1.00 | 2.00 | 0 |
| ATOM | 1044 | N | ILE | 112 | -5.624 | 45.455 | 104.192 | 1.00 | 2.00 | 0 |
| ATOM | 1046 | CA | ILE | 112 | -6.651 | 45.192 | 103.177 | 1.00 | 2.00 | 0 |
| ATOM | 1047 | CB | ILE | 112 | -6.361 | 45.978 | 101.875 | 1.00 | 25.04 | 0 |
| ATOM | 1048 | CG2 | ILE | 112 | -7.414 | 45.656 | 100.814 | 1.00 | 25.04 | 0 |
| ATOM | 1049 | CG1 | ILE | 112 | -6.339 | 47.482 | 102.166 | 1.00 | 25.04 | 0 |
| ATOM | 1050 | CD1 | ILE | 112 | -5.857 | 48.336 | 101.012 | 1.00 | 25.04 | 0 |
| ATOM | 1051 | C | ILE | 112 | -6.706 | 43.706 | 102.829 | 1.00 | 2.00 | 0 |
| ATOM | 1052 | O | ILE | 112 | -7.783 | 43.156 | 102.568 | 1.00 | 25.04 | 0 |
| ATOM | 1053 | N | LYS | 113 | -5.537 | 43.067 | 102.816 | 1.00 | 2.00 | 0 |
| ATOM | 1055 | CA | LYS | 113 | -5.447 | 41.649 | 102.513 | 1.00 | 2.00 | 0 |
| ATOM | 1056 | CB | LYS | 113 | -4.001 | 41.285 | 102.181 | 1.00 | 8.72 | 0 |
| ATOM | 1057 | CG | LYS | 113 | -3.852 | 39.909 | 101.596 | 1.00 | 8.72 | 0 |
| ATOM | 1058 | CD | LYS | 113 | -2.780 | 39.871 | 100.521 | 1.00 | 8.72 | 0 |
| ATOM | 1059 | CE | LYS | 113 | -2.618 | 38.467 | 99.975 | 1.00 | 8.72 | 0 |
| ATOM | 1060 | NZ | LYS | 113 | -3.952 | 37.873 | 99.637 | 1.00 | 8.72 | 0 |
| ATOM | 1064 | C | LYS | 113 | -5.987 | 40.780 | 103.667 | 1.00 | 2.00 | 0 |
| ATOM | 1065 | O | LYS | 113 | -6.620 | 39.742 | 103.435 | 1.00 | 8.72 | 0 |
| ATOM | 1066 | N | TYR | 114 | -5.744 | 41.200 | 104.906 | 1.00 | 9.02 | 0 |
| ATOM | 1068 | CA | TYR | 114 | -6.226 | 40.455 | 106.068 | 1.00 | 8.11 | 0 |
| ATOM | 1069 | CB | TYR | 114 | -5.122 | 39.580 | 106.666 | 1.00 | 12.47 | 0 |
| ATOM | 1070 | CG | TYR | 114 | -4.138 | 38.988 | 105.689 | 1.00 | 12.47 | 0 |
| ATOM | 1071 | CD1 | TYR | 114 | -3.027 | 39.715 | 105.278 | 1.00 | 12.47 | 0 |
| ATOM | 1072 | CE1 | TYR | 114 | -2.111 | 39.191 | 104.397 | 1.00 | 12.47 | 0 |
| ATOM | 1073 | CD2 | TYR | 114 | -4.307 | 37.709 | 105.188 | 1.00 | 12.47 | 0 |
| ATOM | 1074 | CE2 | TYR | 114 | -3.395 | 37.168 | 104.302 | 1.00 | 12.47 | 0 |
| ATOM | 1075 | CZ | TYR | 114 | -2.296 | 37.917 | 103.908 | 1.00 | 12.47 | 0 |
| ATOM | 1076 | OH | TYR | 114 | -1.378 | 37.404 | 103.013 | 1.00 | 12.47 | 0 |

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|---|---|---|---|---|---|---|---|---|---|---|
| ATOM | 1078 | C | TYR | 114 | -6.729 | 41.417 | 107.155 | 1.00 | 9.78 | 0 |
| ATOM | 1079 | O | TYR | 114 | -6.058 | 41.638 | 108.169 | 1.00 | 12.47 | 0 |
| ATOM | 1080 | N | PRO | 115 | -7.928 | 41.985 | 106.968 | 1.00 | 34.30 | 0 |
| ATOM | 1081 | CD | PRO | 115 | -8.843 | 41.845 | 105.826 | 1.00 | 24.86 | 0 |
| ATOM | 1082 | CA | PRO | 115 | -8.488 | 42.912 | 107.944 | 1.00 | 34.30 | 0 |
| ATOM | 1083 | CB | PRO | 115 | -9.862 | 43.227 | 107.365 | 1.00 | 24.86 | 0 |
| ATOM | 1084 | CG | PRO | 115 | -9.640 | 43.117 | 105.921 | 1.00 | 24.86 | 0 |
| ATOM | 1085 | C | PRO | 115 | -8.586 | 42.310 | 109.335 | 1.00 | 34.30 | 0 |
| ATOM | 1086 | O | PRO | 115 | -8.017 | 42.837 | 110.285 | 1.00 | 24.86 | 0 |
| ATOM | 1087 | N | GLU | 116 | -9.275 | 41.181 | 109.445 | 1.00 | 2.00 | 0 |
| ATOM | 1089 | CA | GLU | 116 | -9.477 | 40.538 | 110.742 | 1.00 | 2.00 | 0 |
| ATOM | 1090 | CB | GLU | 116 | -10.577 | 39.469 | 110.637 | 1.00 | 35.30 | 0 |
| ATOM | 1091 | CG | GLU | 116 | -11.673 | 39.726 | 109.593 | 1.00 | 37.08 | 0 |
| ATOM | 1092 | CD | GLU | 116 | -12.739 | 40.728 | 110.027 | 1.00 | 43.38 | 0 |
| ATOM | 1093 | OE1 | GLU | 116 | -13.060 | 41.641 | 109.235 | 1.00 | 47.93 | 0 |
| ATOM | 1094 | OE2 | GLU | 116 | -13.274 | 40.599 | 111.147 | 1.00 | 48.80 | 0 |
| ATOM | 1095 | C | GLU | 116 | -8.213 | 39.902 | 111.358 | 1.00 | 2.00 | 0 |
| ATOM | 1096 | O | GLU | 116 | -8.296 | 39.287 | 112.424 | 1.00 | 32.95 | 0 |
| ATOM | 1097 | N | ASN | 117 | -7.054 | 40.067 | 110.712 | 1.00 | 2.00 | 0 |
| ATOM | 1099 | CA | ASN | 117 | -5.820 | 39.455 | 111.211 | 1.00 | 2.00 | 0 |
| ATOM | 1100 | CB | ASN | 117 | -5.457 | 38.220 | 110.375 | 1.00 | 6.12 | 0 |
| ATOM | 1101 | CG | ASN | 117 | -6.552 | 37.174 | 110.353 | 1.00 | 8.10 | 0 |
| ATOM | 1102 | OD1 | ASN | 117 | -7.584 | 37.351 | 109.700 | 1.00 | 17.57 | 0 |
| ATOM | 1103 | ND2 | ASN | 117 | -6.328 | 36.071 | 111.048 | 1.00 | 14.33 | 0 |
| ATOM | 1106 | C | ASN | 117 | -4.613 | 40.372 | 111.211 | 1.00 | 2.00 | 0 |
| ATOM | 1107 | O | ASN | 117 | -3.496 | 39.952 | 111.506 | 1.00 | 8.94 | 0 |
| ATOM | 1108 | N | PHE | 118 | -4.821 | 41.620 | 110.862 | 1.00 | 2.00 | 0 |
| ATOM | 1110 | CA | PHE | 118 | -3.715 | 42.559 | 110.815 | 1.00 | 2.00 | 0 |
| ATOM | 1111 | CB | PHE | 118 | -3.135 | 42.617 | 109.395 | 1.00 | 2.00 | 0 |
| ATOM | 1112 | CG | PHE | 118 | -1.902 | 43.471 | 109.256 | 1.00 | 2.00 | 0 |
| ATOM | 1113 | CD1 | PHE | 118 | -0.647 | 42.886 | 109.155 | 1.00 | 2.00 | 0 |
| ATOM | 1114 | CD2 | PHE | 118 | -1.995 | 44.857 | 109.177 | 1.00 | 2.00 | 0 |
| ATOM | 1115 | CE1 | PHE | 118 | 0.503 | 43.680 | 108.972 | 1.00 | 2.00 | 0 |
| ATOM | 1116 | CE2 | PHE | 118 | -0.857 | 45.647 | 108.997 | 1.00 | 2.00 | 0 |
| ATOM | 1117 | CZ | PHE | 118 | 0.393 | 45.060 | 108.894 | 1.00 | 2.00 | 0 |
| ATOM | 1118 | C | PHE | 118 | -4.392 | 43.854 | 111.194 | 1.00 | 2.00 | 0 |
| ATOM | 1119 | O | PHE | 118 | -5.384 | 44.259 | 110.576 | 1.00 | 2.00 | 0 |
| ATOM | 1120 | N | PHE | 119 | -3.874 | 44.483 | 112.240 | 1.00 | 12.11 | 0 |
| ATOM | 1122 | CA | PHE | 119 | -4.467 | 45.700 | 112.721 | 1.00 | 12.11 | 0 |
| ATOM | 1123 | CB | PHE | 119 | -5.174 | 45.400 | 114.022 | 1.00 | 2.00 | 0 |
| ATOM | 1124 | CG | PHE | 119 | -6.229 | 44.355 | 113.889 | 1.00 | 2.00 | 0 |
| ATOM | 1125 | CD1 | PHE | 119 | -5.903 | 43.008 | 113.975 | 1.00 | 2.00 | 0 |
| ATOM | 1126 | CD2 | PHE | 119 | -7.556 | 44.716 | 113.655 | 1.00 | 2.00 | 0 |
| ATOM | 1127 | CE1 | PHE | 119 | -6.881 | 42.035 | 113.829 | 1.00 | 2.00 | 0 |
| ATOM | 1128 | CE2 | PHE | 119 | -8.546 | 43.753 | 113.506 | 1.00 | 2.00 | 0 |
| ATOM | 1129 | CZ | PHE | 119 | -8.209 | 42.410 | 113.592 | 1.00 | 2.00 | 0 |
| ATOM | 1130 | C | PHE | 119 | -3.472 | 46.806 | 112.905 | 1.00 | 12.11 | 0 |
| ATOM | 1131 | O | PHE | 119 | -2.342 | 46.577 | 113.346 | 1.00 | 2.00 | 0 |
| ATOM | 1132 | N | LEU | 120 | -3.893 | 48.008 | 112.537 | 1.00 | 2.00 | 0 |
| ATOM | 1134 | CA | LEU | 120 | -3.043 | 49.179 | 112.672 | 1.00 | 2.00 | 0 |
| ATOM | 1135 | CB | LEU | 120 | -2.770 | 49.809 | 111.303 | 1.00 | 2.00 | 0 |
| ATOM | 1136 | CG | LEU | 120 | -2.127 | 48.910 | 110.259 | 1.00 | 2.00 | 0 |
| ATOM | 1137 | CD1 | LEU | 120 | -2.147 | 49.623 | 108.924 | 1.00 | 2.00 | 0 |
| ATOM | 1138 | CD2 | LEU | 120 | -0.731 | 48.539 | 110.685 | 1.00 | 2.00 | 0 |
| ATOM | 1139 | C | LEU | 120 | -3.766 | 50.176 | 113.559 | 1.00 | 2.00 | 0 |
| ATOM | 1140 | O | LEU | 120 | -4.963 | 50.401 | 113.375 | 1.00 | 2.00 | 0 |
| ATOM | 1141 | N | LEU | 121 | -3.069 | 50.730 | 114.542 | 1.00 | 2.00 | 0 |
| ATOM | 1143 | CA | LEU | 121 | -3.670 | 51.714 | 115.415 | 1.00 | 2.00 | 0 |
| ATOM | 1144 | CB | LEU | 121 | -3.351 | 51.428 | 116.890 | 1.00 | 2.00 | 0 |
| ATOM | 1145 | CG | LEU | 121 | -4.142 | 50.320 | 117.598 | 1.00 | 2.00 | 0 |
| ATOM | 1146 | CD1 | LEU | 121 | -3.648 | 50.150 | 119.012 | 1.00 | 2.00 | 0 |
| ATOM | 1147 | CD2 | LEU | 121 | -5.609 | 50.657 | 117.581 | 1.00 | 2.00 | 0 |
| ATOM | 1148 | C | LEU | 121 | -3.106 | 53.060 | 115.004 | 1.00 | 2.00 | 0 |
| ATOM | 1149 | O | LEU | 121 | -2.213 | 53.148 | 114.166 | 1.00 | 2.00 | 0 |
| ATOM | 1150 | N | ARG | 122 | -3.631 | 54.118 | 115.592 | 1.00 | 2.00 | 0 |
| ATOM | 1152 | CA | ARG | 122 | -3.162 | 55.434 | 115.251 | 1.00 | 2.00 | 0 |
| ATOM | 1153 | CB | ARG | 122 | -4.336 | 56.404 | 115.224 | 1.00 | 2.00 | 0 |
| ATOM | 1154 | CG | ARG | 122 | -4.047 | 57.765 | 114.619 | 1.00 | 2.00 | 0 |

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|---|---|---|---|---|---|---|---|---|---|---|
| ATOM | 1155 | CD | ARG | 122 | -5.298 | 58.565 | 114.683 | 1.00 | 2.00 | 0 |
| ATOM | 1156 | NE | ARG | 122 | -5.207 | 59.851 | 114.014 | 1.00 | 2.00 | 0 |
| ATOM | 1158 | CZ | ARG | 122 | -6.274 | 60.578 | 113.685 | 1.00 | 2.00 | 0 |
| ATOM | 1159 | NH1 | ARG | 122 | -7.512 | 60.131 | 113.956 | 1.00 | 2.00 | 0 |
| ATOM | 1162 | NH2 | ARG | 122 | -6.104 | 61.762 | 113.102 | 1.00 | 2.00 | 0 |
| ATOM | 1165 | C | ARG | 122 | -2.104 | 55.942 | 116.208 | 1.00 | 2.00 | 0 |
| ATOM | 1166 | O | ARG | 122 | -2.163 | 55.716 | 117.423 | 1.00 | 2.00 | 0 |
| ATOM | 1167 | N | GLY | 123 | -1.135 | 56.635 | 115.631 | 1.00 | 2.00 | 0 |
| ATOM | 1169 | CA | GLY | 123 | -0.073 | 57.235 | 116.399 | 1.00 | 2.00 | 0 |
| ATOM | 1170 | C | GLY | 123 | -0.205 | 58.730 | 116.198 | 1.00 | 2.00 | 0 |
| ATOM | 1171 | O | GLY | 123 | -0.865 | 59.177 | 115.262 | 1.00 | 86.19 | 0 |
| ATOM | 1172 | N | ASN | 124 | 0.437 | 59.508 | 117.058 | 1.00 | 2.00 | 0 |
| ATOM | 1174 | CA | ASN | 124 | 0.390 | 60.956 | 116.958 | 1.00 | 2.00 | 0 |
| ATOM | 1175 | CB | ASN | 124 | 1.003 | 61.584 | 118.199 | 1.00 | 4.11 | 0 |
| ATOM | 1176 | CG | ASN | 124 | 2.477 | 61.333 | 118.313 | 1.00 | 8.88 | 0 |
| ATOM | 1177 | OD1 | ASN | 124 | 2.940 | 60.187 | 118.486 | 1.00 | 8.54 | 0 |
| ATOM | 1178 | ND2 | ASN | 124 | 3.240 | 62.400 | 118.236 | 1.00 | 6.38 | 0 |
| ATOM | 1181 | C | ASN | 124 | 1.103 | 61.455 | 115.708 | 1.00 | 2.00 | 0 |
| ATOM | 1182 | O | ASN | 124 | 1.143 | 62.664 | 115.430 | 1.00 | 5.53 | 0 |
| ATOM | 1183 | N | HIS | 125 | 1.678 | 60.515 | 114.963 | 1.00 | 18.81 | 0 |
| ATOM | 1185 | CA | HIS | 125 | 2.372 | 60.815 | 113.723 | 1.00 | 19.06 | 0 |
| ATOM | 1186 | CB | HIS | 125 | 3.759 | 60.186 | 113.744 | 1.00 | 13.41 | 0 |
| ATOM | 1187 | CG | HIS | 125 | 4.790 | 61.072 | 114.362 | 1.00 | 13.65 | 0 |
| ATOM | 1188 | CD2 | HIS | 125 | 4.765 | 61.811 | 115.493 | 1.00 | 8.85 | 0 |
| ATOM | 1189 | ND1 | HIS | 125 | 6.006 | 61.322 | 113.772 | 1.00 | 14.49 | 0 |
| ATOM | 1191 | CE1 | HIS | 125 | 6.686 | 62.182 | 114.503 | 1.00 | 13.93 | 0 |
| ATOM | 1192 | NE2 | HIS | 125 | 5.954 | 62.496 | 115.554 | 1.00 | 12.46 | 0 |
| ATOM | 1194 | C | HIS | 125 | 1.555 | 60.338 | 112.523 | 1.00 | 16.39 | 0 |
| ATOM | 1195 | O | HIS | 125 | 2.090 | 59.905 | 111.513 | 1.00 | 13.34 | 0 |
| ATOM | 1196 | N | GLU | 126 | 0.241 | 60.382 | 112.686 | 1.00 | 2.00 | 0 |
| ATOM | 1198 | CA | GLU | 126 | -0.731 | 60.018 | 111.664 | 1.00 | 2.00 | 0 |
| ATOM | 1199 | CB | GLU | 126 | -1.462 | 58.725 | 112.050 | 1.00 | 2.00 | 0 |
| ATOM | 1200 | CG | GLU | 126 | -0.783 | 57.443 | 111.570 | 1.00 | 2.00 | 0 |
| ATOM | 1201 | CD | GLU | 126 | 0.578 | 57.217 | 112.190 | 1.00 | 2.00 | 0 |
| ATOM | 1202 | OE1 | GLU | 126 | 1.615 | 57.346 | 111.504 | 1.00 | 2.00 | 0 |
| ATOM | 1203 | OE2 | GLU | 126 | 0.610 | 56.898 | 113.385 | 1.00 | 2.00 | 0 |
| ATOM | 1204 | C | GLU | 126 | -1.683 | 61.211 | 111.705 | 1.00 | 2.00 | 0 |
| ATOM | 1205 | O | GLU | 126 | -2.903 | 61.073 | 111.837 | 1.00 | 2.00 | 0 |
| ATOM | 1206 | N | CYS | 127 | -1.097 | 62.392 | 111.578 | 1.00 | 2.00 | 0 |
| ATOM | 1208 | CA | CYS | 127 | -1.860 | 63.608 | 111.681 | 1.00 | 2.00 | 0 |
| ATOM | 1209 | CB | CYS | 127 | -2.037 | 63.960 | 113.167 | 1.00 | 26.08 | 0 |
| ATOM | 1210 | SG | CYS | 127 | -3.052 | 65.420 | 113.546 | 1.00 | 39.49 | 0 |
| ATOM | 1211 | C | CYS | 127 | -1.142 | 64.731 | 110.976 | 1.00 | 2.00 | 0 |
| ATOM | 1212 | O | CYS | 127 | 0.048 | 64.974 | 111.204 | 1.00 | 23.46 | 0 |
| ATOM | 1213 | N | ALA | 128 | -1.912 | 65.421 | 110.142 | 1.00 | 2.00 | 0 |
| ATOM | 1215 | CA | ALA | 128 | -1.489 | 66.551 | 109.335 | 1.00 | 2.00 | 0 |
| ATOM | 1216 | CB | ALA | 128 | -2.686 | 67.412 | 109.031 | 1.00 | 2.00 | 0 |
| ATOM | 1217 | C | ALA | 128 | -0.385 | 67.413 | 109.910 | 1.00 | 2.00 | 0 |
| ATOM | 1218 | O | ALA | 128 | 0.690 | 67.456 | 109.346 | 1.00 | 2.00 | 0 |
| ATOM | 1219 | N | SER | 129 | -0.649 | 68.097 | 111.021 | 1.00 | 2.00 | 0 |
| ATOM | 1221 | CA | SER | 129 | 0.331 | 68.981 | 111.675 | 1.00 | 2.00 | 0 |
| ATOM | 1222 | CB | SER | 129 | -0.288 | 69.580 | 112.937 | 1.00 | 28.29 | 0 |
| ATOM | 1223 | OG | SER | 129 | -0.836 | 68.562 | 113.760 | 1.00 | 32.64 | 0 |
| ATOM | 1225 | C | SER | 129 | 1.671 | 68.344 | 112.042 | 1.00 | 2.00 | 0 |
| ATOM | 1226 | O | SER | 129 | 2.669 | 69.048 | 112.186 | 1.00 | 24.43 | 0 |
| ATOM | 1227 | N | ILE | 130 | 1.687 | 67.027 | 112.226 | 1.00 | 2.00 | 0 |
| ATOM | 1229 | CA | ILE | 130 | 2.920 | 66.343 | 112.572 | 1.00 | 2.00 | 0 |
| ATOM | 1230 | CB | ILE | 130 | 2.671 | 65.177 | 113.588 | 1.00 | 2.00 | 0 |
| ATOM | 1231 | CG2 | ILE | 130 | 3.999 | 64.584 | 114.058 | 1.00 | 2.00 | 0 |
| ATOM | 1232 | CG1 | ILE | 130 | 2.012 | 65.717 | 114.854 | 1.00 | 2.00 | 0 |
| ATOM | 1233 | CD1 | ILE | 130 | 2.828 | 66.820 | 115.554 | 1.00 | 2.00 | 0 |
| ATOM | 1234 | C | ILE | 130 | 3.563 | 65.829 | 111.289 | 1.00 | 2.00 | 0 |
| ATOM | 1235 | O | ILE | 130 | 4.776 | 65.962 | 111.113 | 1.00 | 2.00 | 0 |
| ATOM | 1236 | N | ASN | 131 | 2.751 | 65.253 | 110.397 | 1.00 | 15.50 | 0 |
| ATOM | 1238 | CA | ASN | 131 | 3.209 | 64.747 | 109.091 | 1.00 | 12.35 | 0 |
| ATOM | 1239 | CB | ASN | 131 | 2.027 | 64.290 | 108.231 | 1.00 | 2.00 | 0 |
| ATOM | 1240 | CG | ASN | 131 | 1.487 | 62.929 | 108.632 | 1.00 | 2.00 | 0 |
| ATOM | 1241 | OD1 | ASN | 131 | 1.712 | 62.438 | 109.750 | 1.00 | 2.00 | 0 |

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|---|---|---|---|---|---|---|---|---|---|---|
| ATOM | 1242 | ND2 | ASN | 131 | 0.745 | 62.313 | 107.718 | 1.00 | 2.00 | 0 |
| ATOM | 1245 | C | ASN | 131 | 3.849 | 65.914 | 108.374 | 1.00 | 28.24 | 0 |
| ATOM | 1246 | O | ASN | 131 | 5.001 | 65.854 | 107.951 | 1.00 | 2.00 | 0 |
| ATOM | 1247 | N | ARG | 132 | 3.051 | 66.971 | 108.255 | 1.00 | 2.00 | 0 |
| ATOM | 1249 | CA | ARG | 132 | 3.386 | 68.234 | 107.627 | 1.00 | 2.00 | 0 |
| ATOM | 1250 | CB | ARG | 132 | 2.327 | 69.269 | 108.006 | 1.00 | 22.25 | 0 |
| ATOM | 1251 | CG | ARG | 132 | 2.505 | 70.673 | 107.477 | 1.00 | 26.48 | 0 |
| ATOM | 1252 | CD | ARG | 132 | 2.505 | 70.734 | 105.962 | 1.00 | 27.28 | 0 |
| ATOM | 1253 | NE | ARG | 132 | 3.849 | 70.533 | 105.434 | 1.00 | 36.02 | 0 |
| ATOM | 1255 | CZ | ARG | 132 | 4.577 | 71.479 | 104.852 | 1.00 | 34.03 | 0 |
| ATOM | 1256 | NH1 | ARG | 132 | 4.080 | 72.697 | 104.711 | 1.00 | 30.29 | 0 |
| ATOM | 1259 | NH2 | ARG | 132 | 5.808 | 71.211 | 104.424 | 1.00 | 37.77 | 0 |
| ATOM | 1262 | C | ARG | 132 | 4.768 | 68.731 | 107.990 | 1.00 | 2.00 | 0 |
| ATOM | 1263 | O | ARG | 132 | 5.359 | 69.477 | 107.225 | 1.00 | 27.60 | 0 |
| ATOM | 1264 | N | ILE | 133 | 5.314 | 68.324 | 109.127 | 1.00 | 2.00 | 0 |
| ATOM | 1266 | CA | ILE | 133 | 6.652 | 68.801 | 109.457 | 1.00 | 2.00 | 0 |
| ATOM | 1267 | CB | ILE | 133 | 6.652 | 69.644 | 110.746 | 1.00 | 20.12 | 0 |
| ATOM | 1268 | CG2 | ILE | 133 | 6.215 | 71.055 | 110.441 | 1.00 | 19.34 | 0 |
| ATOM | 1269 | CG1 | ILE | 133 | 5.761 | 68.999 | 111.800 | 1.00 | 21.76 | 0 |
| ATOM | 1270 | CD1 | ILE | 133 | 5.687 | 69.792 | 113.065 | 1.00 | 22.74 | 0 |
| ATOM | 1271 | C | ILE | 133 | 7.794 | 67.779 | 109.553 | 1.00 | 2.00 | 0 |
| ATOM | 1272 | O | ILE | 133 | 8.915 | 68.073 | 109.127 | 1.00 | 21.74 | 0 |
| ATOM | 1273 | N | TYR | 134 | 7.521 | 66.583 | 110.080 | 1.00 | 2.00 | 0 |
| ATOM | 1275 | CA | TYR | 134 | 8.571 | 65.567 | 110.270 | 1.00 | 2.00 | 0 |
| ATOM | 1276 | CB | TYR | 134 | 8.330 | 64.766 | 111.561 | 1.00 | 27.01 | 0 |
| ATOM | 1277 | CG | TYR | 134 | 8.270 | 65.648 | 112.767 | 1.00 | 19.94 | 0 |
| ATOM | 1278 | CD1 | TYR | 134 | 7.092 | 65.789 | 113.486 | 1.00 | 23.86 | 0 |
| ATOM | 1279 | CE1 | TYR | 134 | 7.016 | 66.651 | 114.557 | 1.00 | 24.86 | 0 |
| ATOM | 1280 | CD2 | TYR | 134 | 9.380 | 66.392 | 113.160 | 1.00 | 24.55 | 0 |
| ATOM | 1281 | CE2 | TYR | 134 | 9.312 | 67.254 | 114.228 | 1.00 | 23.33 | 0 |
| ATOM | 1282 | CZ | TYR | 134 | 8.128 | 67.384 | 114.925 | 1.00 | 28.93 | 0 |
| ATOM | 1283 | OH | TYR | 134 | 8.043 | 68.259 | 115.984 | 1.00 | 27.73 | 0 |
| ATOM | 1285 | C | TYR | 134 | 8.823 | 64.606 | 109.139 | 1.00 | 2.00 | 0 |
| ATOM | 1286 | O | TYR | 134 | 8.986 | 63.404 | 109.368 | 1.00 | 24.62 | 0 |
| ATOM | 1287 | N | GLY | 135 | 8.847 | 65.127 | 107.922 | 1.00 | 11.68 | 0 |
| ATOM | 1289 | CA | GLY | 135 | 9.134 | 64.275 | 106.787 | 1.00 | 10.40 | 0 |
| ATOM | 1290 | C | GLY | 135 | 8.028 | 63.772 | 105.882 | 1.00 | 9.03 | 0 |
| ATOM | 1291 | O | GLY | 135 | 8.010 | 64.127 | 104.713 | 1.00 | 20.70 | 0 |
| ATOM | 1292 | N | PHE | 136 | 7.110 | 62.963 | 106.393 | 1.00 | 2.00 | 0 |
| ATOM | 1294 | CA | PHE | 136 | 6.062 | 62.412 | 105.549 | 1.00 | 2.00 | 0 |
| ATOM | 1295 | CB | PHE | 136 | 4.951 | 61.757 | 106.347 | 1.00 | 2.00 | 0 |
| ATOM | 1296 | CG | PHE | 136 | 4.091 | 60.831 | 105.524 | 1.00 | 2.00 | 0 |
| ATOM | 1297 | CD1 | PHE | 136 | 4.664 | 59.734 | 104.870 | 1.00 | 2.00 | 0 |
| ATOM | 1298 | CD2 | PHE | 136 | 2.713 | 61.036 | 105.424 | 1.00 | 2.00 | 0 |
| ATOM | 1299 | CE1 | PHE | 136 | 3.882 | 58.846 | 104.131 | 1.00 | 2.00 | 0 |
| ATOM | 1300 | CE2 | PHE | 136 | 1.915 | 60.155 | 104.688 | 1.00 | 2.00 | 0 |
| ATOM | 1301 | CZ | PHE | 136 | 2.507 | 59.050 | 104.037 | 1.00 | 2.00 | 0 |
| ATOM | 1302 | C | PHE | 136 | 5.421 | 63.358 | 104.563 | 1.00 | 2.00 | 0 |
| ATOM | 1303 | O | PHE | 136 | 5.121 | 62.926 | 103.445 | 1.00 | 2.00 | 0 |
| ATOM | 1304 | N | TYR | 137 | 5.199 | 64.616 | 104.940 | 1.00 | 2.00 | 0 |
| ATOM | 1306 | CA | TYR | 137 | 4.606 | 65.530 | 103.977 | 1.00 | 2.00 | 0 |
| ATOM | 1307 | CB | TYR | 137 | 4.243 | 66.859 | 104.598 | 1.00 | 2.00 | 0 |
| ATOM | 1308 | CG | TYR | 137 | 3.886 | 67.921 | 103.564 | 1.00 | 2.00 | 0 |
| ATOM | 1309 | CD1 | TYR | 137 | 2.550 | 68.203 | 103.257 | 1.00 | 2.00 | 0 |
| ATOM | 1310 | CE1 | TYR | 137 | 2.228 | 69.196 | 102.327 | 1.00 | 2.00 | 0 |
| ATOM | 1311 | CD2 | TYR | 137 | 4.893 | 68.666 | 102.901 | 1.00 | 2.00 | 0 |
| ATOM | 1312 | CE2 | TYR | 137 | 4.576 | 69.644 | 101.985 | 1.00 | 2.00 | 0 |
| ATOM | 1313 | CZ | TYR | 137 | 3.247 | 69.903 | 101.707 | 1.00 | 2.00 | 0 |
| ATOM | 1314 | OH | TYR | 137 | 2.920 | 70.893 | 100.823 | 1.00 | 2.00 | 0 |
| ATOM | 1316 | C | TYR | 137 | 5.566 | 65.785 | 102.822 | 1.00 | 2.00 | 0 |
| ATOM | 1317 | O | TYR | 137 | 5.187 | 65.669 | 101.646 | 1.00 | 2.00 | 0 |
| ATOM | 1318 | N | ASP | 138 | 6.802 | 66.153 | 103.155 | 1.00 | 2.00 | 0 |
| ATOM | 1320 | CA | ASP | 138 | 7.822 | 66.439 | 102.147 | 1.00 | 2.00 | 0 |
| ATOM | 1321 | CB | ASP | 138 | 9.102 | 66.971 | 102.810 | 1.00 | 28.59 | 0 |
| ATOM | 1322 | CG | ASP | 138 | 8.832 | 68.173 | 103.705 | 1.00 | 31.85 | 0 |
| ATOM | 1323 | OD1 | ASP | 138 | 8.999 | 69.327 | 103.255 | 1.00 | 34.04 | 0 |
| ATOM | 1324 | OD2 | ASP | 138 | 8.432 | 67.963 | 104.867 | 1.00 | 31.26 | 0 |
| ATOM | 1325 | C | ASP | 138 | 8.118 | 65.203 | 101.308 | 1.00 | 2.00 | 0 |

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|---|---|---|---|---|---|---|---|---|---|---|
| ATOM | 1326 | O | ASP | 138 | 8.322 | 65.309 | 100.102 | 1.00 | 27.39 | 0 |
| ATOM | 1327 | N | GLU | 139 | 8.097 | 64.030 | 101.926 | 1.00 | 31.40 | 0 |
| ATOM | 1329 | CA | GLU | 139 | 8.366 | 62.797 | 101.200 | 1.00 | 28.32 | 0 |
| ATOM | 1330 | CB | GLU | 139 | 8.380 | 61.608 | 102.149 | 1.00 | 2.00 | 0 |
| ATOM | 1331 | CG | GLU | 139 | 8.965 | 60.361 | 101.526 | 1.00 | 4.78 | 0 |
| ATOM | 1332 | CD | GLU | 139 | 9.167 | 59.231 | 102.525 | 1.00 | 3.01 | 0 |
| ATOM | 1333 | OE1 | GLU | 139 | 9.135 | 58.050 | 102.087 | 1.00 | 2.00 | 0 |
| ATOM | 1334 | OE2 | GLU | 139 | 9.372 | 59.518 | 103.738 | 1.00 | 4.61 | 0 |
| ATOM | 1335 | C | GLU | 139 | 7.323 | 62.572 | 100.117 | 1.00 | 30.47 | 0 |
| ATOM | 1336 | O | GLU | 139 | 7.660 | 62.419 | 98.941 | 1.00 | 2.00 | 0 |
| ATOM | 1337 | N | CYS | 140 | 6.055 | 62.553 | 100.511 | 1.00 | 12.32 | 0 |
| ATOM | 1339 | CA | CYS | 140 | 4.981 | 62.355 | 99.553 | 1.00 | 3.99 | 0 |
| ATOM | 1340 | CB | CYS | 140 | 3.625 | 62.543 | 100.221 | 1.00 | 18.56 | 0 |
| ATOM | 1341 | SG | CYS | 140 | 3.313 | 61.308 | 101.477 | 1.00 | 23.54 | 0 |
| ATOM | 1342 | C | CYS | 140 | 5.128 | 63.346 | 98.416 | 1.00 | 12.32 | 0 |
| ATOM | 1343 | O | CYS | 140 | 5.117 | 62.961 | 97.257 | 1.00 | 21.26 | 0 |
| ATOM | 1344 | N | LYS | 141 | 5.305 | 64.616 | 98.763 | 1.00 | 41.55 | 0 |
| ATOM | 1346 | CA | LYS | 141 | 5.446 | 65.696 | 97.786 | 1.00 | 40.86 | 0 |
| ATOM | 1347 | CB | LYS | 141 | 5.655 | 67.023 | 98.531 | 1.00 | 38.66 | 0 |
| ATOM | 1348 | CG | LYS | 141 | 5.853 | 68.246 | 97.646 | 1.00 | 32.19 | 0 |
| ATOM | 1349 | CD | LYS | 141 | 5.886 | 69.522 | 98.468 | 1.00 | 35.28 | 0 |
| ATOM | 1350 | CE | LYS | 141 | 5.895 | 70.750 | 97.584 | 1.00 | 36.09 | 0 |
| ATOM | 1351 | NZ | LYS | 141 | 5.552 | 71.948 | 98.380 | 1.00 | 40.44 | 0 |
| ATOM | 1355 | C | LYS | 141 | 6.586 | 65.467 | 96.791 | 1.00 | 40.27 | 0 |
| ATOM | 1356 | O | LYS | 141 | 6.431 | 65.642 | 95.582 | 1.00 | 28.60 | 0 |
| ATOM | 1357 | N | ARG | 142 | 7.731 | 65.073 | 97.319 | 1.00 | 23.84 | 0 |
| ATOM | 1359 | CA | ARG | 142 | 8.912 | 64.834 | 96.512 | 1.00 | 23.84 | 0 |
| ATOM | 1360 | CB | ARG | 142 | 10.097 | 64.566 | 97.444 | 1.00 | 22.75 | 0 |
| ATOM | 1361 | CG | ARG | 142 | 11.368 | 64.101 | 96.778 | 1.00 | 24.10 | 0 |
| ATOM | 1362 | CD | ARG | 142 | 12.474 | 64.073 | 97.799 | 1.00 | 33.58 | 0 |
| ATOM | 1363 | NE | ARG | 142 | 12.099 | 63.283 | 98.963 | 1.00 | 37.62 | 0 |
| ATOM | 1365 | CZ | ARG | 142 | 12.464 | 62.018 | 99.150 | 1.00 | 46.30 | 0 |
| ATOM | 1366 | NH1 | ARG | 142 | 13.224 | 61.404 | 98.249 | 1.00 | 44.23 | 0 |
| ATOM | 1369 | NH2 | ARG | 142 | 12.060 | 61.363 | 100.234 | 1.00 | 42.22 | 0 |
| ATOM | 1372 | C | ARG | 142 | 8.732 | 63.689 | 95.519 | 1.00 | 23.84 | 0 |
| ATOM | 1373 | O | ARG | 142 | 8.995 | 63.838 | 94.330 | 1.00 | 24.93 | 0 |
| ATOM | 1374 | N | ARG | 143 | 8.268 | 62.550 | 95.999 | 1.00 | 2.00 | 0 |
| ATOM | 1376 | CA | ARG | 143 | 8.104 | 61.413 | 95.125 | 1.00 | 2.00 | 0 |
| ATOM | 1377 | CB | ARG | 143 | 8.267 | 60.134 | 95.941 | 1.00 | 2.86 | 0 |
| ATOM | 1378 | CG | ARG | 143 | 9.686 | 59.941 | 96.455 | 1.00 | 2.86 | 0 |
| ATOM | 1379 | CD | ARG | 143 | 9.792 | 58.874 | 97.530 | 1.00 | 8.64 | 0 |
| ATOM | 1380 | NE | ARG | 143 | 9.490 | 57.527 | 97.049 | 1.00 | 4.03 | 0 |
| ATOM | 1382 | CZ | ARG | 143 | 9.492 | 56.439 | 97.816 | 1.00 | 6.91 | 0 |
| ATOM | 1383 | NH1 | ARG | 143 | 9.782 | 56.527 | 99.115 | 1.00 | 7.13 | 0 |
| ATOM | 1386 | NH2 | ARG | 143 | 9.203 | 55.257 | 97.287 | 1.00 | 12.97 | 0 |
| ATOM | 1389 | C | ARG | 143 | 6.796 | 61.411 | 94.367 | 1.00 | 2.00 | 0 |
| ATOM | 1390 | O | ARG | 143 | 6.707 | 60.818 | 93.295 | 1.00 | 12.04 | 0 |
| ATOM | 1391 | N | TYR | 144 | 5.791 | 62.097 | 94.897 | 1.00 | 2.00 | 0 |
| ATOM | 1393 | CA | TYR | 144 | 4.459 | 62.120 | 94.274 | 1.00 | 2.00 | 0 |
| ATOM | 1394 | CB | TYR | 144 | 3.509 | 61.150 | 95.021 | 1.00 | 2.00 | 0 |
| ATOM | 1395 | CG | TYR | 144 | 3.902 | 59.689 | 94.953 | 1.00 | 2.00 | 0 |
| ATOM | 1396 | CD1 | TYR | 144 | 4.946 | 59.203 | 95.716 | 1.00 | 2.00 | 0 |
| ATOM | 1397 | CE1 | TYR | 144 | 5.336 | 57.885 | 95.635 | 1.00 | 2.00 | 0 |
| ATOM | 1398 | CD2 | TYR | 144 | 3.248 | 58.804 | 94.102 | 1.00 | 2.00 | 0 |
| ATOM | 1399 | CE2 | TYR | 144 | 3.633 | 57.483 | 94.017 | 1.00 | 2.00 | 0 |
| ATOM | 1400 | CZ | TYR | 144 | 4.683 | 57.034 | 94.786 | 1.00 | 2.00 | 0 |
| ATOM | 1401 | OH | TYR | 144 | 5.113 | 55.738 | 94.703 | 1.00 | 2.00 | 0 |
| ATOM | 1403 | C | TYR | 144 | 3.789 | 63.502 | 94.169 | 1.00 | 2.00 | 0 |
| ATOM | 1404 | O | TYR | 144 | 4.129 | 64.316 | 93.297 | 1.00 | 2.00 | 0 |
| ATOM | 1405 | N | ASN | 145 | 2.827 | 63.750 | 95.058 | 1.00 | 2.00 | 0 |
| ATOM | 1407 | CA | ASN | 145 | 2.081 | 65.000 | 95.083 | 1.00 | 2.00 | 0 |
| ATOM | 1408 | CB | ASN | 145 | 1.159 | 65.078 | 93.867 | 1.00 | 7.57 | 0 |
| ATOM | 1409 | CG | ASN | 145 | 0.255 | 63.861 | 93.748 | 1.00 | 5.76 | 0 |
| ATOM | 1410 | OD1 | ASN | 145 | -0.823 | 63.826 | 94.329 | 1.00 | 9.42 | 0 |
| ATOM | 1411 | ND2 | ASN | 145 | 0.702 | 62.851 | 93.007 | 1.00 | 5.88 | 0 |
| ATOM | 1414 | C | ASN | 145 | 1.229 | 65.137 | 96.354 | 1.00 | 2.00 | 0 |
| ATOM | 1415 | O | ASN | 145 | 0.760 | 64.143 | 96.938 | 1.00 | 11.61 | 0 |
| ATOM | 1416 | N | ILE | 146 | 1.001 | 66.391 | 96.737 | 1.00 | 2.00 | 0 |

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|---|---|---|---|---|---|---|---|---|---|---|
| ATOM | 1418 | CA | ILE | 146 | 0.217 | 66.745 | 97.901 | 1.00 | 2.00 | 0 |
| ATOM | 1419 | CB | ILE | 146 | 0.168 | 68.278 | 98.048 | 1.00 | 2.00 | 0 |
| ATOM | 1420 | CG2 | ILE | 146 | -0.607 | 68.690 | 99.278 | 1.00 | 2.00 | 0 |
| ATOM | 1421 | CG1 | ILE | 146 | 1.591 | 68.798 | 98.201 | 1.00 | 2.00 | 0 |
| ATOM | 1422 | CD1 | ILE | 146 | 1.679 | 70.270 | 98.360 | 1.00 | 2.00 | 0 |
| ATOM | 1423 | C | ILE | 146 | -1.181 | 66.143 | 97.851 | 1.00 | 2.00 | 0 |
| ATOM | 1424 | O | ILE | 146 | -1.805 | 65.927 | 98.881 | 1.00 | 2.00 | 0 |
| ATOM | 1425 | N | LYS | 147 | -1.680 | 65.839 | 96.668 | 1.00 | 2.00 | 0 |
| ATOM | 1427 | CA | LYS | 147 | -3.000 | 65.241 | 96.594 | 1.00 | 2.00 | 0 |
| ATOM | 1428 | CB | LYS | 147 | -3.412 | 65.007 | 95.131 | 1.00 | 15.32 | 0 |
| ATOM | 1429 | CG | LYS | 147 | -4.880 | 64.643 | 94.902 | 1.00 | 21.64 | 0 |
| ATOM | 1430 | CD | LYS | 147 | -5.024 | 63.248 | 94.280 | 1.00 | 29.48 | 0 |
| ATOM | 1431 | CE | LYS | 147 | -4.704 | 62.128 | 95.300 | 1.00 | 25.79 | 0 |
| ATOM | 1432 | NZ | LYS | 147 | -4.388 | 60.777 | 94.716 | 1.00 | 22.31 | 0 |
| ATOM | 1436 | C | LYS | 147 | -2.864 | 63.928 | 97.345 | 1.00 | 2.00 | 0 |
| ATOM | 1437 | O | LYS | 147 | -3.652 | 63.630 | 98.233 | 1.00 | 8.30 | 0 |
| ATOM | 1438 | N | LEU | 148 | -1.815 | 63.180 | 97.023 | 1.00 | 9.36 | 0 |
| ATOM | 1440 | CA | LEU | 148 | -1.582 | 61.892 | 97.651 | 1.00 | 9.36 | 0 |
| ATOM | 1441 | CB | LEU | 148 | -0.360 | 61.202 | 97.037 | 1.00 | 2.00 | 0 |
| ATOM | 1442 | CG | LEU | 148 | -0.207 | 59.721 | 97.415 | 1.00 | 2.00 | 0 |
| ATOM | 1443 | CD1 | LEU | 148 | -1.398 | 58.910 | 96.924 | 1.00 | 2.00 | 0 |
| ATOM | 1444 | CD2 | LEU | 148 | 1.078 | 59.168 | 96.835 | 1.00 | 2.00 | 0 |
| ATOM | 1445 | C | LEU | 148 | -1.423 | 62.040 | 99.157 | 1.00 | 9.36 | 0 |
| ATOM | 1446 | O | LEU | 148 | -2.097 | 61.351 | 99.899 | 1.00 | 2.00 | 0 |
| ATOM | 1447 | N | TRP | 149 | -0.555 | 62.943 | 99.611 | 1.00 | 2.00 | 0 |
| ATOM | 1449 | CA | TRP | 149 | -0.360 | 63.166 | 101.042 | 1.00 | 2.00 | 0 |
| ATOM | 1450 | CB | TRP | 149 | 0.559 | 64.359 | 101.276 | 1.00 | 9.48 | 0 |
| ATOM | 1451 | CG | TRP | 149 | 0.690 | 64.767 | 102.748 | 1.00 | 13.35 | 0 |
| ATOM | 1452 | CD2 | TRP | 149 | 0.095 | 65.915 | 103.387 | 1.00 | 9.36 | 0 |
| ATOM | 1453 | CE2 | TRP | 149 | 0.512 | 65.907 | 104.725 | 1.00 | 12.67 | 0 |
| ATOM | 1454 | CE3 | TRP | 149 | -0.751 | 66.946 | 102.951 | 1.00 | 9.36 | 0 |
| ATOM | 1455 | CD1 | TRP | 149 | 1.415 | 64.135 | 103.713 | 1.00 | 12.84 | 0 |
| ATOM | 1456 | NE1 | TRP | 149 | 1.315 | 64.811 | 104.895 | 1.00 | 14.40 | 0 |
| ATOM | 1458 | CZ2 | TRP | 149 | 0.119 | 66.880 | 105.632 | 1.00 | 10.82 | 0 |
| ATOM | 1459 | CZ3 | TRP | 149 | -1.138 | 67.912 | 103.858 | 1.00 | 10.25 | 0 |
| ATOM | 1460 | CH2 | TRP | 149 | -0.702 | 67.870 | 105.182 | 1.00 | 21.34 | 0 |
| ATOM | 1461 | C | TRP | 149 | -1.712 | 63.427 | 101.707 | 1.00 | 2.00 | 0 |
| ATOM | 1462 | O | TRP | 149 | -2.095 | 62.726 | 102.647 | 1.00 | 9.36 | 0 |
| ATOM | 1463 | N | LYS | 150 | -2.429 | 64.434 | 101.216 | 1.00 | 2.00 | 0 |
| ATOM | 1465 | CA | LYS | 150 | -3.756 | 64.777 | 101.725 | 1.00 | 2.00 | 0 |
| ATOM | 1466 | CB | LYS | 150 | -4.392 | 65.810 | 100.819 | 1.00 | 25.82 | 0 |
| ATOM | 1467 | CG | LYS | 150 | -3.695 | 67.135 | 100.844 | 1.00 | 27.78 | 0 |
| ATOM | 1468 | CD | LYS | 150 | -4.145 | 67.981 | 99.676 | 1.00 | 24.78 | 0 |
| ATOM | 1469 | CE | LYS | 150 | -4.236 | 69.442 | 100.053 | 1.00 | 28.33 | 0 |
| ATOM | 1470 | NZ | LYS | 150 | -5.243 | 69.673 | 101.132 | 1.00 | 35.49 | 0 |
| ATOM | 1474 | C | LYS | 150 | -4.661 | 63.536 | 101.786 | 1.00 | 2.00 | 0 |
| ATOM | 1475 | O | LYS | 150 | -5.468 | 63.397 | 102.701 | 1.00 | 28.71 | 0 |
| ATOM | 1476 | N | THR | 151 | -4.525 | 62.638 | 100.809 | 1.00 | 2.00 | 0 |
| ATOM | 1478 | CA | THR | 151 | -5.315 | 61.403 | 100.758 | 1.00 | 2.00 | 0 |
| ATOM | 1479 | CB | THR | 151 | -5.111 | 60.670 | 99.408 | 1.00 | 18.71 | 0 |
| ATOM | 1480 | OG1 | THR | 151 | -5.491 | 61.532 | 98.332 | 1.00 | 21.97 | 0 |
| ATOM | 1482 | CG2 | THR | 151 | -5.964 | 59.434 | 99.332 | 1.00 | 19.85 | 0 |
| ATOM | 1483 | C | THR | 151 | -4.920 | 60.487 | 101.925 | 1.00 | 2.00 | 0 |
| ATOM | 1484 | O | THR | 151 | -5.760 | 59.773 | 102.489 | 1.00 | 14.71 | 0 |
| ATOM | 1485 | N | PHE | 152 | -3.645 | 60.529 | 102.297 | 1.00 | 2.00 | 0 |
| ATOM | 1487 | CA | PHE | 152 | -3.161 | 59.729 | 103.398 | 1.00 | 2.00 | 0 |
| ATOM | 1488 | CB | PHE | 152 | -1.638 | 59.759 | 103.502 | 1.00 | 13.78 | 0 |
| ATOM | 1489 | CG | PHE | 152 | -0.956 | 58.586 | 102.830 | 1.00 | 13.78 | 0 |
| ATOM | 1490 | CD1 | PHE | 152 | 0.034 | 58.792 | 101.864 | 1.00 | 13.78 | 0 |
| ATOM | 1491 | CD2 | PHE | 152 | -1.289 | 57.277 | 103.178 | 1.00 | 13.78 | 0 |
| ATOM | 1492 | CE1 | PHE | 152 | 0.679 | 57.717 | 101.260 | 1.00 | 13.78 | 0 |
| ATOM | 1493 | CE2 | PHE | 152 | -0.648 | 56.194 | 102.578 | 1.00 | 13.78 | 0 |
| ATOM | 1494 | CZ | PHE | 152 | 0.340 | 56.417 | 101.617 | 1.00 | 13.78 | 0 |
| ATOM | 1495 | C | PHE | 152 | -3.767 | 60.246 | 104.673 | 1.00 | 2.00 | 0 |
| ATOM | 1496 | O | PHE | 152 | -4.380 | 59.470 | 105.397 | 1.00 | 13.78 | 0 |
| ATOM | 1497 | N | THR | 153 | -3.657 | 61.547 | 104.944 | 1.00 | 2.00 | 0 |
| ATOM | 1499 | CA | THR | 153 | -4.217 | 62.064 | 106.192 | 1.00 | 2.00 | 0 |
| ATOM | 1500 | CB | THR | 153 | -4.166 | 63.604 | 106.318 | 1.00 | 19.49 | 0 |

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|---|---|---|---|---|---|---|---|---|---|---|
| ATOM | 1501 | OG1 | THR | 153 | -4.912 | 64.207 | 105.265 | 1.00 | 24.34 | 0 |
| ATOM | 1503 | CG2 | THR | 153 | -2.739 | 64.095 | 106.293 | 1.00 | 23.93 | 0 |
| ATOM | 1504 | C | THR | 153 | -5.653 | 61.607 | 106.348 | 1.00 | 2.00 | 0 |
| ATOM | 1505 | O | THR | 153 | -6.054 | 61.158 | 107.414 | 1.00 | 29.22 | 0 |
| ATOM | 1506 | N | ASP | 154 | -6.415 | 61.667 | 105.276 | 1.00 | 2.00 | 0 |
| ATOM | 1508 | CA | ASP | 154 | -7.801 | 61.250 | 105.332 | 1.00 | 2.00 | 0 |
| ATOM | 1509 | CB | ASP | 154 | -8.442 | 61.393 | 103.945 | 1.00 | 21.48 | 0 |
| ATOM | 1510 | CG | ASP | 154 | -9.965 | 61.345 | 103.987 | 1.00 | 21.21 | 0 |
| ATOM | 1511 | OD1 | ASP | 154 | -10.576 | 61.750 | 102.971 | 1.00 | 27.37 | 0 |
| ATOM | 1512 | OD2 | ASP | 154 | -10.548 | 60.912 | 105.018 | 1.00 | 20.95 | 0 |
| ATOM | 1513 | C | ASP | 154 | -7.889 | 59.806 | 105.801 | 1.00 | 2.00 | 0 |
| ATOM | 1514 | O | ASP | 154 | -8.783 | 59.444 | 106.569 | 1.00 | 11.19 | 0 |
| ATOM | 1515 | N | CYS | 155 | -6.968 | 58.981 | 105.319 | 1.00 | 2.00 | 0 |
| ATOM | 1517 | CA | CYS | 155 | -6.951 | 57.571 | 105.691 | 1.00 | 2.00 | 0 |
| ATOM | 1518 | CB | CYS | 155 | -5.904 | 56.822 | 104.865 | 1.00 | 2.00 | 0 |
| ATOM | 1519 | SG | CYS | 155 | -5.770 | 55.072 | 105.254 | 1.00 | 2.00 | 0 |
| ATOM | 1520 | C | CYS | 155 | -6.627 | 57.479 | 107.178 | 1.00 | 2.00 | 0 |
| ATOM | 1521 | O | CYS | 155 | -7.267 | 56.741 | 107.931 | 1.00 | 2.00 | 0 |
| ATOM | 1522 | N | PHE | 156 | -5.641 | 58.273 | 107.583 | 1.00 | 8.58 | 0 |
| ATOM | 1524 | CA | PHE | 156 | -5.172 | 58.366 | 108.954 | 1.00 | 8.58 | 0 |
| ATOM | 1525 | CB | PHE | 156 | -4.056 | 59.409 | 109.018 | 1.00 | 2.00 | 0 |
| ATOM | 1526 | CG | PHE | 156 | -2.766 | 58.945 | 108.437 | 1.00 | 2.00 | 0 |
| ATOM | 1527 | CD1 | PHE | 156 | -2.537 | 57.585 | 108.206 | 1.00 | 2.00 | 0 |
| ATOM | 1528 | CD2 | PHE | 156 | -1.756 | 59.847 | 108.160 | 1.00 | 2.00 | 0 |
| ATOM | 1529 | CE1 | PHE | 156 | -1.309 | 57.130 | 107.710 | 1.00 | 2.00 | 0 |
| ATOM | 1530 | CE2 | PHE | 156 | -0.518 | 59.400 | 107.662 | 1.00 | 2.00 | 0 |
| ATOM | 1531 | CZ | PHE | 156 | -0.295 | 58.039 | 107.439 | 1.00 | 2.00 | 0 |
| ATOM | 1532 | C | PHE | 156 | -6.287 | 58.743 | 109.931 | 1.00 | 8.58 | 0 |
| ATOM | 1533 | O | PHE | 156 | -6.463 | 58.119 | 110.974 | 1.00 | 2.00 | 0 |
| ATOM | 1534 | N | ASN | 157 | -7.055 | 59.758 | 109.572 | 1.00 | 2.00 | 0 |
| ATOM | 1536 | CA | ASN | 157 | -8.144 | 60.233 | 110.405 | 1.00 | 2.00 | 0 |
| ATOM | 1537 | CB | ASN | 157 | -8.811 | 61.475 | 109.779 | 1.00 | 2.00 | 0 |
| ATOM | 1538 | CG | ASN | 157 | -7.861 | 62.661 | 109.577 | 1.00 | 2.00 | 0 |
| ATOM | 1539 | OD1 | ASN | 157 | -8.226 | 63.629 | 108.922 | 1.00 | 2.00 | 0 |
| ATOM | 1540 | ND2 | ASN | 157 | -6.669 | 62.601 | 110.143 | 1.00 | 2.00 | 0 |
| ATOM | 1543 | C | ASN | 157 | -9.230 | 59.179 | 110.631 | 1.00 | 2.00 | 0 |
| ATOM | 1544 | O | ASN | 157 | -10.242 | 59.489 | 111.240 | 1.00 | 2.00 | 0 |
| ATOM | 1545 | N | CYS | 158 | -9.064 | 57.962 | 110.120 | 1.00 | 2.00 | 0 |
| ATOM | 1547 | CA | CYS | 158 | -10.074 | 56.914 | 110.304 | 1.00 | 2.00 | 0 |
| ATOM | 1548 | CB | CYS | 158 | -10.751 | 56.567 | 108.970 | 1.00 | 2.00 | 0 |
| ATOM | 1549 | SG | CYS | 158 | -11.898 | 57.864 | 108.331 | 1.00 | 2.00 | 0 |
| ATOM | 1550 | C | CYS | 158 | -9.482 | 55.665 | 110.924 | 1.00 | 2.00 | 0 |
| ATOM | 1551 | O | CYS | 158 | -10.148 | 54.648 | 111.049 | 1.00 | 2.00 | 0 |
| ATOM | 1552 | N | LEU | 159 | -8.216 | 55.772 | 111.304 | 1.00 | 2.00 | 0 |
| ATOM | 1554 | CA | LEU | 159 | -7.433 | 54.714 | 111.945 | 1.00 | 2.00 | 0 |
| ATOM | 1555 | CB | LEU | 159 | -5.985 | 55.219 | 112.037 | 1.00 | 2.00 | 0 |
| ATOM | 1556 | CG | LEU | 159 | -4.747 | 54.363 | 111.781 | 1.00 | 2.00 | 0 |
| ATOM | 1557 | CD1 | LEU | 159 | -4.993 | 53.449 | 110.617 | 1.00 | 2.00 | 0 |
| ATOM | 1558 | CD2 | LEU | 159 | -3.536 | 55.269 | 111.503 | 1.00 | 2.00 | 0 |
| ATOM | 1559 | C | LEU | 159 | -8.010 | 54.454 | 113.361 | 1.00 | 2.00 | 0 |
| ATOM | 1560 | O | LEU | 159 | -8.548 | 55.367 | 113.980 | 1.00 | 2.00 | 0 |
| ATOM | 1561 | N | PRO | 160 | -7.951 | 53.209 | 113.871 | 1.00 | 2.00 | 0 |
| ATOM | 1562 | CD | PRO | 160 | -7.504 | 51.978 | 113.208 | 1.00 | 2.00 | 0 |
| ATOM | 1563 | CA | PRO | 160 | -8.473 | 52.896 | 115.209 | 1.00 | 2.00 | 0 |
| ATOM | 1564 | CB | PRO | 160 | -8.398 | 51.375 | 115.269 | 1.00 | 2.00 | 0 |
| ATOM | 1565 | CG | PRO | 160 | -8.416 | 50.956 | 113.838 | 1.00 | 2.00 | 0 |
| ATOM | 1566 | C | PRO | 160 | -7.535 | 53.516 | 116.228 | 1.00 | 2.00 | 0 |
| ATOM | 1567 | O | PRO | 160 | -6.329 | 53.463 | 116.031 | 1.00 | 2.00 | 0 |
| ATOM | 1568 | N | ILE | 161 | -8.062 | 54.073 | 117.315 | 1.00 | 10.42 | 0 |
| ATOM | 1570 | CA | ILE | 161 | -7.206 | 54.717 | 118.312 | 1.00 | 10.42 | 0 |
| ATOM | 1571 | CB | ILE | 161 | -7.862 | 55.995 | 118.918 | 1.00 | 2.00 | 0 |
| ATOM | 1572 | CG2 | ILE | 161 | -8.493 | 56.837 | 117.823 | 1.00 | 2.00 | 0 |
| ATOM | 1573 | CG1 | ILE | 161 | -8.899 | 55.612 | 119.987 | 1.00 | 2.00 | 0 |
| ATOM | 1574 | CD1 | ILE | 161 | -9.428 | 56.766 | 120.775 | 1.00 | 2.00 | 0 |
| ATOM | 1575 | C | ILE | 161 | -6.741 | 53.859 | 119.492 | 1.00 | 10.42 | 0 |
| ATOM | 1576 | O | ILE | 161 | -5.808 | 54.254 | 120.193 | 1.00 | 2.00 | 0 |
| ATOM | 1577 | N | ALA | 162 | -7.387 | 52.712 | 119.720 | 1.00 | 16.67 | 0 |
| ATOM | 1579 | CA | ALA | 162 | -7.036 | 51.832 | 120.837 | 1.00 | 16.67 | 0 |

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|---|---|---|---|---|---|---|---|---|---|---|
| ATOM | 1580 | CB | ALA | 162 | -7.580 | 52.409 | 122.120 | 1.00 | 2.00 | 0 |
| ATOM | 1581 | C | ALA | 162 | -7.567 | 50.414 | 120.637 | 1.00 | 16.67 | 0 |
| ATOM | 1582 | O | ALA | 162 | -8.494 | 50.203 | 119.861 | 1.00 | 2.00 | 0 |
| ATOM | 1583 | N | ALA | 163 | -6.984 | 49.455 | 121.356 | 1.00 | 2.00 | 0 |
| ATOM | 1585 | CA | ALA | 163 | -7.379 | 48.052 | 121.267 | 1.00 | 2.00 | 0 |
| ATOM | 1586 | CB | ALA | 163 | -6.559 | 47.374 | 120.197 | 1.00 | 14.80 | 0 |
| ATOM | 1587 | C | ALA | 163 | -7.232 | 47.283 | 122.604 | 1.00 | 2.00 | 0 |
| ATOM | 1588 | O | ALA | 163 | -6.373 | 47.620 | 123.425 | 1.00 | 8.24 | 0 |
| ATOM | 1589 | N | ILE | 164 | -8.069 | 46.263 | 122.813 | 1.00 | 8.09 | 0 |
| ATOM | 1591 | CA | ILE | 164 | -8.036 | 45.424 | 124.018 | 1.00 | 8.09 | 0 |
| ATOM | 1592 | CB | ILE | 164 | -9.323 | 45.590 | 124.860 | 1.00 | 10.56 | 0 |
| ATOM | 1593 | CG2 | ILE | 164 | -9.200 | 44.830 | 126.150 | 1.00 | 10.56 | 0 |
| ATOM | 1594 | CG1 | ILE | 164 | -9.566 | 47.055 | 125.187 | 1.00 | 10.56 | 0 |
| ATOM | 1595 | CD1 | ILE | 164 | -10.886 | 47.285 | 125.837 | 1.00 | 10.56 | 0 |
| ATOM | 1596 | C | ILE | 164 | -7.910 | 43.938 | 123.623 | 1.00 | 8.09 | 0 |
| ATOM | 1597 | O | ILE | 164 | -8.866 | 43.328 | 123.127 | 1.00 | 10.56 | 0 |
| ATOM | 1598 | N | VAL | 165 | -6.739 | 43.353 | 123.856 | 1.00 | 20.53 | 0 |
| ATOM | 1600 | CA | VAL | 165 | -6.510 | 41.958 | 123.503 | 1.00 | 21.83 | 0 |
| ATOM | 1601 | CB | VAL | 165 | -5.041 | 41.664 | 123.243 | 1.00 | 2.00 | 0 |
| ATOM | 1602 | CG1 | VAL | 165 | -4.905 | 40.241 | 122.717 | 1.00 | 2.00 | 0 |
| ATOM | 1603 | CG2 | VAL | 165 | -4.460 | 42.686 | 122.273 | 1.00 | 2.00 | 0 |
| ATOM | 1604 | C | VAL | 165 | -6.973 | 40.987 | 124.570 | 1.00 | 22.04 | 0 |
| ATOM | 1605 | O | VAL | 165 | -6.546 | 41.064 | 125.728 | 1.00 | 2.00 | 0 |
| ATOM | 1606 | N | ASP | 166 | -7.841 | 40.066 | 124.163 | 1.00 | 10.50 | 0 |
| ATOM | 1608 | CA | ASP | 166 | -8.401 | 39.057 | 125.046 | 1.00 | 16.73 | 0 |
| ATOM | 1609 | CB | ASP | 166 | -7.348 | 37.980 | 125.337 | 1.00 | 24.26 | 0 |
| ATOM | 1610 | CG | ASP | 166 | -7.245 | 36.914 | 124.212 | 1.00 | 24.02 | 0 |
| ATOM | 1611 | OD1 | ASP | 166 | -8.258 | 36.207 | 123.944 | 1.00 | 22.19 | 0 |
| ATOM | 1612 | OD2 | ASP | 166 | -6.145 | 36.776 | 123.611 | 1.00 | 26.91 | 0 |
| ATOM | 1613 | C | ASP | 166 | -8.963 | 39.674 | 126.326 | 1.00 | 15.15 | 0 |
| ATOM | 1614 | O | ASP | 166 | -9.139 | 39.006 | 127.336 | 1.00 | 12.89 | 0 |
| ATOM | 1615 | N | GLU | 167 | -9.262 | 40.967 | 126.231 | 1.00 | 2.00 | 0 |
| ATOM | 1617 | CA | GLU | 167 | -9.833 | 41.811 | 127.289 | 1.00 | 2.00 | 0 |
| ATOM | 1618 | CB | GLU | 167 | -11.280 | 41.394 | 127.555 | 1.00 | 83.32 | 0 |
| ATOM | 1619 | CG | GLU | 167 | -12.129 | 41.397 | 126.273 | 1.00 | 2.00 | 0 |
| ATOM | 1620 | CD | GLU | 167 | -11.819 | 42.603 | 125.305 | 1.00 | 2.00 | 0 |
| ATOM | 1621 | OE1 | GLU | 167 | -11.133 | 42.398 | 124.242 | 1.00 | 2.00 | 0 |
| ATOM | 1622 | OE2 | GLU | 167 | -12.268 | 43.750 | 125.622 | 1.00 | 2.00 | 0 |
| ATOM | 1623 | C | GLU | 167 | -9.056 | 41.981 | 128.585 | 1.00 | 2.00 | 0 |
| ATOM | 1624 | O | GLU | 167 | -9.634 | 42.138 | 129.657 | 1.00 | 74.79 | 0 |
| ATOM | 1625 | N | LYS | 168 | -7.733 | 41.984 | 128.460 | 1.00 | 22.77 | 0 |
| ATOM | 1627 | CA | LYS | 168 | -6.829 | 42.154 | 129.589 | 1.00 | 14.49 | 0 |
| ATOM | 1628 | CB | LYS | 168 | -6.098 | 40.844 | 129.910 | 1.00 | 21.81 | 0 |
| ATOM | 1629 | CG | LYS | 168 | -6.956 | 39.798 | 130.600 | 1.00 | 17.49 | 0 |
| ATOM | 1630 | CD | LYS | 168 | -7.677 | 40.404 | 131.802 | 1.00 | 18.27 | 0 |
| ATOM | 1631 | CE | LYS | 168 | -8.654 | 39.411 | 132.466 | 1.00 | 26.28 | 0 |
| ATOM | 1632 | NZ | LYS | 168 | -9.658 | 40.080 | 133.373 | 1.00 | 29.04 | 0 |
| ATOM | 1636 | C | LYS | 168 | -5.811 | 43.225 | 129.237 | 1.00 | 11.04 | 0 |
| ATOM | 1637 | O | LYS | 168 | -5.665 | 44.214 | 129.947 | 1.00 | 17.06 | 0 |
| ATOM | 1638 | N | ILE | 169 | -5.109 | 43.015 | 128.131 | 1.00 | 2.00 | 0 |
| ATOM | 1640 | CA | ILE | 169 | -4.093 | 43.950 | 127.663 | 1.00 | 2.00 | 0 |
| ATOM | 1641 | CB | ILE | 169 | -3.151 | 43.267 | 126.648 | 1.00 | 2.00 | 0 |
| ATOM | 1642 | CG2 | ILE | 169 | -1.989 | 44.184 | 126.302 | 1.00 | 2.00 | 0 |
| ATOM | 1643 | CG1 | ILE | 169 | -2.632 | 41.952 | 127.215 | 1.00 | 2.00 | 0 |
| ATOM | 1644 | CD1 | ILE | 169 | -1.691 | 41.218 | 126.297 | 1.00 | 2.00 | 0 |
| ATOM | 1645 | C | ILE | 169 | -4.731 | 45.144 | 126.964 | 1.00 | 2.00 | 0 |
| ATOM | 1646 | O | ILE | 169 | -5.393 | 44.973 | 125.938 | 1.00 | 2.00 | 0 |
| ATOM | 1647 | N | PHE | 170 | -4.572 | 46.337 | 127.524 | 1.00 | 17.81 | 0 |
| ATOM | 1649 | CA | PHE | 170 | -5.110 | 47.525 | 126.877 | 1.00 | 19.78 | 0 |
| ATOM | 1650 | CB | PHE | 170 | -5.486 | 48.610 | 127.885 | 1.00 | 2.00 | 0 |
| ATOM | 1651 | CG | PHE | 170 | -5.895 | 49.920 | 127.252 | 1.00 | 2.00 | 0 |
| ATOM | 1652 | CD1 | PHE | 170 | -7.095 | 50.028 | 126.538 | 1.00 | 2.00 | 0 |
| ATOM | 1653 | CD2 | PHE | 170 | -5.092 | 51.056 | 127.390 | 1.00 | 2.00 | 0 |
| ATOM | 1654 | CE1 | PHE | 170 | -7.493 | 51.248 | 125.976 | 1.00 | 2.00 | 0 |
| ATOM | 1655 | CE2 | PHE | 170 | -5.473 | 52.282 | 126.836 | 1.00 | 2.00 | 0 |
| ATOM | 1656 | CZ | PHE | 170 | -6.680 | 52.377 | 126.127 | 1.00 | 2.00 | 0 |
| ATOM | 1657 | C | PHE | 170 | -3.943 | 47.992 | 126.038 | 1.00 | 23.45 | 0 |
| ATOM | 1658 | O | PHE | 170 | -2.809 | 47.983 | 126.518 | 1.00 | 2.00 | 0 |

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|---|---|---|---|---|---|---|---|---|---|
| ATOM | 1659 | N | CYS | 171 | -4.208 | 48.375 | 124.790 | 1.00 | 2.00 | 0 |
| ATOM | 1661 | CA | CYS | 171 | -3.158 | 48.836 | 123.898 | 1.00 | 2.00 | 0 |
| ATOM | 1662 | CB | CYS | 171 | -2.952 | 47.843 | 122.766 | 1.00 | 26.14 | 0 |
| ATOM | 1663 | SG | CYS | 171 | -2.524 | 46.203 | 123.305 | 1.00 | 16.13 | 0 |
| ATOM | 1664 | C | CYS | 171 | -3.499 | 50.189 | 123.310 | 1.00 | 2.00 | 0 |
| ATOM | 1665 | O | CYS | 171 | -4.652 | 50.453 | 122.943 | 1.00 | 26.14 | 0 |
| ATOM | 1666 | N | CYS | 172 | -2.495 | 51.058 | 123.265 | 1.00 | 2.00 | 0 |
| ATOM | 1668 | CA | CYS | 172 | -2.635 | 52.378 | 122.668 | 1.00 | 2.00 | 0 |
| ATOM | 1669 | CB | CYS | 172 | -3.403 | 53.356 | 123.597 | 1.00 | 14.54 | 0 |
| ATOM | 1670 | SG | CYS | 172 | -2.593 | 53.995 | 125.094 | 1.00 | 15.67 | 0 |
| ATOM | 1671 | C | CYS | 172 | -1.231 | 52.890 | 122.287 | 1.00 | 2.00 | 0 |
| ATOM | 1672 | O | CYS | 172 | -0.227 | 52.277 | 122.657 | 1.00 | 7.48 | 0 |
| ATOM | 1673 | N | HIS | 173 | -1.154 | 53.951 | 121.488 | 1.00 | 2.00 | 0 |
| ATOM | 1675 | CA | HIS | 173 | 0.146 | 54.461 | 121.112 | 1.00 | 2.00 | 0 |
| ATOM | 1676 | C | HIS | 173 | 0.815 | 55.130 | 122.297 | 1.00 | 2.00 | 0 |
| ATOM | 1677 | O | HIS | 173 | 1.893 | 54.707 | 122.722 | 1.00 | 2.00 | 0 |
| ATOM | 1678 | CB | HIS | 173 | 0.056 | 55.457 | 119.944 | 1.00 | 2.00 | 0 |
| ATOM | 1679 | CG | HIS | 173 | 1.377 | 56.074 | 119.588 | 1.00 | 2.00 | 0 |
| ATOM | 1680 | ND1 | HIS | 173 | 2.487 | 55.347 | 119.234 | 1.00 | 2.00 | 0 |
| ATOM | 1682 | CD2 | HIS | 173 | 1.774 | 57.372 | 119.585 | 1.00 | 2.00 | 0 |
| ATOM | 1683 | NE2 | HIS | 173 | 3.123 | 57.441 | 119.241 | 1.00 | 2.00 | 0 |
| ATOM | 1684 | CE1 | HIS | 173 | 3.492 | 56.189 | 119.045 | 1.00 | 2.00 | 0 |
| ATOM | 1685 | N | GLY | 174 | 0.168 | 56.172 | 122.817 | 1.00 | 2.00 | 0 |
| ATOM | 1687 | CA | GLY | 174 | 0.711 | 56.933 | 123.935 | 1.00 | 2.00 | 0 |
| ATOM | 1688 | C | GLY | 174 | 0.568 | 56.450 | 125.386 | 1.00 | 2.00 | 0 |
| ATOM | 1689 | O | GLY | 174 | 1.556 | 56.111 | 126.041 | 1.00 | 2.00 | 0 |
| ATOM | 1690 | N | GLY | 175 | -0.648 | 56.453 | 125.913 | 1.00 | 16.98 | 0 |
| ATOM | 1692 | CA | GLY | 175 | -0.830 | 56.028 | 127.283 | 1.00 | 16.98 | 0 |
| ATOM | 1693 | C | GLY | 175 | -2.227 | 56.343 | 127.763 | 1.00 | 16.98 | 0 |
| ATOM | 1694 | O | GLY | 175 | -3.190 | 56.231 | 126.999 | 1.00 | 66.77 | 0 |
| ATOM | 1695 | N | LEU | 176 | -2.341 | 56.764 | 129.021 | 1.00 | 11.28 | 0 |
| ATOM | 1697 | CA | LEU | 176 | -3.637 | 57.063 | 129.604 | 1.00 | 11.28 | 0 |
| ATOM | 1698 | CB | LEU | 176 | -3.740 | 56.427 | 130.976 | 1.00 | 2.00 | 0 |
| ATOM | 1699 | CG | LEU | 176 | -3.443 | 54.934 | 130.966 | 1.00 | 2.00 | 0 |
| ATOM | 1700 | CD1 | LEU | 176 | -3.469 | 54.407 | 132.374 | 1.00 | 2.00 | 0 |
| ATOM | 1701 | CD2 | LEU | 176 | -4.463 | 54.218 | 130.121 | 1.00 | 2.00 | 0 |
| ATOM | 1702 | C | LEU | 176 | -3.876 | 58.545 | 129.692 | 1.00 | 11.28 | 0 |
| ATOM | 1703 | O | LEU | 176 | -2.943 | 59.329 | 129.645 | 1.00 | 2.00 | 0 |
| ATOM | 1704 | N | SER | 177 | -5.138 | 58.913 | 129.850 | 1.00 | 6.18 | 0 |
| ATOM | 1706 | CA | SER | 177 | -5.567 | 60.304 | 129.918 | 1.00 | 6.86 | 0 |
| ATOM | 1707 | CB | SER | 177 | -6.476 | 60.587 | 128.718 | 1.00 | 12.19 | 0 |
| ATOM | 1708 | OG | SER | 177 | -7.189 | 61.804 | 128.835 | 1.00 | 12.19 | 0 |
| ATOM | 1710 | C | SER | 177 | -6.356 | 60.573 | 131.193 | 1.00 | 7.79 | 0 |
| ATOM | 1711 | O | SER | 177 | -7.170 | 59.749 | 131.606 | 1.00 | 12.19 | 0 |
| ATOM | 1712 | N | PRO | 178 | -6.150 | 61.736 | 131.824 | 1.00 | 2.00 | 0 |
| ATOM | 1713 | CD | PRO | 178 | -5.223 | 62.827 | 131.505 | 1.00 | 29.89 | 0 |
| ATOM | 1714 | CA | PRO | 178 | -6.895 | 62.054 | 133.041 | 1.00 | 2.00 | 0 |
| ATOM | 1715 | CB | PRO | 178 | -6.231 | 63.337 | 133.518 | 1.00 | 25.57 | 0 |
| ATOM | 1716 | CG | PRO | 178 | -5.842 | 63.973 | 132.274 | 1.00 | 21.36 | 0 |
| ATOM | 1717 | C | PRO | 178 | -8.394 | 62.266 | 132.757 | 1.00 | 2.00 | 0 |
| ATOM | 1718 | O | PRO | 178 | -9.140 | 62.740 | 133.617 | 1.00 | 24.04 | 0 |
| ATOM | 1719 | N | ASP | 179 | -8.821 | 61.933 | 131.543 | 1.00 | 38.94 | 0 |
| ATOM | 1721 | CA | ASP | 179 | -10.206 | 62.078 | 131.129 | 1.00 | 37.05 | 0 |
| ATOM | 1722 | CB | ASP | 179 | -10.264 | 62.870 | 129.837 | 1.00 | 33.34 | 0 |
| ATOM | 1723 | CG | ASP | 179 | -9.964 | 64.320 | 130.048 | 1.00 | 30.55 | 0 |
| ATOM | 1724 | OD1 | ASP | 179 | -10.923 | 65.045 | 130.386 | 1.00 | 31.71 | 0 |
| ATOM | 1725 | OD2 | ASP | 179 | -8.786 | 64.728 | 129.889 | 1.00 | 32.17 | 0 |
| ATOM | 1726 | C | ASP | 179 | -10.871 | 60.735 | 130.923 | 1.00 | 40.05 | 0 |
| ATOM | 1727 | O | ASP | 179 | -12.096 | 60.638 | 130.873 | 1.00 | 34.46 | 0 |
| ATOM | 1728 | N | LEU | 180 | -10.057 | 59.699 | 130.791 | 1.00 | 15.43 | 0 |
| ATOM | 1730 | CA | LEU | 180 | -10.570 | 58.362 | 130.590 | 1.00 | 12.98 | 0 |
| ATOM | 1731 | CB | LEU | 180 | -9.446 | 57.467 | 130.058 | 1.00 | 2.00 | 0 |
| ATOM | 1732 | CG | LEU | 180 | -9.867 | 56.186 | 129.338 | 1.00 | 2.00 | 0 |
| ATOM | 1733 | CD1 | LEU | 180 | -10.706 | 56.511 | 128.110 | 1.00 | 2.00 | 0 |
| ATOM | 1734 | CD2 | LEU | 180 | -8.633 | 55.413 | 128.953 | 1.00 | 2.00 | 0 |
| ATOM | 1735 | C | LEU | 180 | -11.157 | 57.806 | 131.902 | 1.00 | 14.43 | 0 |
| ATOM | 1736 | O | LEU | 180 | -10.470 | 57.709 | 132.931 | 1.00 | 2.00 | 0 |
| ATOM | 1737 | N | GLN | 181 | -12.448 | 57.492 | 131.862 | 1.00 | 5.88 | 0 |

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|---|---|---|---|---|---|---|---|---|---|
| ATOM | 1739 | CA | GLN | 181 | -13.184 | 56.917 | 132.992 | 1.00 | 5.88 | 0 |
| ATOM | 1740 | CB | GLN | 181 | -14.379 | 57.787 | 133.375 | 1.00 | 32.99 | 0 |
| ATOM | 1741 | CG | GLN | 181 | -14.002 | 59.152 | 133.900 | 1.00 | 36.07 | 0 |
| ATOM | 1742 | CD | GLN | 181 | -15.101 | 60.172 | 133.676 | 1.00 | 38.35 | 0 |
| ATOM | 1743 | OE1 | GLN | 181 | -16.285 | 59.886 | 133.877 | 1.00 | 41.53 | 0 |
| ATOM | 1744 | NE2 | GLN | 181 | -14.717 | 61.366 | 133.242 | 1.00 | 38.39 | 0 |
| ATOM | 1747 | C | GLN | 181 | -13.672 | 55.563 | 132.500 | 1.00 | 5.88 | 0 |
| ATOM | 1748 | O | GLN | 181 | -13.572 | 54.554 | 133.205 | 1.00 | 24.31 | 0 |
| ATOM | 1749 | N | SER | 182 | -14.188 | 55.544 | 131.274 | 1.00 | 2.20 | 0 |
| ATOM | 1751 | CA | SER | 182 | -14.651 | 54.310 | 130.664 | 1.00 | 9.71 | 0 |
| ATOM | 1752 | CB | SER | 182 | -16.174 | 54.255 | 130.614 | 1.00 | 15.80 | 0 |
| ATOM | 1753 | OG | SER | 182 | -16.668 | 54.856 | 129.433 | 1.00 | 17.25 | 0 |
| ATOM | 1755 | C | SER | 182 | -14.112 | 54.177 | 129.248 | 1.00 | 3.77 | 0 |
| ATOM | 1756 | O | SER | 182 | -13.359 | 55.019 | 128.751 | 1.00 | 15.80 | 0 |
| ATOM | 1757 | N | MET | 183 | -14.526 | 53.091 | 128.615 | 1.00 | 2.00 | 0 |
| ATOM | 1759 | CA | MET | 183 | -14.156 | 52.780 | 127.251 | 1.00 | 2.00 | 0 |
| ATOM | 1760 | CB | MET | 183 | -14.100 | 51.272 | 127.064 | 1.00 | 2.00 | 0 |
| ATOM | 1761 | CG | MET | 183 | -13.171 | 50.616 | 128.048 | 1.00 | 2.00 | 0 |
| ATOM | 1762 | SD | MET | 183 | -11.620 | 51.473 | 128.022 | 1.00 | 2.00 | 0 |
| ATOM | 1763 | CE | MET | 183 | -10.520 | 50.135 | 127.900 | 1.00 | 2.00 | 0 |
| ATOM | 1764 | C | MET | 183 | -15.204 | 53.373 | 126.326 | 1.00 | 2.00 | 0 |
| ATOM | 1765 | O | MET | 183 | -14.959 | 53.550 | 125.129 | 1.00 | 2.00 | 0 |
| ATOM | 1766 | N | GLU | 184 | -16.370 | 53.700 | 126.882 | 1.00 | 2.00 | 0 |
| ATOM | 1768 | CA | GLU | 184 | -17.432 | 54.280 | 126.082 | 1.00 | 2.00 | 0 |
| ATOM | 1769 | CB | GLU | 184 | -18.668 | 54.531 | 126.910 | 1.00 | 6.25 | 0 |
| ATOM | 1770 | CG | GLU | 184 | -19.830 | 54.977 | 126.073 | 1.00 | 8.82 | 0 |
| ATOM | 1771 | CD | GLU | 184 | -20.273 | 53.927 | 125.068 | 1.00 | 13.01 | 0 |
| ATOM | 1772 | OE1 | GLU | 184 | -19.846 | 52.744 | 125.181 | 1.00 | 14.09 | 0 |
| ATOM | 1773 | OE2 | GLU | 184 | -21.064 | 54.293 | 124.164 | 1.00 | 20.29 | 0 |
| ATOM | 1774 | C | GLU | 184 | -16.978 | 55.586 | 125.481 | 1.00 | 2.00 | 0 |
| ATOM | 1775 | O | GLU | 184 | -17.399 | 55.946 | 124.392 | 1.00 | 23.33 | 0 |
| ATOM | 1776 | N | GLN | 185 | -16.117 | 56.295 | 126.198 | 1.00 | 12.32 | 0 |
| ATOM | 1778 | CA | GLN | 185 | -15.599 | 57.561 | 125.714 | 1.00 | 14.30 | 0 |
| ATOM | 1779 | CB | GLN | 185 | -14.697 | 58.190 | 126.758 | 1.00 | 43.49 | 0 |
| ATOM | 1780 | CG | GLN | 185 | -15.454 | 58.629 | 127.990 | 1.00 | 47.40 | 0 |
| ATOM | 1781 | CD | GLN | 185 | -14.537 | 58.929 | 129.139 | 1.00 | 49.32 | 0 |
| ATOM | 1782 | OE1 | GLN | 185 | -13.994 | 58.016 | 129.753 | 1.00 | 56.49 | 0 |
| ATOM | 1783 | NE2 | GLN | 185 | -14.350 | 60.208 | 129.437 | 1.00 | 49.76 | 0 |
| ATOM | 1786 | C | GLN | 185 | -14.834 | 57.307 | 124.432 | 1.00 | 16.93 | 0 |
| ATOM | 1787 | O | GLN | 185 | -14.973 | 58.053 | 123.461 | 1.00 | 43.79 | 0 |
| ATOM | 1788 | N | ILE | 186 | -14.044 | 56.238 | 124.420 | 1.00 | 5.67 | 0 |
| ATOM | 1790 | CA | ILE | 186 | -13.280 | 55.880 | 123.235 | 1.00 | 5.67 | 0 |
| ATOM | 1791 | CB | ILE | 186 | -12.436 | 54.613 | 123.470 | 1.00 | 16.18 | 0 |
| ATOM | 1792 | CG2 | ILE | 186 | -11.675 | 54.243 | 122.208 | 1.00 | 11.85 | 0 |
| ATOM | 1793 | CG1 | ILE | 186 | -11.489 | 54.825 | 124.642 | 1.00 | 13.18 | 0 |
| ATOM | 1794 | CD1 | ILE | 186 | -10.545 | 55.954 | 124.459 | 1.00 | 17.92 | 0 |
| ATOM | 1795 | C | ILE | 186 | -14.294 | 55.566 | 122.143 | 1.00 | 5.67 | 0 |
| ATOM | 1796 | O | ILE | 186 | -14.260 | 56.145 | 121.060 | 1.00 | 19.35 | 0 |
| ATOM | 1797 | N | ARG | 187 | -15.207 | 54.655 | 122.471 | 1.00 | 17.59 | 0 |
| ATOM | 1799 | CA | ARG | 187 | -16.243 | 54.205 | 121.561 | 1.00 | 16.33 | 0 |
| ATOM | 1800 | CB | ARG | 187 | -17.141 | 53.165 | 122.237 | 1.00 | 20.41 | 0 |
| ATOM | 1801 | CG | ARG | 187 | -16.468 | 51.900 | 122.723 | 1.00 | 29.32 | 0 |
| ATOM | 1802 | CD | ARG | 187 | -17.497 | 51.006 | 123.447 | 1.00 | 31.43 | 0 |
| ATOM | 1803 | NE | ARG | 187 | -16.888 | 49.888 | 124.165 | 1.00 | 38.34 | 0 |
| ATOM | 1805 | CZ | ARG | 187 | -16.311 | 48.838 | 123.580 | 1.00 | 34.30 | 0 |
| ATOM | 1806 | NH1 | ARG | 187 | -16.256 | 48.747 | 122.252 | 1.00 | 41.37 | 0 |
| ATOM | 1809 | NH2 | ARG | 187 | -15.783 | 47.873 | 124.322 | 1.00 | 34.50 | 0 |
| ATOM | 1812 | C | ARG | 187 | -17.148 | 55.302 | 121.011 | 1.00 | 15.89 | 0 |
| ATOM | 1813 | O | ARG | 187 | -17.937 | 55.032 | 120.108 | 1.00 | 20.82 | 0 |
| ATOM | 1814 | N | ARG | 188 | -17.071 | 56.524 | 121.529 | 1.00 | 2.00 | 0 |
| ATOM | 1816 | CA | ARG | 188 | -17.964 | 57.557 | 121.012 | 1.00 | 2.00 | 0 |
| ATOM | 1817 | CB | ARG | 188 | -18.878 | 58.105 | 122.106 | 1.00 | 31.38 | 0 |
| ATOM | 1818 | CG | ARG | 188 | -18.184 | 58.827 | 123.228 | 1.00 | 29.44 | 0 |
| ATOM | 1819 | CD | ARG | 188 | -19.202 | 59.586 | 124.034 | 1.00 | 31.32 | 0 |
| ATOM | 1820 | NE | ARG | 188 | -20.410 | 58.802 | 124.237 | 1.00 | 33.18 | 0 |
| ATOM | 1822 | CZ | ARG | 188 | -21.637 | 59.285 | 124.112 | 1.00 | 29.63 | 0 |
| ATOM | 1823 | NH1 | ARG | 188 | -21.827 | 60.561 | 123.777 | 1.00 | 36.26 | 0 |
| ATOM | 1826 | NH2 | ARG | 188 | -22.671 | 58.484 | 124.332 | 1.00 | 32.06 | 0 |

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|---|---|---|---|---|---|---|---|---|---|---|
| ATOM | 1829 | C | ARG | 188 | -17.255 | 58.682 | 120.332 | 1.00 | 2.00 | 0 |
| ATOM | 1830 | O | ARG | 188 | -17.758 | 59.804 | 120.250 | 1.00 | 31.89 | 0 |
| ATOM | 1831 | N | ILE | 189 | -16.070 | 58.369 | 119.846 | 1.00 | 17.06 | 0 |
| ATOM | 1833 | CA | ILE | 189 | -15.263 | 59.333 | 119.136 | 1.00 | 16.98 | 0 |
| ATOM | 1834 | CB | ILE | 189 | -13.759 | 59.043 | 119.345 | 1.00 | 16.67 | 0 |
| ATOM | 1835 | CG2 | ILE | 189 | -12.924 | 59.973 | 118.493 | 1.00 | 17.43 | 0 |
| ATOM | 1836 | CG1 | ILE | 189 | -13.411 | 59.205 | 120.826 | 1.00 | 17.65 | 0 |
| ATOM | 1837 | CD1 | ILE | 189 | -11.970 | 58.946 | 121.173 | 1.00 | 16.74 | 0 |
| ATOM | 1838 | C | ILE | 189 | -15.620 | 59.244 | 117.656 | 1.00 | 19.51 | 0 |
| ATOM | 1839 | O | ILE | 189 | -15.448 | 58.184 | 117.044 | 1.00 | 25.93 | 0 |
| ATOM | 1840 | N | MET | 190 | -16.158 | 60.342 | 117.108 | 1.00 | 22.12 | 0 |
| ATOM | 1842 | CA | MET | 190 | -16.514 | 60.420 | 115.685 | 1.00 | 24.92 | 0 |
| ATOM | 1843 | CB | MET | 190 | -17.051 | 61.812 | 115.320 | 1.00 | 46.39 | 0 |
| ATOM | 1844 | CG | MET | 190 | -17.366 | 61.977 | 113.826 | 1.00 | 46.97 | 0 |
| ATOM | 1845 | SD | MET | 190 | -17.820 | 63.658 | 113.312 | 1.00 | 58.03 | 0 |
| ATOM | 1846 | CE | MET | 190 | -16.271 | 64.266 | 112.598 | 1.00 | 52.38 | 0 |
| ATOM | 1847 | C | MET | 190 | -15.173 | 60.194 | 115.015 | 1.00 | 25.36 | 0 |
| ATOM | 1848 | O | MET | 190 | -14.287 | 61.041 | 115.106 | 1.00 | 32.57 | 0 |
| ATOM | 1849 | N | ARG | 191 | -15.023 | 59.057 | 114.346 | 1.00 | 2.00 | 0 |
| ATOM | 1851 | CA | ARG | 191 | -13.732 | 58.738 | 113.772 | 1.00 | 2.00 | 0 |
| ATOM | 1852 | CB | ARG | 191 | -13.731 | 57.384 | 113.089 | 1.00 | 2.00 | 0 |
| ATOM | 1853 | CG | ARG | 191 | -12.300 | 56.900 | 112.821 | 1.00 | 11.31 | 0 |
| ATOM | 1854 | CD | ARG | 191 | -11.978 | 55.799 | 113.752 | 1.00 | 11.31 | 0 |
| ATOM | 1855 | NE | ARG | 191 | -13.139 | 54.935 | 113.762 | 1.00 | 2.00 | 0 |
| ATOM | 1857 | CZ | ARG | 191 | -13.124 | 53.663 | 113.416 | 1.00 | 2.00 | 0 |
| ATOM | 1858 | NH1 | ARG | 191 | -11.985 | 53.085 | 113.047 | 1.00 | 2.00 | 0 |
| ATOM | 1861 | NH2 | ARG | 191 | -14.263 | 52.984 | 113.430 | 1.00 | 2.00 | 0 |
| ATOM | 1864 | C | ARG | 191 | -13.084 | 59.769 | 112.857 | 1.00 | 2.00 | 0 |
| ATOM | 1865 | O | ARG | 191 | -11.995 | 60.267 | 113.202 | 1.00 | 6.10 | 0 |
| ATOM | 1866 | N | PRO | 192 | -13.685 | 60.065 | 111.670 | 1.00 | 37.06 | 0 |
| ATOM | 1867 | CD | PRO | 192 | -14.912 | 59.530 | 111.045 | 1.00 | 2.00 | 0 |
| ATOM | 1868 | CA | PRO | 192 | -13.048 | 61.068 | 110.799 | 1.00 | 36.28 | 0 |
| ATOM | 1869 | CB | PRO | 192 | -14.114 | 61.335 | 109.749 | 1.00 | 2.00 | 0 |
| ATOM | 1870 | CG | PRO | 192 | -14.743 | 59.973 | 109.602 | 1.00 | 2.00 | 0 |
| ATOM | 1871 | C | PRO | 192 | -12.787 | 62.261 | 111.693 | 1.00 | 37.24 | 0 |
| ATOM | 1872 | O | PRO | 192 | -13.697 | 63.033 | 112.004 | 1.00 | 2.00 | 0 |
| ATOM | 1873 | N | THR | 193 | -11.552 | 62.348 | 112.168 | 1.00 | 2.00 | 0 |
| ATOM | 1875 | CA | THR | 193 | -11.182 | 63.396 | 113.089 | 1.00 | 2.00 | 0 |
| ATOM | 1876 | CB | THR | 193 | -11.627 | 63.063 | 114.540 | 1.00 | 22.05 | 0 |
| ATOM | 1877 | OG1 | THR | 193 | -11.349 | 64.183 | 115.392 | 1.00 | 31.69 | 0 |
| ATOM | 1879 | CG2 | THR | 193 | -10.862 | 61.859 | 115.089 | 1.00 | 21.46 | 0 |
| ATOM | 1880 | C | THR | 193 | -9.700 | 63.661 | 113.152 | 1.00 | 2.00 | 0 |
| ATOM | 1881 | O | THR | 193 | -8.865 | 62.795 | 112.860 | 1.00 | 17.62 | 0 |
| ATOM | 1882 | N | ASP | 194 | -9.394 | 64.879 | 113.572 | 1.00 | 2.00 | 0 |
| ATOM | 1884 | CA | ASP | 194 | -8.031 | 65.311 | 113.744 | 1.00 | 2.00 | 0 |
| ATOM | 1885 | CB | ASP | 194 | -7.927 | 66.805 | 113.431 | 1.00 | 49.25 | 0 |
| ATOM | 1886 | CG | ASP | 194 | -6.561 | 67.197 | 112.912 | 1.00 | 49.25 | 0 |
| ATOM | 1887 | OD1 | ASP | 194 | -6.132 | 68.334 | 113.194 | 1.00 | 49.25 | 0 |
| ATOM | 1888 | OD2 | ASP | 194 | -5.920 | 66.371 | 112.217 | 1.00 | 49.25 | 0 |
| ATOM | 1889 | C | ASP | 194 | -7.686 | 65.041 | 115.216 | 1.00 | 2.00 | 0 |
| ATOM | 1890 | O | ASP | 194 | -8.571 | 64.978 | 116.077 | 1.00 | 54.62 | 0 |
| ATOM | 1891 | N | VAL | 195 | -6.408 | 64.836 | 115.488 | 1.00 | 17.01 | 0 |
| ATOM | 1893 | CA | VAL | 195 | -5.948 | 64.611 | 116.839 | 1.00 | 12.88 | 0 |
| ATOM | 1894 | CB | VAL | 195 | -4.509 | 64.017 | 116.818 | 1.00 | 9.98 | 0 |
| ATOM | 1895 | CG1 | VAL | 195 | -3.934 | 63.875 | 118.239 | 1.00 | 9.98 | 0 |
| ATOM | 1896 | CG2 | VAL | 195 | -4.532 | 62.675 | 116.124 | 1.00 | 9.98 | 0 |
| ATOM | 1897 | C | VAL | 195 | -5.971 | 65.994 | 117.511 | 1.00 | 12.88 | 0 |
| ATOM | 1898 | O | VAL | 195 | -5.343 | 66.934 | 117.038 | 1.00 | 9.98 | 0 |
| ATOM | 1899 | N | PRO | 196 | -6.771 | 66.152 | 118.567 | 1.00 | 16.08 | 0 |
| ATOM | 1900 | CD | PRO | 196 | -7.805 | 65.214 | 119.033 | 1.00 | 26.02 | 0 |
| ATOM | 1901 | CA | PRO | 196 | -6.862 | 67.429 | 119.284 | 1.00 | 21.91 | 0 |
| ATOM | 1902 | CB | PRO | 196 | -8.026 | 67.195 | 120.240 | 1.00 | 25.86 | 0 |
| ATOM | 1903 | CG | PRO | 196 | -8.874 | 66.153 | 119.496 | 1.00 | 25.31 | 0 |
| ATOM | 1904 | C | PRO | 196 | -5.560 | 67.735 | 120.027 | 1.00 | 24.64 | 0 |
| ATOM | 1905 | O | PRO | 196 | -4.809 | 66.818 | 120.349 | 1.00 | 23.54 | 0 |
| ATOM | 1906 | N | ASP | 197 | -5.291 | 69.010 | 120.302 | 1.00 | 39.93 | 0 |
| ATOM | 1908 | CA | ASP | 197 | -4.058 | 69.377 | 121.005 | 1.00 | 38.76 | 0 |
| ATOM | 1909 | CB | ASP | 197 | -3.605 | 70.789 | 120.612 | 1.00 | 78.93 | 0 |

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|---|---|---|---|---|---|---|---|---|---|
| ATOM | 1910 | CG | ASP | 197 | -4.726 | 71.800 | 120.658 | 1.00 | 84.50 | 0 |
| ATOM | 1911 | OD1 | ASP | 197 | -5.071 | 72.263 | 121.768 | 1.00 | 83.41 | 0 |
| ATOM | 1912 | OD2 | ASP | 197 | -5.258 | 72.134 | 119.578 | 1.00 | 90.03 | 0 |
| ATOM | 1913 | C | ASP | 197 | -4.162 | 69.256 | 122.520 | 1.00 | 41.84 | 0 |
| ATOM | 1914 | O | ASP | 197 | -3.227 | 69.577 | 123.255 | 1.00 | 85.35 | 0 |
| ATOM | 1915 | N | GLN | 198 | -5.316 | 68.789 | 122.973 | 1.00 | 2.00 | 0 |
| ATOM | 1917 | CA | GLN | 198 | -5.581 | 68.588 | 124.385 | 1.00 | 2.00 | 0 |
| ATOM | 1918 | CB | GLN | 198 | -5.686 | 69.937 | 125.120 | 1.00 | 27.32 | 0 |
| ATOM | 1919 | CG | GLN | 198 | -6.621 | 70.967 | 124.503 | 1.00 | 32.39 | 0 |
| ATOM | 1920 | CD | GLN | 198 | -7.981 | 71.041 | 125.192 | 1.00 | 29.94 | 0 |
| ATOM | 1921 | OE1 | GLN | 198 | -8.108 | 70.793 | 126.397 | 1.00 | 32.81 | 0 |
| ATOM | 1922 | NE2 | GLN | 198 | -9.007 | 71.391 | 124.424 | 1.00 | 29.42 | 0 |
| ATOM | 1925 | C | GLN | 198 | -6.863 | 67.793 | 124.492 | 1.00 | 2.00 | 0 |
| ATOM | 1926 | O | GLN | 198 | -7.748 | 67.909 | 123.640 | 1.00 | 26.90 | 0 |
| ATOM | 1927 | N | GLY | 199 | -6.943 | 66.949 | 125.509 | 1.00 | 15.20 | 0 |
| ATOM | 1929 | CA | GLY | 199 | -8.137 | 66.148 | 125.692 | 1.00 | 15.56 | 0 |
| ATOM | 1930 | C | GLY | 199 | -7.820 | 64.670 | 125.631 | 1.00 | 13.32 | 0 |
| ATOM | 1931 | O | GLY | 199 | -6.655 | 64.283 | 125.502 | 1.00 | 2.00 | 0 |
| ATOM | 1932 | N | LEU | 200 | -8.857 | 63.842 | 125.684 | 1.00 | 2.00 | 0 |
| ATOM | 1934 | CA | LEU | 200 | -8.690 | 62.402 | 125.666 | 1.00 | 2.00 | 0 |
| ATOM | 1935 | CB | LEU | 200 | -10.049 | 61.701 | 125.667 | 1.00 | 2.00 | 0 |
| ATOM | 1936 | CG | LEU | 200 | -9.945 | 60.224 | 126.081 | 1.00 | 2.00 | 0 |
| ATOM | 1937 | CD1 | LEU | 200 | -11.126 | 59.800 | 126.947 | 1.00 | 2.00 | 0 |
| ATOM | 1938 | CD2 | LEU | 200 | -9.842 | 59.380 | 124.847 | 1.00 | 2.00 | 0 |
| ATOM | 1939 | C | LEU | 200 | -7.850 | 61.875 | 124.521 | 1.00 | 2.00 | 0 |
| ATOM | 1940 | O | LEU | 200 | -6.764 | 61.323 | 124.764 | 1.00 | 2.00 | 0 |
| ATOM | 1941 | N | LEU | 201 | -8.344 | 62.045 | 123.283 | 1.00 | 2.00 | 0 |
| ATOM | 1943 | CA | LEU | 201 | -7.663 | 61.566 | 122.070 | 1.00 | 2.00 | 0 |
| ATOM | 1944 | CB | LEU | 201 | -8.378 | 62.041 | 120.811 | 1.00 | 2.00 | 0 |
| ATOM | 1945 | CG | LEU | 201 | -8.369 | 61.100 | 119.589 | 1.00 | 2.00 | 0 |
| ATOM | 1946 | CD1 | LEU | 201 | -8.895 | 61.855 | 118.375 | 1.00 | 2.00 | 0 |
| ATOM | 1947 | CD2 | LEU | 201 | -6.981 | 60.569 | 119.277 | 1.00 | 2.00 | 0 |
| ATOM | 1948 | C | LEU | 201 | -6.246 | 62.078 | 122.059 | 1.00 | 2.00 | 0 |
| ATOM | 1949 | O | LEU | 201 | -5.319 | 61.347 | 121.715 | 1.00 | 2.00 | 0 |
| ATOM | 1950 | N | CYS | 202 | -6.071 | 63.333 | 122.446 | 1.00 | 2.00 | 0 |
| ATOM | 1952 | CA | CYS | 202 | -4.733 | 63.891 | 122.484 | 1.00 | 2.00 | 0 |
| ATOM | 1953 | CB | CYS | 202 | -4.722 | 65.306 | 123.024 | 1.00 | 2.00 | 0 |
| ATOM | 1954 | SG | CYS | 202 | -3.012 | 65.850 | 123.209 | 1.00 | 2.00 | 0 |
| ATOM | 1955 | C | CYS | 202 | -3.850 | 63.076 | 123.394 | 1.00 | 2.00 | 0 |
| ATOM | 1956 | O | CYS | 202 | -2.719 | 62.715 | 123.036 | 1.00 | 2.00 | 0 |
| ATOM | 1957 | N | ASP | 203 | -4.385 | 62.798 | 124.584 | 1.00 | 15.07 | 0 |
| ATOM | 1959 | CA | ASP | 203 | -3.673 | 62.057 | 125.611 | 1.00 | 11.86 | 0 |
| ATOM | 1960 | CB | ASP | 203 | -4.429 | 62.142 | 126.931 | 1.00 | 13.71 | 0 |
| ATOM | 1961 | CG | ASP | 203 | -4.449 | 63.538 | 127.497 | 1.00 | 15.77 | 0 |
| ATOM | 1962 | OD1 | ASP | 203 | -3.529 | 64.315 | 127.162 | 1.00 | 11.73 | 0 |
| ATOM | 1963 | OD2 | ASP | 203 | -5.380 | 63.861 | 128.271 | 1.00 | 16.16 | 0 |
| ATOM | 1964 | C | ASP | 203 | -3.369 | 60.615 | 125.262 | 1.00 | 13.81 | 0 |
| ATOM | 1965 | O | ASP | 203 | -2.254 | 60.155 | 125.492 | 1.00 | 23.94 | 0 |
| ATOM | 1966 | N | LEU | 204 | -4.330 | 59.902 | 124.695 | 1.00 | 10.49 | 0 |
| ATOM | 1968 | CA | LEU | 204 | -4.097 | 58.509 | 124.332 | 1.00 | 10.49 | 0 |
| ATOM | 1969 | CB | LEU | 204 | -5.351 | 57.912 | 123.717 | 1.00 | 10.22 | 0 |
| ATOM | 1970 | CG | LEU | 204 | -6.478 | 57.606 | 124.696 | 1.00 | 10.22 | 0 |
| ATOM | 1971 | CD1 | LEU | 204 | -7.667 | 57.281 | 123.866 | 1.00 | 10.22 | 0 |
| ATOM | 1972 | CD2 | LEU | 204 | -6.143 | 56.441 | 125.620 | 1.00 | 10.22 | 0 |
| ATOM | 1973 | C | LEU | 204 | -2.930 | 58.347 | 123.361 | 1.00 | 10.49 | 0 |
| ATOM | 1974 | O | LEU | 204 | -2.204 | 57.352 | 123.392 | 1.00 | 10.22 | 0 |
| ATOM | 1975 | N | LEU | 205 | -2.748 | 59.336 | 122.501 | 1.00 | 2.00 | 0 |
| ATOM | 1977 | CA | LEU | 205 | -1.679 | 59.301 | 121.525 | 1.00 | 2.00 | 0 |
| ATOM | 1978 | CB | LEU | 205 | -2.161 | 59.933 | 120.219 | 1.00 | 2.00 | 0 |
| ATOM | 1979 | CG | LEU | 205 | -3.459 | 59.463 | 119.551 | 1.00 | 2.00 | 0 |
| ATOM | 1980 | CD1 | LEU | 205 | -3.595 | 60.238 | 118.259 | 1.00 | 2.00 | 0 |
| ATOM | 1981 | CD2 | LEU | 205 | -3.459 | 57.954 | 119.269 | 1.00 | 2.00 | 0 |
| ATOM | 1982 | C | LEU | 205 | -0.409 | 60.018 | 121.967 | 1.00 | 2.00 | 0 |
| ATOM | 1983 | O | LEU | 205 | 0.620 | 59.890 | 121.314 | 1.00 | 2.00 | 0 |
| ATOM | 1984 | N | TRP | 206 | -0.472 | 60.756 | 123.072 | 1.00 | 10.02 | 0 |
| ATOM | 1986 | CA | TRP | 206 | 0.678 | 61.526 | 123.545 | 1.00 | 10.02 | 0 |
| ATOM | 1987 | CB | TRP | 206 | 0.362 | 62.994 | 123.408 | 1.00 | 2.00 | 0 |
| ATOM | 1988 | CG | TRP | 206 | 0.413 | 63.485 | 122.052 | 1.00 | 2.00 | 0 |

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|---|---|---|---|---|---|---|---|---|---|---|
| ATOM | 1989 | CD2 | TRP | 206 | 1.532 | 64.103 | 121.420 | 1.00 | 2.00 | 0 |
| ATOM | 1990 | CE2 | TRP | 206 | 1.105 | 64.535 | 120.148 | 1.00 | 2.00 | 0 |
| ATOM | 1991 | CE3 | TRP | 206 | 2.854 | 64.355 | 121.813 | 1.00 | 2.00 | 0 |
| ATOM | 1992 | CD1 | TRP | 206 | -0.616 | 63.541 | 121.162 | 1.00 | 2.00 | 0 |
| ATOM | 1993 | NE1 | TRP | 206 | -0.212 | 64.178 | 120.017 | 1.00 | 2.00 | 0 |
| ATOM | 1995 | CZ2 | TRP | 206 | 1.950 | 65.207 | 119.263 | 1.00 | 2.00 | 0 |
| ATOM | 1996 | CZ3 | TRP | 206 | 3.697 | 65.024 | 120.932 | 1.00 | 2.00 | 0 |
| ATOM | 1997 | CH2 | TRP | 206 | 3.238 | 65.443 | 119.669 | 1.00 | 2.00 | 0 |
| ATOM | 1998 | C | TRP | 206 | 1.246 | 61.330 | 124.955 | 1.00 | 10.02 | 0 |
| ATOM | 1999 | O | TRP | 206 | 2.419 | 61.639 | 125.194 | 1.00 | 2.00 | 0 |
| ATOM | 2000 | N | SER | 207 | 0.418 | 60.867 | 125.886 | 1.00 | 2.00 | 0 |
| ATOM | 2002 | CA | SER | 207 | 0.830 | 60.690 | 127.267 | 1.00 | 2.00 | 0 |
| ATOM | 2003 | CB | SER | 207 | -0.363 | 60.273 | 128.121 | 1.00 | 29.76 | 0 |
| ATOM | 2004 | OG | SER | 207 | -0.482 | 61.120 | 129.256 | 1.00 | 35.73 | 0 |
| ATOM | 2006 | C | SER | 207 | 1.951 | 59.699 | 127.446 | 1.00 | 2.00 | 0 |
| ATOM | 2007 | O | SER | 207 | 2.075 | 58.743 | 126.681 | 1.00 | 31.05 | 0 |
| ATOM | 2008 | N | ASP | 208 | 2.777 | 59.943 | 128.462 | 1.00 | 2.00 | 0 |
| ATOM | 2010 | CA | ASP | 208 | 3.899 | 59.056 | 128.764 | 1.00 | 2.00 | 0 |
| ATOM | 2011 | CB | ASP | 208 | 5.257 | 59.714 | 128.505 | 1.00 | 42.39 | 0 |
| ATOM | 2012 | CG | ASP | 208 | 5.296 | 60.532 | 127.256 | 1.00 | 46.59 | 0 |
| ATOM | 2013 | OD1 | ASP | 208 | 5.695 | 61.706 | 127.362 | 1.00 | 48.93 | 0 |
| ATOM | 2014 | OD2 | ASP | 208 | 4.959 | 60.008 | 126.180 | 1.00 | 44.70 | 0 |
| ATOM | 2015 | C | ASP | 208 | 3.903 | 58.705 | 130.231 | 1.00 | 2.00 | 0 |
| ATOM | 2016 | O | ASP | 208 | 3.580 | 59.537 | 131.072 | 1.00 | 45.54 | 0 |
| ATOM | 2017 | N | PRO | 209 | 4.244 | 57.457 | 130.559 | 1.00 | 10.98 | 0 |
| ATOM | 2018 | CD | PRO | 209 | 4.509 | 56.316 | 129.673 | 1.00 | 2.00 | 0 |
| ATOM | 2019 | CA | PRO | 209 | 4.299 | 57.040 | 131.957 | 1.00 | 10.98 | 0 |
| ATOM | 2020 | CB | PRO | 209 | 4.407 | 55.522 | 131.845 | 1.00 | 2.00 | 0 |
| ATOM | 2021 | CG | PRO | 209 | 5.197 | 55.356 | 130.604 | 1.00 | 2.00 | 0 |
| ATOM | 2022 | C | PRO | 209 | 5.584 | 57.675 | 132.507 | 1.00 | 10.98 | 0 |
| ATOM | 2023 | O | PRO | 209 | 6.448 | 58.078 | 131.712 | 1.00 | 2.00 | 0 |
| ATOM | 2024 | N | ASP | 210 | 5.724 | 57.774 | 133.833 | 1.00 | 2.00 | 0 |
| ATOM | 2026 | CA | ASP | 210 | 6.931 | 58.360 | 134.413 | 1.00 | 2.00 | 0 |
| ATOM | 2027 | CB | ASP | 210 | 6.755 | 59.863 | 134.614 | 1.00 | 31.00 | 0 |
| ATOM | 2028 | CG | ASP | 210 | 8.050 | 60.570 | 134.990 | 1.00 | 36.69 | 0 |
| ATOM | 2029 | OD1 | ASP | 210 | 9.132 | 59.956 | 134.874 | 1.00 | 33.32 | 0 |
| ATOM | 2030 | OD2 | ASP | 210 | 7.989 | 61.756 | 135.396 | 1.00 | 38.93 | 0 |
| ATOM | 2031 | C | ASP | 210 | 7.304 | 57.734 | 135.729 | 1.00 | 2.00 | 0 |
| ATOM | 2032 | O | ASP | 210 | 6.448 | 57.320 | 136.496 | 1.00 | 28.60 | 0 |
| ATOM | 2033 | N | LYS | 211 | 8.608 | 57.666 | 135.966 | 1.00 | 4.23 | 0 |
| ATOM | 2035 | CA | LYS | 211 | 9.170 | 57.136 | 137.211 | 1.00 | 9.37 | 0 |
| ATOM | 2036 | CB | LYS | 211 | 10.647 | 56.760 | 137.024 | 1.00 | 17.66 | 0 |
| ATOM | 2037 | CG | LYS | 211 | 10.941 | 55.441 | 136.345 | 1.00 | 29.60 | 0 |
| ATOM | 2038 | CD | LYS | 211 | 12.451 | 55.184 | 136.403 | 1.00 | 32.82 | 0 |
| ATOM | 2039 | CE | LYS | 211 | 12.852 | 53.831 | 135.809 | 1.00 | 42.70 | 0 |
| ATOM | 2040 | NZ | LYS | 211 | 14.336 | 53.616 | 135.852 | 1.00 | 41.45 | 0 |
| ATOM | 2044 | C | LYS | 211 | 9.100 | 58.157 | 138.367 | 1.00 | 7.69 | 0 |
| ATOM | 2045 | O | LYS | 211 | 8.746 | 57.803 | 139.481 | 1.00 | 18.85 | 0 |
| ATOM | 2046 | N | ASP | 212 | 9.456 | 59.414 | 138.093 | 1.00 | 2.00 | 0 |
| ATOM | 2048 | CA | ASP | 212 | 9.468 | 60.483 | 139.101 | 1.00 | 2.00 | 0 |
| ATOM | 2049 | CB | ASP | 212 | 10.322 | 61.669 | 138.624 | 1.00 | 39.78 | 0 |
| ATOM | 2050 | CG | ASP | 212 | 11.483 | 61.254 | 137.754 | 1.00 | 46.31 | 0 |
| ATOM | 2051 | OD1 | ASP | 212 | 11.823 | 62.030 | 136.834 | 1.00 | 41.85 | 0 |
| ATOM | 2052 | OD2 | ASP | 212 | 12.051 | 60.166 | 137.987 | 1.00 | 46.28 | 0 |
| ATOM | 2053 | C | ASP | 212 | 8.074 | 61.033 | 139.412 | 1.00 | 2.00 | 0 |
| ATOM | 2054 | O | ASP | 212 | 7.943 | 62.164 | 139.903 | 1.00 | 41.82 | 0 |
| ATOM | 2055 | N | VAL | 213 | 7.040 | 60.250 | 139.124 | 1.00 | 2.00 | 0 |
| ATOM | 2057 | CA | VAL | 213 | 5.669 | 60.690 | 139.340 | 1.00 | 2.00 | 0 |
| ATOM | 2058 | CB | VAL | 213 | 5.137 | 61.376 | 138.050 | 1.00 | 2.00 | 0 |
| ATOM | 2059 | CG1 | VAL | 213 | 3.652 | 61.247 | 137.922 | 1.00 | 2.00 | 0 |
| ATOM | 2060 | CG2 | VAL | 213 | 5.505 | 62.826 | 138.076 | 1.00 | 2.00 | 0 |
| ATOM | 2061 | C | VAL | 213 | 4.767 | 59.526 | 139.763 | 1.00 | 2.00 | 0 |
| ATOM | 2062 | O | VAL | 213 | 5.007 | 58.356 | 139.390 | 1.00 | 2.00 | 0 |
| ATOM | 2063 | N | LEU | 214 | 3.748 | 59.844 | 140.564 | 1.00 | 21.53 | 0 |
| ATOM | 2065 | CA | LEU | 214 | 2.815 | 58.830 | 141.022 | 1.00 | 19.34 | 0 |
| ATOM | 2066 | CB | LEU | 214 | 2.742 | 58.809 | 142.543 | 1.00 | 14.66 | 0 |
| ATOM | 2067 | CG | LEU | 214 | 2.371 | 57.438 | 143.097 | 1.00 | 15.86 | 0 |
| ATOM | 2068 | CD1 | LEU | 214 | 3.507 | 56.477 | 142.816 | 1.00 | 9.71 | 0 |

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|---|---|---|---|---|---|---|---|---|---|---|
| ATOM | 2069 | CD2 | LEU | 214 | 2.109 | 57.530 | 144.588 | 1.00 | 17.44 | 0 |
| ATOM | 2070 | C | LEU | 214 | 1.433 | 59.068 | 140.439 | 1.00 | 19.87 | 0 |
| ATOM | 2071 | O | LEU | 214 | 0.757 | 58.124 | 140.033 | 1.00 | 9.54 | 0 |
| ATOM | 2072 | N | GLY | 215 | 1.003 | 60.322 | 140.411 | 1.00 | 16.98 | 0 |
| ATOM | 2074 | CA | GLY | 215 | -0.299 | 60.640 | 139.852 | 1.00 | 11.19 | 0 |
| ATOM | 2075 | C | GLY | 215 | -0.081 | 61.255 | 138.487 | 1.00 | 12.07 | 0 |
| ATOM | 2076 | O | GLY | 215 | 0.772 | 60.796 | 137.739 | 1.00 | 10.02 | 0 |
| ATOM | 2077 | N | TRP | 216 | -0.824 | 62.303 | 138.167 | 1.00 | 2.00 | 0 |
| ATOM | 2079 | CA | TRP | 216 | -0.684 | 62.979 | 136.890 | 1.00 | 2.00 | 0 |
| ATOM | 2080 | CB | TRP | 216 | -2.030 | 63.535 | 136.458 | 1.00 | 2.00 | 0 |
| ATOM | 2081 | CG | TRP | 216 | -2.903 | 62.452 | 136.050 | 1.00 | 2.00 | 0 |
| ATOM | 2082 | CD2 | TRP | 216 | -2.840 | 61.741 | 134.804 | 1.00 | 2.00 | 0 |
| ATOM | 2083 | CE2 | TRP | 216 | -3.806 | 60.713 | 134.865 | 1.00 | 2.00 | 0 |
| ATOM | 2084 | CE3 | TRP | 216 | -2.050 | 61.865 | 133.648 | 1.00 | 2.00 | 0 |
| ATOM | 2085 | CD1 | TRP | 216 | -3.879 | 61.860 | 136.789 | 1.00 | 2.00 | 0 |
| ATOM | 2086 | NE1 | TRP | 216 | -4.425 | 60.811 | 136.087 | 1.00 | 2.00 | 0 |
| ATOM | 2088 | CZ2 | TRP | 216 | -4.005 | 59.812 | 133.809 | 1.00 | 2.00 | 0 |
| ATOM | 2089 | CZ3 | TRP | 216 | -2.251 | 60.970 | 132.605 | 1.00 | 2.00 | 0 |
| ATOM | 2090 | CH2 | TRP | 216 | -3.217 | 59.961 | 132.695 | 1.00 | 2.00 | 0 |
| ATOM | 2091 | C | TRP | 216 | 0.310 | 64.101 | 136.985 | 1.00 | 2.00 | 0 |
| ATOM | 2092 | O | TRP | 216 | 0.261 | 64.883 | 137.926 | 1.00 | 2.00 | 0 |
| ATOM | 2093 | N | GLY | 217 | 1.213 | 64.182 | 136.021 | 1.00 | 12.63 | 0 |
| ATOM | 2095 | CA | GLY | 217 | 2.199 | 65.245 | 136.028 | 1.00 | 15.52 | 0 |
| ATOM | 2096 | C | GLY | 217 | 2.312 | 65.928 | 134.675 | 1.00 | 10.15 | 0 |
| ATOM | 2097 | O | GLY | 217 | 1.627 | 65.559 | 133.720 | 1.00 | 26.84 | 0 |
| ATOM | 2098 | N | GLU | 218 | 3.189 | 66.923 | 134.594 | 1.00 | 23.86 | 0 |
| ATOM | 2100 | CA | GLU | 218 | 3.434 | 67.686 | 133.364 | 1.00 | 22.47 | 0 |
| ATOM | 2101 | CB | GLU | 218 | 4.198 | 68.978 | 133.729 | 1.00 | 65.82 | 0 |
| ATOM | 2102 | CG | GLU | 218 | 5.082 | 69.595 | 132.641 | 1.00 | 67.96 | 0 |
| ATOM | 2103 | CD | GLU | 218 | 6.577 | 69.562 | 132.987 | 1.00 | 67.00 | 0 |
| ATOM | 2104 | OE1 | GLU | 218 | 7.056 | 70.519 | 133.631 | 1.00 | 68.41 | 0 |
| ATOM | 2105 | OE2 | GLU | 218 | 7.276 | 68.589 | 132.616 | 1.00 | 63.29 | 0 |
| ATOM | 2106 | C | GLU | 218 | 4.232 | 66.841 | 132.371 | 1.00 | 25.48 | 0 |
| ATOM | 2107 | O | GLU | 218 | 4.808 | 65.820 | 132.750 | 1.00 | 67.07 | 0 |
| ATOM | 2108 | N | ASN | 219 | 4.253 | 67.245 | 131.103 | 1.00 | 21.19 | 0 |
| ATOM | 2110 | CA | ASN | 219 | 5.039 | 66.510 | 130.108 | 1.00 | 21.18 | 0 |
| ATOM | 2111 | CB | ASN | 219 | 4.140 | 65.888 | 129.048 | 1.00 | 10.60 | 0 |
| ATOM | 2112 | CG | ASN | 219 | 4.832 | 64.791 | 128.282 | 1.00 | 14.78 | 0 |
| ATOM | 2113 | OD1 | ASN | 219 | 6.052 | 64.646 | 128.341 | 1.00 | 9.20 | 0 |
| ATOM | 2114 | ND2 | ASN | 219 | 4.057 | 64.003 | 127.560 | 1.00 | 8.28 | 0 |
| ATOM | 2117 | C | ASN | 219 | 6.058 | 67.411 | 129.425 | 1.00 | 21.70 | 0 |
| ATOM | 2118 | O | ASN | 219 | 5.776 | 68.576 | 129.151 | 1.00 | 9.52 | 0 |
| ATOM | 2119 | N | ASP | 220 | 7.246 | 66.886 | 129.151 | 1.00 | 35.32 | 0 |
| ATOM | 2121 | CA | ASP | 220 | 8.266 | 67.690 | 128.485 | 1.00 | 34.19 | 0 |
| ATOM | 2122 | CB | ASP | 220 | 9.585 | 66.900 | 128.358 | 1.00 | 48.55 | 0 |
| ATOM | 2123 | CG | ASP | 220 | 9.469 | 65.673 | 127.447 | 1.00 | 92.38 | 0 |
| ATOM | 2124 | OD1 | ASP | 220 | 9.083 | 64.584 | 127.938 | 1.00 | 48.43 | 0 |
| ATOM | 2125 | OD2 | ASP | 220 | 9.778 | 65.797 | 126.237 | 1.00 | 92.09 | 0 |
| ATOM | 2126 | C | ASP | 220 | 7.763 | 68.148 | 127.100 | 1.00 | 33.44 | 0 |
| ATOM | 2127 | O | ASP | 220 | 8.045 | 69.262 | 126.661 | 1.00 | 47.84 | 0 |
| ATOM | 2128 | N | ARG | 221 | 6.986 | 67.287 | 126.444 | 1.00 | 22.98 | 0 |
| ATOM | 2130 | CA | ARG | 221 | 6.427 | 67.552 | 125.127 | 1.00 | 22.11 | 0 |
| ATOM | 2131 | CB | ARG | 221 | 5.578 | 66.382 | 124.672 | 1.00 | 2.00 | 0 |
| ATOM | 2132 | CG | ARG | 221 | 6.251 | 65.056 | 124.739 | 1.00 | 2.00 | 0 |
| ATOM | 2133 | CD | ARG | 221 | 5.241 | 63.981 | 124.421 | 1.00 | 2.00 | 0 |
| ATOM | 2134 | NE | ARG | 221 | 5.828 | 62.658 | 124.590 | 1.00 | 2.00 | 0 |
| ATOM | 2136 | CZ | ARG | 221 | 6.785 | 62.154 | 123.811 | 1.00 | 2.00 | 0 |
| ATOM | 2137 | NH1 | ARG | 221 | 7.255 | 62.866 | 122.790 | 1.00 | 2.00 | 0 |
| ATOM | 2140 | NH2 | ARG | 221 | 7.285 | 60.947 | 124.064 | 1.00 | 2.00 | 0 |
| ATOM | 2143 | C | ARG | 221 | 5.546 | 68.776 | 125.109 | 1.00 | 18.96 | 0 |
| ATOM | 2144 | O | ARG | 221 | 5.164 | 69.239 | 124.052 | 1.00 | 2.00 | 0 |
| ATOM | 2145 | N | GLY | 222 | 5.188 | 69.280 | 126.280 | 1.00 | 2.00 | 0 |
| ATOM | 2147 | CA | GLY | 222 | 4.328 | 70.447 | 126.343 | 1.00 | 2.00 | 0 |
| ATOM | 2148 | C | GLY | 222 | 2.939 | 70.103 | 125.844 | 1.00 | 2.00 | 0 |
| ATOM | 2149 | O | GLY | 222 | 2.142 | 70.988 | 125.509 | 1.00 | 29.15 | 0 |
| ATOM | 2150 | N | VAL | 223 | 2.658 | 68.804 | 125.776 | 1.00 | 2.00 | 0 |
| ATOM | 2152 | CA | VAL | 223 | 1.356 | 68.313 | 125.342 | 1.00 | 2.00 | 0 |
| ATOM | 2153 | CB | VAL | 223 | 1.364 | 67.860 | 123.839 | 1.00 | 2.00 | 0 |

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|---|---|---|---|---|---|---|---|---|---|---|
| ATOM | 2154 | CG1 | VAL | 223 | -0.063 | 67.888 | 123.280 | 1.00 | 2.00 | 0 |
| ATOM | 2155 | CG2 | VAL | 223 | 2.258 | 68.762 | 123.004 | 1.00 | 2.00 | 0 |
| ATOM | 2156 | C | VAL | 223 | 1.071 | 67.125 | 126.250 | 1.00 | 2.00 | 0 |
| ATOM | 2157 | O | VAL | 223 | 2.004 | 66.431 | 126.656 | 1.00 | 2.00 | 0 |
| ATOM | 2158 | N | SER | 224 | -0.205 | 66.897 | 126.550 | 1.00 | 12.21 | 0 |
| ATOM | 2160 | CA | SER | 224 | -0.661 | 65.825 | 127.440 | 1.00 | 15.55 | 0 |
| ATOM | 2161 | CB | SER | 224 | -0.609 | 64.453 | 126.759 | 1.00 | 6.64 | 0 |
| ATOM | 2162 | OG | SER | 224 | 0.713 | 64.003 | 126.546 | 1.00 | 10.80 | 0 |
| ATOM | 2164 | C | SER | 224 | 0.077 | 65.779 | 128.787 | 1.00 | 20.53 | 0 |
| ATOM | 2165 | O | SER | 224 | 0.814 | 66.706 | 129.153 | 1.00 | 8.42 | 0 |
| ATOM | 2166 | N | PHE | 225 | -0.124 | 64.700 | 129.533 | 1.00 | 6.68 | 0 |
| ATOM | 2168 | CA | PHE | 225 | 0.484 | 64.586 | 130.839 | 1.00 | 6.68 | 0 |
| ATOM | 2169 | CB | PHE | 225 | -0.625 | 64.489 | 131.890 | 1.00 | 14.03 | 0 |
| ATOM | 2170 | CG | PHE | 225 | -1.670 | 65.552 | 131.758 | 1.00 | 11.21 | 0 |
| ATOM | 2171 | CD1 | PHE | 225 | -2.925 | 65.248 | 131.239 | 1.00 | 11.66 | 0 |
| ATOM | 2172 | CD2 | PHE | 225 | -1.396 | 66.869 | 132.131 | 1.00 | 11.41 | 0 |
| ATOM | 2173 | CE1 | PHE | 225 | -3.899 | 66.241 | 131.086 | 1.00 | 11.76 | 0 |
| ATOM | 2174 | CE2 | PHE | 225 | -2.363 | 67.869 | 131.983 | 1.00 | 14.72 | 0 |
| ATOM | 2175 | CZ | PHE | 225 | -3.618 | 67.553 | 131.458 | 1.00 | 16.73 | 0 |
| ATOM | 2176 | C | PHE | 225 | 1.405 | 63.392 | 130.957 | 1.00 | 6.68 | 0 |
| ATOM | 2177 | O | PHE | 225 | 1.902 | 62.850 | 129.966 | 1.00 | 15.31 | 0 |
| ATOM | 2178 | N | THR | 226 | 1.663 | 63.022 | 132.203 | 1.00 | 2.00 | 0 |
| ATOM | 2180 | CA | THR | 226 | 2.473 | 61.872 | 132.509 | 1.00 | 2.00 | 0 |
| ATOM | 2181 | CB | THR | 226 | 3.898 | 62.226 | 132.853 | 1.00 | 13.51 | 0 |
| ATOM | 2182 | OG1 | THR | 226 | 4.607 | 61.012 | 133.094 | 1.00 | 13.51 | 0 |
| ATOM | 2184 | CG2 | THR | 226 | 3.961 | 63.081 | 134.086 | 1.00 | 13.51 | 0 |
| ATOM | 2185 | C | THR | 226 | 1.809 | 61.217 | 133.686 | 1.00 | 2.00 | 0 |
| ATOM | 2186 | O | THR | 226 | 1.039 | 61.861 | 134.394 | 1.00 | 13.51 | 0 |
| ATOM | 2187 | N | PHE | 227 | 2.086 | 59.938 | 133.883 | 1.00 | 2.00 | 0 |
| ATOM | 2189 | CA | PHE | 227 | 1.466 | 59.191 | 134.957 | 1.00 | 2.00 | 0 |
| ATOM | 2190 | CB | PHE | 227 | 0.206 | 58.448 | 134.472 | 1.00 | 18.74 | 0 |
| ATOM | 2191 | CG | PHE | 227 | 0.362 | 57.793 | 133.131 | 1.00 | 21.51 | 0 |
| ATOM | 2192 | CD1 | PHE | 227 | 0.717 | 56.453 | 133.034 | 1.00 | 18.55 | 0 |
| ATOM | 2193 | CD2 | PHE | 227 | 0.188 | 58.532 | 131.954 | 1.00 | 20.45 | 0 |
| ATOM | 2194 | CE1 | PHE | 227 | 0.902 | 55.857 | 131.787 | 1.00 | 19.97 | 0 |
| ATOM | 2195 | CE2 | PHE | 227 | 0.371 | 57.948 | 130.698 | 1.00 | 14.44 | 0 |
| ATOM | 2196 | CZ | PHE | 227 | 0.729 | 56.612 | 130.612 | 1.00 | 17.09 | 0 |
| ATOM | 2197 | C | PHE | 227 | 2.427 | 58.224 | 135.562 | 1.00 | 2.00 | 0 |
| ATOM | 2198 | O | PHE | 227 | 3.282 | 57.668 | 134.888 | 1.00 | 20.11 | 0 |
| ATOM | 2199 | N | GLY | 228 | 2.294 | 58.066 | 136.867 | 1.00 | 21.90 | 0 |
| ATOM | 2201 | CA | GLY | 228 | 3.143 | 57.165 | 137.607 | 1.00 | 20.86 | 0 |
| ATOM | 2202 | C | GLY | 228 | 2.424 | 55.859 | 137.815 | 1.00 | 24.57 | 0 |
| ATOM | 2203 | O | GLY | 228 | 1.365 | 55.615 | 137.223 | 1.00 | 2.00 | 0 |
| ATOM | 2204 | N | ALA | 229 | 2.974 | 55.041 | 138.704 | 1.00 | 2.00 | 0 |
| ATOM | 2206 | CA | ALA | 229 | 2.422 | 53.722 | 138.971 | 1.00 | 2.00 | 0 |
| ATOM | 2207 | CB | ALA | 229 | 3.372 | 52.924 | 139.835 | 1.00 | 2.00 | 0 |
| ATOM | 2208 | C | ALA | 229 | 1.055 | 53.706 | 139.576 | 1.00 | 2.00 | 0 |
| ATOM | 2209 | O | ALA | 229 | 0.359 | 52.705 | 139.460 | 1.00 | 2.00 | 0 |
| ATOM | 2210 | N | GLU | 230 | 0.666 | 54.802 | 140.220 | 1.00 | 2.00 | 0 |
| ATOM | 2212 | CA | GLU | 230 | -0.648 | 54.881 | 140.875 | 1.00 | 2.00 | 0 |
| ATOM | 2213 | CB | GLU | 230 | -0.787 | 56.193 | 141.647 | 1.00 | 66.07 | 0 |
| ATOM | 2214 | CG | GLU | 230 | -1.123 | 56.014 | 143.111 | 1.00 | 71.18 | 0 |
| ATOM | 2215 | CD | GLU | 230 | -2.376 | 55.175 | 143.337 | 1.00 | 2.00 | 0 |
| ATOM | 2216 | OE1 | GLU | 230 | -2.275 | 53.918 | 143.199 | 1.00 | 2.00 | 0 |
| ATOM | 2217 | OE2 | GLU | 230 | -3.448 | 55.773 | 143.663 | 1.00 | 2.00 | 0 |
| ATOM | 2218 | C | GLU | 230 | -1.769 | 54.777 | 139.862 | 1.00 | 2.00 | 0 |
| ATOM | 2219 | O | GLU | 230 | -2.649 | 53.922 | 139.966 | 1.00 | 60.28 | 0 |
| ATOM | 2220 | N | VAL | 231 | -1.684 | 55.652 | 138.861 | 1.00 | 12.41 | 0 |
| ATOM | 2222 | CA | VAL | 231 | -2.649 | 55.749 | 137.772 | 1.00 | 9.72 | 0 |
| ATOM | 2223 | CB | VAL | 231 | -2.186 | 56.789 | 136.717 | 1.00 | 2.00 | 0 |
| ATOM | 2224 | CG1 | VAL | 231 | -3.304 | 57.063 | 135.718 | 1.00 | 2.00 | 0 |
| ATOM | 2225 | CG2 | VAL | 231 | -1.728 | 58.077 | 137.396 | 1.00 | 2.00 | 0 |
| ATOM | 2226 | C | VAL | 231 | -2.816 | 54.393 | 137.102 | 1.00 | 11.88 | 0 |
| ATOM | 2227 | O | VAL | 231 | -3.937 | 53.966 | 136.849 | 1.00 | 2.00 | 0 |
| ATOM | 2228 | N | VAL | 232 | -1.695 | 53.723 | 136.832 | 1.00 | 2.00 | 0 |
| ATOM | 2230 | CA | VAL | 232 | -1.678 | 52.397 | 136.203 | 1.00 | 2.00 | 0 |
| ATOM | 2231 | CB | VAL | 232 | -0.245 | 51.817 | 136.151 | 1.00 | 2.00 | 0 |
| ATOM | 2232 | CG1 | VAL | 232 | -0.264 | 50.442 | 135.548 | 1.00 | 2.00 | 0 |

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|---|---|---|---|---|---|---|---|---|---|---|
| ATOM | 2233 | CG2 | VAL | 232 | 0.664 | 52.724 | 135.376 | 1.00 | 2.00 | 0 |
| ATOM | 2234 | C | VAL | 232 | -2.533 | 51.413 | 136.992 | 1.00 | 2.00 | 0 |
| ATOM | 2235 | O | VAL | 232 | -3.449 | 50.787 | 136.454 | 1.00 | 2.00 | 0 |
| ATOM | 2236 | N | ALA | 233 | -2.217 | 51.292 | 138.275 | 1.00 | 38.57 | 0 |
| ATOM | 2238 | CA | ALA | 233 | -2.920 | 50.395 | 139.173 | 1.00 | 38.57 | 0 |
| ATOM | 2239 | CB | ALA | 233 | -2.297 | 50.487 | 140.542 | 1.00 | 13.20 | 0 |
| ATOM | 2240 | C | ALA | 233 | -4.426 | 50.681 | 139.245 | 1.00 | 38.57 | 0 |
| ATOM | 2241 | O | ALA | 233 | -5.255 | 49.763 | 139.166 | 1.00 | 9.05 | 0 |
| ATOM | 2242 | N | LYS | 234 | -4.780 | 51.954 | 139.397 | 1.00 | 2.00 | 0 |
| ATOM | 2244 | CA | LYS | 234 | -6.177 | 52.355 | 139.477 | 1.00 | 2.00 | 0 |
| ATOM | 2245 | CB | LYS | 234 | -6.270 | 53.843 | 139.803 | 1.00 | 22.96 | 0 |
| ATOM | 2246 | CG | LYS | 234 | -5.776 | 54.160 | 141.205 | 1.00 | 31.42 | 0 |
| ATOM | 2247 | CD | LYS | 234 | -6.667 | 53.499 | 142.257 | 1.00 | 42.09 | 0 |
| ATOM | 2248 | CE | LYS | 234 | -5.916 | 53.151 | 143.543 | 1.00 | 40.07 | 0 |
| ATOM | 2249 | NZ | LYS | 234 | -5.104 | 51.892 | 143.444 | 1.00 | 41.59 | 0 |
| ATOM | 2253 | C | LYS | 234 | -6.920 | 52.036 | 138.183 | 1.00 | 2.00 | 0 |
| ATOM | 2254 | O | LYS | 234 | -7.936 | 51.319 | 138.206 | 1.00 | 20.45 | 0 |
| ATOM | 2255 | N | PHE | 235 | -6.389 | 52.532 | 137.061 | 1.00 | 14.37 | 0 |
| ATOM | 2257 | CA | PHE | 235 | -6.973 | 52.319 | 135.733 | 1.00 | 14.37 | 0 |
| ATOM | 2258 | CB | PHE | 235 | -6.055 | 52.880 | 134.640 | 1.00 | 2.00 | 0 |
| ATOM | 2259 | CG | PHE | 235 | -6.438 | 52.452 | 133.249 | 1.00 | 2.00 | 0 |
| ATOM | 2260 | CD1 | PHE | 235 | -7.352 | 53.199 | 132.502 | 1.00 | 2.00 | 0 |
| ATOM | 2261 | CD2 | PHE | 235 | -5.924 | 51.270 | 132.706 | 1.00 | 2.00 | 0 |
| ATOM | 2262 | CE1 | PHE | 235 | -7.760 | 52.777 | 131.236 | 1.00 | 2.00 | 0 |
| ATOM | 2263 | CE2 | PHE | 235 | -6.316 | 50.834 | 131.452 | 1.00 | 2.00 | 0 |
| ATOM | 2264 | CZ | PHE | 235 | -7.242 | 51.588 | 130.710 | 1.00 | 2.00 | 0 |
| ATOM | 2265 | C | PHE | 235 | -7.229 | 50.849 | 135.444 | 1.00 | 14.37 | 0 |
| ATOM | 2266 | O | PHE | 235 | -8.312 | 50.471 | 134.977 | 1.00 | 2.00 | 0 |
| ATOM | 2267 | N | LEU | 236 | -6.217 | 50.029 | 135.690 | 1.00 | 3.08 | 0 |
| ATOM | 2269 | CA | LEU | 236 | -6.339 | 48.606 | 135.447 | 1.00 | 5.72 | 0 |
| ATOM | 2270 | CB | LEU | 236 | -5.018 | 47.900 | 135.731 | 1.00 | 2.00 | 0 |
| ATOM | 2271 | CG | LEU | 236 | -3.915 | 48.136 | 134.710 | 1.00 | 2.00 | 0 |
| ATOM | 2272 | CD1 | LEU | 236 | -2.699 | 47.332 | 135.096 | 1.00 | 2.00 | 0 |
| ATOM | 2273 | CD2 | LEU | 236 | -4.405 | 47.737 | 133.321 | 1.00 | 2.00 | 0 |
| ATOM | 2274 | C | LEU | 236 | -7.452 | 47.978 | 136.278 | 1.00 | 10.30 | 0 |
| ATOM | 2275 | O | LEU | 236 | -8.389 | 47.398 | 135.712 | 1.00 | 2.00 | 0 |
| ATOM | 2276 | N | HIS | 237 | -7.368 | 48.118 | 137.606 | 1.00 | 8.44 | 0 |
| ATOM | 2278 | CA | HIS | 237 | -8.368 | 47.540 | 138.504 | 1.00 | 8.44 | 0 |
| ATOM | 2279 | CB | HIS | 237 | -8.088 | 47.885 | 139.980 | 1.00 | 38.56 | 0 |
| ATOM | 2280 | CG | HIS | 237 | -9.141 | 47.380 | 140.935 | 1.00 | 46.82 | 0 |
| ATOM | 2281 | CD2 | HIS | 237 | -10.323 | 47.916 | 141.329 | 1.00 | 46.01 | 0 |
| ATOM | 2282 | ND1 | HIS | 237 | -9.035 | 46.173 | 141.599 | 1.00 | 46.38 | 0 |
| ATOM | 2284 | CE1 | HIS | 237 | -10.103 | 45.989 | 142.355 | 1.00 | 50.85 | 0 |
| ATOM | 2285 | NE2 | HIS | 237 | -10.900 | 47.031 | 142.210 | 1.00 | 49.26 | 0 |
| ATOM | 2287 | C | HIS | 237 | -9.747 | 48.033 | 138.138 | 1.00 | 8.44 | 0 |
| ATOM | 2288 | O | HIS | 237 | -10.672 | 47.232 | 138.027 | 1.00 | 35.43 | 0 |
| ATOM | 2289 | N | LYS | 238 | -9.882 | 49.346 | 137.947 | 1.00 | 2.00 | 0 |
| ATOM | 2291 | CA | LYS | 238 | -11.183 | 49.923 | 137.607 | 1.00 | 2.00 | 0 |
| ATOM | 2292 | CB | LYS | 238 | -11.071 | 51.424 | 137.327 | 1.00 | 28.00 | 0 |
| ATOM | 2293 | CG | LYS | 238 | -12.427 | 52.103 | 137.104 | 1.00 | 29.80 | 0 |
| ATOM | 2294 | CD | LYS | 238 | -12.322 | 53.628 | 136.829 | 1.00 | 36.02 | 0 |
| ATOM | 2295 | CE | LYS | 238 | -11.917 | 54.444 | 138.083 | 1.00 | 32.99 | 0 |
| ATOM | 2296 | NZ | LYS | 238 | -11.833 | 55.925 | 137.845 | 1.00 | 30.09 | 0 |
| ATOM | 2300 | C | LYS | 238 | -11.776 | 49.215 | 136.403 | 1.00 | 2.00 | 0 |
| ATOM | 2301 | O | LYS | 238 | -12.991 | 49.205 | 136.234 | 1.00 | 29.21 | 0 |
| ATOM | 2302 | N | HIS | 239 | -10.913 | 48.607 | 135.584 | 1.00 | 2.00 | 0 |
| ATOM | 2304 | CA | HIS | 239 | -11.340 | 47.897 | 134.384 | 1.00 | 2.00 | 0 |
| ATOM | 2305 | CB | HIS | 239 | -10.784 | 48.603 | 133.148 | 1.00 | 2.00 | 0 |
| ATOM | 2306 | CG | HIS | 239 | -11.125 | 50.056 | 133.091 | 1.00 | 2.00 | 0 |
| ATOM | 2307 | CD2 | HIS | 239 | -12.282 | 50.689 | 132.785 | 1.00 | 2.00 | 0 |
| ATOM | 2308 | ND1 | HIS | 239 | -10.217 | 51.046 | 133.397 | 1.00 | 2.00 | 0 |
| ATOM | 2310 | CE1 | HIS | 239 | -10.797 | 52.225 | 133.284 | 1.00 | 2.00 | 0 |
| ATOM | 2311 | NE2 | HIS | 239 | -12.052 | 52.036 | 132.914 | 1.00 | 2.00 | 0 |
| ATOM | 2313 | C | HIS | 239 | -10.946 | 46.417 | 134.352 | 1.00 | 2.00 | 0 |
| ATOM | 2314 | O | HIS | 239 | -10.938 | 45.798 | 133.295 | 1.00 | 2.00 | 0 |
| ATOM | 2315 | N | ASP | 240 | -10.642 | 45.838 | 135.503 | 1.00 | 37.96 | 0 |
| ATOM | 2317 | CA | ASP | 240 | -10.251 | 44.433 | 135.564 | 1.00 | 37.83 | 0 |
| ATOM | 2318 | CB | ASP | 240 | -11.482 | 43.512 | 135.737 | 1.00 | 39.81 | 0 |

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|---|---|---|---|---|---|---|---|---|---|
| ATOM | 2319 | CG | ASP | 240 | -12.676 | 43.919 | 134.870 | 1.00 | 47.06 | 0 |
| ATOM | 2320 | OD1 | ASP | 240 | -12.687 | 43.571 | 133.666 | 1.00 | 50.73 | 0 |
| ATOM | 2321 | OD2 | ASP | 240 | -13.610 | 44.578 | 135.396 | 1.00 | 47.58 | 0 |
| ATOM | 2322 | C | ASP | 240 | -9.393 | 43.985 | 134.385 | 1.00 | 37.76 | 0 |
| ATOM | 2323 | O | ASP | 240 | -9.626 | 42.933 | 133.797 | 1.00 | 40.81 | 0 |
| ATOM | 2324 | N | LEU | 241 | -8.417 | 44.823 | 134.040 | 1.00 | 2.00 | 0 |
| ATOM | 2326 | CA | LEU | 241 | -7.462 | 44.551 | 132.955 | 1.00 | 2.00 | 0 |
| ATOM | 2327 | CB | LEU | 241 | -7.086 | 45.858 | 132.229 | 1.00 | 2.00 | 0 |
| ATOM | 2328 | CG | LEU | 241 | -8.185 | 46.590 | 131.429 | 1.00 | 2.00 | 0 |
| ATOM | 2329 | CD1 | LEU | 241 | -7.795 | 48.047 | 131.224 | 1.00 | 2.00 | 0 |
| ATOM | 2330 | CD2 | LEU | 241 | -8.435 | 45.899 | 130.087 | 1.00 | 2.00 | 0 |
| ATOM | 2331 | C | LEU | 241 | -6.225 | 43.925 | 133.601 | 1.00 | 2.00 | 0 |
| ATOM | 2332 | O | LEU | 241 | -6.157 | 43.832 | 134.818 | 1.00 | 2.00 | 0 |
| ATOM | 2333 | N | ASP | 242 | -5.235 | 43.534 | 132.817 | 1.00 | 2.00 | 0 |
| ATOM | 2335 | CA | ASP | 242 | -4.046 | 42.895 | 133.380 | 1.00 | 2.00 | 0 |
| ATOM | 2336 | CB | ASP | 242 | -3.974 | 41.455 | 132.915 | 1.00 | 25.69 | 0 |
| ATOM | 2337 | CG | ASP | 242 | -4.683 | 40.511 | 133.822 | 1.00 | 12.83 | 0 |
| ATOM | 2338 | OD1 | ASP | 242 | -5.751 | 40.853 | 134.365 | 1.00 | 16.91 | 0 |
| ATOM | 2339 | OD2 | ASP | 242 | -4.149 | 39.404 | 133.976 | 1.00 | 15.37 | 0 |
| ATOM | 2340 | C | ASP | 242 | -2.711 | 43.506 | 133.033 | 1.00 | 2.00 | 0 |
| ATOM | 2341 | O | ASP | 242 | -1.702 | 43.214 | 133.671 | 1.00 | 25.69 | 0 |
| ATOM | 2342 | N | LEU | 243 | -2.689 | 44.317 | 131.994 | 1.00 | 23.97 | 0 |
| ATOM | 2344 | CA | LEU | 243 | -1.440 | 44.899 | 131.539 | 1.00 | 18.84 | 0 |
| ATOM | 2345 | CB | LEU | 243 | -0.644 | 43.799 | 130.822 | 1.00 | 2.00 | 0 |
| ATOM | 2346 | CG | LEU | 243 | 0.698 | 43.831 | 130.097 | 1.00 | 2.00 | 0 |
| ATOM | 2347 | CD1 | LEU | 243 | 0.410 | 43.690 | 128.660 | 1.00 | 2.00 | 0 |
| ATOM | 2348 | CD2 | LEU | 243 | 1.526 | 45.058 | 130.397 | 1.00 | 2.00 | 0 |
| ATOM | 2349 | C | LEU | 243 | -1.804 | 46.013 | 130.590 | 1.00 | 19.91 | 0 |
| ATOM | 2350 | O | LEU | 243 | -2.960 | 46.149 | 130.183 | 1.00 | 2.00 | 0 |
| ATOM | 2351 | N | ILE | 244 | -0.834 | 46.849 | 130.283 | 1.00 | 24.04 | 0 |
| ATOM | 2353 | CA | ILE | 244 | -1.070 | 47.919 | 129.354 | 1.00 | 22.40 | 0 |
| ATOM | 2354 | CB | ILE | 244 | -1.164 | 49.269 | 130.067 | 1.00 | 2.00 | 0 |
| ATOM | 2355 | CG2 | ILE | 244 | -1.235 | 50.405 | 129.026 | 1.00 | 2.00 | 0 |
| ATOM | 2356 | CG1 | ILE | 244 | -2.395 | 49.255 | 130.994 | 1.00 | 2.00 | 0 |
| ATOM | 2357 | CD1 | ILE | 244 | -2.607 | 50.530 | 131.803 | 1.00 | 2.00 | 0 |
| ATOM | 2358 | C | ILE | 244 | 0.069 | 47.902 | 128.369 | 1.00 | 25.54 | 0 |
| ATOM | 2359 | O | ILE | 244 | 1.234 | 47.715 | 128.755 | 1.00 | 2.00 | 0 |
| ATOM | 2360 | N | CYS | 245 | -0.286 | 48.063 | 127.096 | 1.00 | 2.00 | 0 |
| ATOM | 2362 | CA | CYS | 245 | 0.675 | 48.074 | 126.019 | 1.00 | 2.00 | 0 |
| ATOM | 2363 | CB | CYS | 245 | 0.403 | 46.930 | 125.077 | 1.00 | 7.03 | 0 |
| ATOM | 2364 | SG | CYS | 245 | 1.849 | 45.913 | 124.986 | 1.00 | 12.49 | 0 |
| ATOM | 2365 | C | CYS | 245 | 0.668 | 49.389 | 125.275 | 1.00 | 2.00 | 0 |
| ATOM | 2366 | O | CYS | 245 | -0.362 | 49.842 | 124.782 | 1.00 | 8.03 | 0 |
| ATOM | 2367 | N | ARG | 246 | 1.829 | 50.014 | 125.235 | 1.00 | 2.00 | 0 |
| ATOM | 2369 | CA | ARG | 246 | 1.987 | 51.277 | 124.562 | 1.00 | 2.00 | 0 |
| ATOM | 2370 | CB | ARG | 246 | 1.763 | 52.438 | 125.541 | 1.00 | 2.00 | 0 |
| ATOM | 2371 | CG | ARG | 246 | 2.658 | 52.453 | 126.783 | 1.00 | 2.00 | 0 |
| ATOM | 2372 | CD | ARG | 246 | 3.969 | 53.245 | 126.623 | 1.00 | 2.00 | 0 |
| ATOM | 2373 | NE | ARG | 246 | 3.714 | 54.656 | 126.383 | 1.00 | 2.00 | 0 |
| ATOM | 2375 | CZ | ARG | 246 | 4.610 | 55.622 | 126.519 | 1.00 | 2.00 | 0 |
| ATOM | 2376 | NH1 | ARG | 246 | 5.842 | 55.334 | 126.895 | 1.00 | 2.00 | 0 |
| ATOM | 2379 | NH2 | ARG | 246 | 4.263 | 56.881 | 126.289 | 1.00 | 2.00 | 0 |
| ATOM | 2382 | C | ARG | 246 | 3.374 | 51.342 | 123.938 | 1.00 | 2.00 | 0 |
| ATOM | 2383 | O | ARG | 246 | 4.216 | 50.471 | 124.168 | 1.00 | 2.00 | 0 |
| ATOM | 2384 | N | ALA | 247 | 3.605 | 52.345 | 123.108 | 1.00 | 2.00 | 0 |
| ATOM | 2386 | CA | ALA | 247 | 4.906 | 52.489 | 122.484 | 1.00 | 2.00 | 0 |
| ATOM | 2387 | CB | ALA | 247 | 4.791 | 52.272 | 120.975 | 1.00 | 61.76 | 0 |
| ATOM | 2388 | C | ALA | 247 | 5.351 | 53.902 | 122.819 | 1.00 | 2.00 | 0 |
| ATOM | 2389 | O | ALA | 247 | 5.806 | 54.172 | 123.922 | 1.00 | 61.76 | 0 |
| ATOM | 2390 | N | HIS | 248 | 5.187 | 54.801 | 121.870 | 1.00 | 2.00 | 0 |
| ATOM | 2392 | CA | HIS | 248 | 5.512 | 56.193 | 122.042 | 1.00 | 2.00 | 0 |
| ATOM | 2393 | C | HIS | 248 | 6.959 | 56.579 | 122.361 | 1.00 | 2.00 | 0 |
| ATOM | 2394 | O | HIS | 248 | 7.507 | 57.453 | 121.672 | 1.00 | 2.00 | 0 |
| ATOM | 2395 | CB | HIS | 248 | 4.539 | 56.793 | 123.054 | 1.00 | 2.00 | 0 |
| ATOM | 2396 | CG | HIS | 248 | 4.255 | 58.246 | 122.837 | 1.00 | 2.00 | 0 |
| ATOM | 2397 | ND1 | HIS | 248 | 5.262 | 59.147 | 122.594 | 1.00 | 2.00 | 0 |
| ATOM | 2398 | CE1 | HIS | 248 | 4.677 | 60.327 | 122.535 | 1.00 | 2.00 | 0 |
| ATOM | 2399 | CD2 | HIS | 248 | 3.074 | 58.906 | 122.913 | 1.00 | 2.00 | 0 |

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|---|---|---|---|---|---|---|---|---|---|---|
| ATOM | 2400 | NE2 | HIS | 248 | 3.359 | 60.234 | 122.721 | 1.00 | 2.00 | 0 |
| ATOM | 2402 | N | GLN | 249 | 7.588 | 55.942 | 123.348 | 1.00 | 7.57 | 0 |
| ATOM | 2404 | CA | GLN | 249 | 8.967 | 56.283 | 123.731 | 1.00 | 7.57 | 0 |
| ATOM | 2405 | CB | GLN | 249 | 9.010 | 56.722 | 125.192 | 1.00 | 30.82 | 0 |
| ATOM | 2406 | CG | GLN | 249 | 7.987 | 57.759 | 125.566 | 1.00 | 32.63 | 0 |
| ATOM | 2407 | CD | GLN | 249 | 8.159 | 58.253 | 126.983 | 1.00 | 33.33 | 0 |
| ATOM | 2408 | OE1 | GLN | 249 | 7.871 | 59.406 | 127.274 | 1.00 | 39.63 | 0 |
| ATOM | 2409 | NE2 | GLN | 249 | 8.640 | 57.389 | 127.874 | 1.00 | 32.74 | 0 |
| ATOM | 2412 | C | GLN | 249 | 10.052 | 55.222 | 123.529 | 1.00 | 7.57 | 0 |
| ATOM | 2413 | O | GLN | 249 | 9.884 | 54.057 | 123.888 | 1.00 | 28.32 | 0 |
| ATOM | 2414 | N | VAL | 250 | 11.185 | 55.664 | 122.988 | 1.00 | 20.32 | 0 |
| ATOM | 2416 | CA | VAL | 250 | 12.339 | 54.805 | 122.735 | 1.00 | 20.32 | 0 |
| ATOM | 2417 | CB | VAL | 250 | 13.571 | 55.628 | 122.300 | 1.00 | 6.81 | 0 |
| ATOM | 2418 | CG1 | VAL | 250 | 14.641 | 54.714 | 121.706 | 1.00 | 6.81 | 0 |
| ATOM | 2419 | CG2 | VAL | 250 | 13.161 | 56.708 | 121.311 | 1.00 | 6.81 | 0 |
| ATOM | 2420 | C | VAL | 250 | 12.733 | 54.034 | 123.998 | 1.00 | 20.32 | 0 |
| ATOM | 2421 | O | VAL | 250 | 12.471 | 54.474 | 125.120 | 1.00 | 6.81 | 0 |
| ATOM | 2422 | N | VAL | 251 | 13.372 | 52.887 | 123.797 | 1.00 | 2.00 | 0 |
| ATOM | 2424 | CA | VAL | 251 | 13.820 | 52.023 | 124.871 | 1.00 | 2.00 | 0 |
| ATOM | 2425 | CB | VAL | 251 | 12.655 | 51.150 | 125.391 | 1.00 | 9.99 | 0 |
| ATOM | 2426 | CG1 | VAL | 251 | 11.778 | 51.967 | 126.311 | 1.00 | 9.99 | 0 |
| ATOM | 2427 | CG2 | VAL | 251 | 11.803 | 50.661 | 124.247 | 1.00 | 9.99 | 0 |
| ATOM | 2428 | C | VAL | 251 | 14.960 | 51.167 | 124.316 | 1.00 | 2.00 | 0 |
| ATOM | 2429 | O | VAL | 251 | 14.792 | 50.470 | 123.319 | 1.00 | 9.99 | 0 |
| ATOM | 2430 | N | GLU | 252 | 16.118 | 51.224 | 124.972 | 1.00 | 21.55 | 0 |
| ATOM | 2432 | CA | GLU | 252 | 17.312 | 50.509 | 124.519 | 1.00 | 19.34 | 0 |
| ATOM | 2433 | CB | GLU | 252 | 18.452 | 50.605 | 125.542 | 1.00 | 11.04 | 0 |
| ATOM | 2434 | CG | GLU | 252 | 19.819 | 50.220 | 124.933 | 1.00 | 18.95 | 0 |
| ATOM | 2435 | CD | GLU | 252 | 20.926 | 49.966 | 125.962 | 1.00 | 20.82 | 0 |
| ATOM | 2436 | OE1 | GLU | 252 | 21.938 | 49.303 | 125.597 | 1.00 | 17.37 | 0 |
| ATOM | 2437 | OE2 | GLU | 252 | 20.782 | 50.422 | 127.126 | 1.00 | 29.06 | 0 |
| ATOM | 2438 | C | GLU | 252 | 17.144 | 49.055 | 124.145 | 1.00 | 19.22 | 0 |
| ATOM | 2439 | O | GLU | 252 | 17.838 | 48.571 | 123.261 | 1.00 | 8.64 | 0 |
| ATOM | 2440 | N | ASP | 253 | 16.240 | 48.356 | 124.815 | 1.00 | 2.00 | 0 |
| ATOM | 2442 | CA | ASP | 253 | 16.025 | 46.936 | 124.544 | 1.00 | 2.00 | 0 |
| ATOM | 2443 | CB | ASP | 253 | 16.125 | 46.144 | 125.850 | 1.00 | 78.16 | 0 |
| ATOM | 2444 | CG | ASP | 253 | 17.543 | 46.106 | 126.401 | 1.00 | 84.05 | 0 |
| ATOM | 2445 | OD1 | ASP | 253 | 18.060 | 44.995 | 126.635 | 1.00 | 89.15 | 0 |
| ATOM | 2446 | OD2 | ASP | 253 | 18.148 | 47.181 | 126.598 | 1.00 | 87.62 | 0 |
| ATOM | 2447 | C | ASP | 253 | 14.710 | 46.645 | 123.836 | 1.00 | 2.00 | 0 |
| ATOM | 2448 | O | ASP | 253 | 14.201 | 45.528 | 123.881 | 1.00 | 63.68 | 0 |
| ATOM | 2449 | N | GLY | 254 | 14.161 | 47.660 | 123.181 | 1.00 | 2.00 | 0 |
| ATOM | 2451 | CA | GLY | 254 | 12.919 | 47.483 | 122.457 | 1.00 | 2.00 | 0 |
| ATOM | 2452 | C | GLY | 254 | 11.715 | 47.547 | 123.354 | 1.00 | 2.00 | 0 |
| ATOM | 2453 | O | GLY | 254 | 10.694 | 48.124 | 122.993 | 1.00 | 43.70 | 0 |
| ATOM | 2454 | N | TYR | 255 | 11.823 | 46.922 | 124.516 | 1.00 | 2.00 | 0 |
| ATOM | 2456 | CA | TYR | 255 | 10.749 | 46.956 | 125.484 | 1.00 | 2.00 | 0 |
| ATOM | 2457 | CB | TYR | 255 | 10.047 | 45.614 | 125.571 | 1.00 | 2.00 | 0 |
| ATOM | 2458 | CG | TYR | 255 | 10.853 | 44.510 | 126.185 | 1.00 | 2.00 | 0 |
| ATOM | 2459 | CD1 | TYR | 255 | 12.103 | 44.175 | 125.696 | 1.00 | 2.00 | 0 |
| ATOM | 2460 | CE1 | TYR | 255 | 12.824 | 43.121 | 126.248 | 1.00 | 2.00 | 0 |
| ATOM | 2461 | CD2 | TYR | 255 | 10.337 | 43.770 | 127.246 | 1.00 | 2.00 | 0 |
| ATOM | 2462 | CE2 | TYR | 255 | 11.041 | 42.721 | 127.802 | 1.00 | 2.00 | 0 |
| ATOM | 2463 | CZ | TYR | 255 | 12.279 | 42.397 | 127.301 | 1.00 | 2.00 | 0 |
| ATOM | 2464 | OH | TYR | 255 | 12.946 | 41.328 | 127.839 | 1.00 | 2.00 | 0 |
| ATOM | 2466 | C | TYR | 255 | 11.262 | 47.375 | 126.847 | 1.00 | 2.00 | 0 |
| ATOM | 2467 | O | TYR | 255 | 12.453 | 47.283 | 127.150 | 1.00 | 2.00 | 0 |
| ATOM | 2468 | N | GLU | 256 | 10.336 | 47.853 | 127.656 | 1.00 | 2.00 | 0 |
| ATOM | 2470 | CA | GLU | 256 | 10.632 | 48.341 | 128.979 | 1.00 | 2.00 | 0 |
| ATOM | 2471 | CB | GLU | 256 | 11.092 | 49.798 | 128.910 | 1.00 | 20.70 | 0 |
| ATOM | 2472 | CG | GLU | 256 | 11.264 | 50.457 | 130.269 | 1.00 | 27.98 | 0 |
| ATOM | 2473 | CD | GLU | 256 | 11.485 | 51.961 | 130.179 | 1.00 | 31.28 | 0 |
| ATOM | 2474 | OE1 | GLU | 256 | 10.726 | 52.725 | 130.834 | 1.00 | 33.21 | 0 |
| ATOM | 2475 | OE2 | GLU | 256 | 12.418 | 52.378 | 129.453 | 1.00 | 39.87 | 0 |
| ATOM | 2476 | C | GLU | 256 | 9.362 | 48.238 | 129.800 | 1.00 | 2.00 | 0 |
| ATOM | 2477 | O | GLU | 256 | 8.299 | 48.743 | 129.420 | 1.00 | 18.74 | 0 |
| ATOM | 2478 | N | PHE | 257 | 9.474 | 47.540 | 130.919 | 1.00 | 2.00 | 0 |
| ATOM | 2480 | CA | PHE | 257 | 8.357 | 47.364 | 131.806 | 1.00 | 2.00 | 0 |

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|---|---|---|---|---|---|---|---|---|---|---|
| ATOM | 2481 | CB | PHE | 257 | 8.578 | 46.139 | 132.661 | 1.00 | 2.00 | 0 |
| ATOM | 2482 | CG | PHE | 257 | 8.222 | 44.865 | 131.978 | 1.00 | 2.00 | 0 |
| ATOM | 2483 | CD1 | PHE | 257 | 9.187 | 43.926 | 131.694 | 1.00 | 2.00 | 0 |
| ATOM | 2484 | CD2 | PHE | 257 | 6.906 | 44.594 | 131.649 | 1.00 | 2.00 | 0 |
| ATOM | 2485 | CE1 | PHE | 257 | 8.849 | 42.740 | 131.101 | 1.00 | 2.00 | 0 |
| ATOM | 2486 | CE2 | PHE | 257 | 6.560 | 43.417 | 131.058 | 1.00 | 2.00 | 0 |
| ATOM | 2487 | CZ | PHE | 257 | 7.533 | 42.481 | 130.781 | 1.00 | 2.00 | 0 |
| ATOM | 2488 | C | PHE | 257 | 8.257 | 48.593 | 132.671 | 1.00 | 2.00 | 0 |
| ATOM | 2489 | O | PHE | 257 | 9.215 | 49.360 | 132.782 | 1.00 | 2.00 | 0 |
| ATOM | 2490 | N | PHE | 258 | 7.104 | 48.777 | 133.286 | 1.00 | 25.02 | 0 |
| ATOM | 2492 | CA | PHE | 258 | 6.884 | 49.916 | 134.147 | 1.00 | 25.02 | 0 |
| ATOM | 2493 | CB | PHE | 258 | 6.417 | 51.086 | 133.299 | 1.00 | 2.00 | 0 |
| ATOM | 2494 | CG | PHE | 258 | 5.831 | 52.237 | 134.072 | 1.00 | 2.00 | 0 |
| ATOM | 2495 | CD1 | PHE | 258 | 6.625 | 53.325 | 134.431 | 1.00 | 2.00 | 0 |
| ATOM | 2496 | CD2 | PHE | 258 | 4.468 | 52.271 | 134.369 | 1.00 | 2.00 | 0 |
| ATOM | 2497 | CE1 | PHE | 258 | 6.070 | 54.439 | 135.070 | 1.00 | 2.00 | 0 |
| ATOM | 2498 | CE2 | PHE | 258 | 3.900 | 53.369 | 135.003 | 1.00 | 2.00 | 0 |
| ATOM | 2499 | CZ | PHE | 258 | 4.698 | 54.461 | 135.356 | 1.00 | 2.00 | 0 |
| ATOM | 2500 | C | PHE | 258 | 5.837 | 49.508 | 135.160 | 1.00 | 25.02 | 0 |
| ATOM | 2501 | O | PHE | 258 | 4.965 | 48.675 | 134.859 | 1.00 | 2.00 | 0 |
| ATOM | 2502 | N | ALA | 259 | 5.953 | 50.063 | 136.368 | 1.00 | 13.61 | 0 |
| ATOM | 2504 | CA | ALA | 259 | 5.027 | 49.775 | 137.457 | 1.00 | 11.22 | 0 |
| ATOM | 2505 | CB | ALA | 259 | 3.626 | 50.318 | 137.122 | 1.00 | 2.00 | 0 |
| ATOM | 2506 | C | ALA | 259 | 4.951 | 48.286 | 137.729 | 1.00 | 12.73 | 0 |
| ATOM | 2507 | O | ALA | 259 | 3.876 | 47.718 | 137.660 | 1.00 | 2.00 | 0 |
| ATOM | 2508 | N | LYS | 260 | 6.091 | 47.657 | 138.016 | 1.00 | 2.00 | 0 |
| ATOM | 2510 | CA | LYS | 260 | 6.140 | 46.214 | 138.304 | 1.00 | 9.39 | 0 |
| ATOM | 2511 | CB | LYS | 260 | 5.594 | 45.925 | 139.704 | 1.00 | 20.75 | 0 |
| ATOM | 2512 | CG | LYS | 260 | 6.589 | 46.151 | 140.844 | 1.00 | 28.17 | 0 |
| ATOM | 2513 | CD | LYS | 260 | 6.797 | 47.622 | 141.177 | 1.00 | 36.91 | 0 |
| ATOM | 2514 | CE | LYS | 260 | 7.615 | 47.765 | 142.449 | 1.00 | 36.02 | 0 |
| ATOM | 2515 | NZ | LYS | 260 | 6.919 | 47.158 | 143.633 | 1.00 | 29.33 | 0 |
| ATOM | 2519 | C | LYS | 260 | 5.370 | 45.375 | 137.279 | 1.00 | 2.00 | 0 |
| ATOM | 2520 | O | LYS | 260 | 4.443 | 44.633 | 137.641 | 1.00 | 15.95 | 0 |
| ATOM | 2521 | N | ARG | 261 | 5.764 | 45.531 | 136.004 | 1.00 | 2.00 | 0 |
| ATOM | 2523 | CA | ARG | 261 | 5.173 | 44.843 | 134.851 | 1.00 | 2.00 | 0 |
| ATOM | 2524 | CB | ARG | 261 | 5.410 | 43.335 | 134.964 | 1.00 | 21.35 | 0 |
| ATOM | 2525 | CG | ARG | 261 | 6.881 | 42.969 | 134.928 | 1.00 | 21.35 | 0 |
| ATOM | 2526 | CD | ARG | 261 | 7.088 | 41.473 | 134.970 | 1.00 | 9.03 | 0 |
| ATOM | 2527 | NE | ARG | 261 | 8.408 | 41.097 | 134.460 | 1.00 | 14.18 | 0 |
| ATOM | 2529 | CZ | ARG | 261 | 8.801 | 39.842 | 134.222 | 1.00 | 14.38 | 0 |
| ATOM | 2530 | NH1 | ARG | 261 | 7.976 | 38.820 | 134.462 | 1.00 | 16.12 | 0 |
| ATOM | 2533 | NH2 | ARG | 261 | 10.018 | 39.603 | 133.729 | 1.00 | 18.11 | 0 |
| ATOM | 2536 | C | ARG | 261 | 3.692 | 45.136 | 134.592 | 1.00 | 2.00 | 0 |
| ATOM | 2537 | O | ARG | 261 | 3.009 | 44.343 | 133.933 | 1.00 | 21.35 | 0 |
| ATOM | 2538 | N | GLN | 262 | 3.215 | 46.283 | 135.092 | 1.00 | 7.73 | 0 |
| ATOM | 2540 | CA | GLN | 262 | 1.821 | 46.727 | 134.927 | 1.00 | 7.73 | 0 |
| ATOM | 2541 | CB | GLN | 262 | 1.379 | 47.620 | 136.100 | 1.00 | 2.00 | 0 |
| ATOM | 2542 | CG | GLN | 262 | 1.106 | 46.888 | 137.434 | 1.00 | 2.00 | 0 |
| ATOM | 2543 | CD | GLN | 262 | 0.859 | 47.840 | 138.601 | 1.00 | 2.00 | 0 |
| ATOM | 2544 | OE1 | GLN | 262 | -0.277 | 48.137 | 138.930 | 1.00 | 2.00 | 0 |
| ATOM | 2545 | NE2 | GLN | 262 | 1.922 | 48.304 | 139.237 | 1.00 | 2.00 | 0 |
| ATOM | 2548 | C | GLN | 262 | 1.635 | 47.495 | 133.628 | 1.00 | 7.73 | 0 |
| ATOM | 2549 | O | GLN | 262 | 0.526 | 47.650 | 133.154 | 1.00 | 2.00 | 0 |
| ATOM | 2550 | N | LEU | 263 | 2.730 | 47.996 | 133.078 | 1.00 | 2.00 | 0 |
| ATOM | 2552 | CA | LEU | 263 | 2.723 | 48.726 | 131.819 | 1.00 | 2.00 | 0 |
| ATOM | 2553 | CB | LEU | 263 | 2.754 | 50.244 | 132.069 | 1.00 | 2.00 | 0 |
| ATOM | 2554 | CG | LEU | 263 | 3.070 | 51.201 | 130.890 | 1.00 | 2.00 | 0 |
| ATOM | 2555 | CD1 | LEU | 263 | 2.404 | 52.532 | 131.133 | 1.00 | 2.00 | 0 |
| ATOM | 2556 | CD2 | LEU | 263 | 4.575 | 51.408 | 130.679 | 1.00 | 2.00 | 0 |
| ATOM | 2557 | C | LEU | 263 | 3.991 | 48.305 | 131.089 | 1.00 | 2.00 | 0 |
| ATOM | 2558 | O | LEU | 263 | 5.018 | 48.082 | 131.736 | 1.00 | 2.00 | 0 |
| ATOM | 2559 | N | VAL | 264 | 3.932 | 48.207 | 129.759 | 1.00 | 42.92 | 0 |
| ATOM | 2561 | CA | VAL | 264 | 5.105 | 47.850 | 128.949 | 1.00 | 41.59 | 0 |
| ATOM | 2562 | CB | VAL | 264 | 5.014 | 46.373 | 128.433 | 1.00 | 2.00 | 0 |
| ATOM | 2563 | CG1 | VAL | 264 | 3.952 | 46.242 | 127.372 | 1.00 | 2.00 | 0 |
| ATOM | 2564 | CG2 | VAL | 264 | 6.349 | 45.908 | 127.929 | 1.00 | 2.00 | 0 |
| ATOM | 2565 | C | VAL | 264 | 5.193 | 48.840 | 127.772 | 1.00 | 42.79 | 0 |

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|---|---|---|---|---|---|---|---|---|---|---|
| ATOM | 2566 | O | VAL | 264 | 4.164 | 49.261 | 127.242 | 1.00 | 2.00 | 0 |
| ATOM | 2567 | N | THR | 265 | 6.409 | 49.237 | 127.400 | 1.00 | 2.00 | 0 |
| ATOM | 2569 | CA | THR | 265 | 6.639 | 50.177 | 126.292 | 1.00 | 2.00 | 0 |
| ATOM | 2570 | CB | THR | 265 | 7.420 | 51.412 | 126.789 | 1.00 | 2.00 | 0 |
| ATOM | 2571 | OG1 | THR | 265 | 6.534 | 52.253 | 127.531 | 1.00 | 2.00 | 0 |
| ATOM | 2573 | CG2 | THR | 265 | 8.021 | 52.191 | 125.648 | 1.00 | 2.00 | 0 |
| ATOM | 2574 | C | THR | 265 | 7.405 | 49.523 | 125.132 | 1.00 | 2.00 | 0 |
| ATOM | 2575 | O | THR | 265 | 8.612 | 49.245 | 125.246 | 1.00 | 2.00 | 0 |
| ATOM | 2576 | N | LEU | 266 | 6.712 | 49.280 | 124.019 | 1.00 | 7.19 | 0 |
| ATOM | 2578 | CA | LEU | 266 | 7.330 | 48.653 | 122.857 | 1.00 | 7.19 | 0 |
| ATOM | 2579 | CB | LEU | 266 | 6.338 | 47.721 | 122.176 | 1.00 | 2.00 | 0 |
| ATOM | 2580 | CG | LEU | 266 | 5.815 | 46.505 | 122.948 | 1.00 | 2.00 | 0 |
| ATOM | 2581 | CD1 | LEU | 266 | 4.859 | 45.733 | 122.057 | 1.00 | 2.00 | 0 |
| ATOM | 2582 | CD2 | LEU | 266 | 6.955 | 45.599 | 123.368 | 1.00 | 2.00 | 0 |
| ATOM | 2583 | C | LEU | 266 | 7.898 | 49.618 | 121.819 | 1.00 | 7.19 | 0 |
| ATOM | 2584 | O | LEU | 266 | 7.329 | 50.675 | 121.537 | 1.00 | 2.00 | 0 |
| ATOM | 2585 | N | PHE | 267 | 9.033 | 49.249 | 121.247 | 1.00 | 2.00 | 0 |
| ATOM | 2587 | CA | PHE | 267 | 9.665 | 50.068 | 120.222 | 1.00 | 2.00 | 0 |
| ATOM | 2588 | CB | PHE | 267 | 10.763 | 50.960 | 120.821 | 1.00 | 2.00 | 0 |
| ATOM | 2589 | CG | PHE | 267 | 10.937 | 52.260 | 120.091 | 1.00 | 2.00 | 0 |
| ATOM | 2590 | CD1 | PHE | 267 | 9.985 | 53.261 | 120.206 | 1.00 | 2.00 | 0 |
| ATOM | 2591 | CD2 | PHE | 267 | 12.021 | 52.468 | 119.255 | 1.00 | 2.00 | 0 |
| ATOM | 2592 | CE1 | PHE | 267 | 10.108 | 54.445 | 119.493 | 1.00 | 2.00 | 0 |
| ATOM | 2593 | CE2 | PHE | 267 | 12.146 | 53.652 | 118.540 | 1.00 | 2.00 | 0 |
| ATOM | 2594 | CZ | PHE | 267 | 11.187 | 54.636 | 118.661 | 1.00 | 2.00 | 0 |
| ATOM | 2595 | C | PHE | 267 | 10.246 | 49.076 | 119.227 | 1.00 | 2.00 | 0 |
| ATOM | 2596 | O | PHE | 267 | 11.418 | 48.693 | 119.321 | 1.00 | 2.00 | 0 |
| ATOM | 2597 | N | SER | 268 | 9.387 | 48.638 | 118.302 | 1.00 | 12.94 | 0 |
| ATOM | 2599 | CA | SER | 268 | 9.707 | 47.648 | 117.267 | 1.00 | 12.94 | 0 |
| ATOM | 2600 | CB | SER | 268 | 8.420 | 47.043 | 116.723 | 1.00 | 11.11 | 0 |
| ATOM | 2601 | OG | SER | 268 | 7.593 | 46.579 | 117.771 | 1.00 | 11.11 | 0 |
| ATOM | 2603 | C | SER | 268 | 10.450 | 48.231 | 116.103 | 1.00 | 12.94 | 0 |
| ATOM | 2604 | O | SER | 268 | 10.150 | 49.344 | 115.711 | 1.00 | 11.11 | 0 |
| ATOM | 2605 | N | ALA | 269 | 11.391 | 47.454 | 115.556 | 1.00 | 71.01 | 0 |
| ATOM | 2607 | CA | ALA | 269 | 12.222 | 47.779 | 114.378 | 1.00 | 71.72 | 0 |
| ATOM | 2608 | CB | ALA | 269 | 11.383 | 48.513 | 113.295 | 1.00 | 82.00 | 0 |
| ATOM | 2609 | C | ALA | 269 | 13.585 | 48.469 | 114.543 | 1.00 | 74.82 | 0 |
| ATOM | 2610 | O | ALA | 269 | 14.609 | 47.889 | 114.186 | 1.00 | 91.21 | 0 |
| ATOM | 2611 | N | PRO | 270 | 13.619 | 49.704 | 115.076 | 1.00 | 28.82 | 0 |
| ATOM | 2612 | CD | PRO | 270 | 12.436 | 50.466 | 115.513 | 1.00 | 2.00 | 0 |
| ATOM | 2613 | CA | PRO | 270 | 14.788 | 50.542 | 115.316 | 1.00 | 31.86 | 0 |
| ATOM | 2614 | CB | PRO | 270 | 14.340 | 51.374 | 116.502 | 1.00 | 2.00 | 0 |
| ATOM | 2615 | CG | PRO | 270 | 13.034 | 51.783 | 116.023 | 1.00 | 2.00 | 0 |
| ATOM | 2616 | C | PRO | 270 | 16.254 | 50.192 | 115.428 | 1.00 | 29.52 | 0 |
| ATOM | 2617 | O | PRO | 270 | 16.716 | 49.072 | 115.272 | 1.00 | 2.00 | 0 |
| ATOM | 2618 | N | ASN | 271 | 16.928 | 51.318 | 115.593 | 1.00 | 2.00 | 0 |
| ATOM | 2620 | CA | ASN | 271 | 18.346 | 51.621 | 115.754 | 1.00 | 2.00 | 0 |
| ATOM | 2621 | CB | ASN | 271 | 19.168 | 50.935 | 114.663 | 1.00 | 35.96 | 0 |
| ATOM | 2622 | CG | ASN | 271 | 18.483 | 50.953 | 113.300 | 1.00 | 61.96 | 0 |
| ATOM | 2623 | OD1 | ASN | 271 | 17.605 | 51.787 | 113.034 | 1.00 | 36.11 | 0 |
| ATOM | 2624 | ND2 | ASN | 271 | 18.872 | 50.015 | 112.432 | 1.00 | 36.31 | 0 |
| ATOM | 2627 | C | ASN | 271 | 18.199 | 53.143 | 115.475 | 1.00 | 2.00 | 0 |
| ATOM | 2628 | O | ASN | 271 | 19.072 | 53.807 | 114.915 | 1.00 | 61.69 | 0 |
| ATOM | 2629 | N | TYR | 272 | 17.039 | 53.638 | 115.930 | 1.00 | 2.00 | 0 |
| ATOM | 2631 | CA | TYR | 272 | 16.489 | 54.978 | 115.793 | 1.00 | 2.00 | 0 |
| ATOM | 2632 | CB | TYR | 272 | 15.772 | 55.358 | 117.090 | 1.00 | 17.33 | 0 |
| ATOM | 2633 | CG | TYR | 272 | 14.528 | 56.208 | 116.897 | 1.00 | 10.41 | 0 |
| ATOM | 2634 | CD1 | TYR | 272 | 13.458 | 55.769 | 116.105 | 1.00 | 11.86 | 0 |
| ATOM | 2635 | CE1 | TYR | 272 | 12.313 | 56.571 | 115.917 | 1.00 | 14.32 | 0 |
| ATOM | 2636 | CD2 | TYR | 272 | 14.421 | 57.454 | 117.493 | 1.00 | 10.66 | 0 |
| ATOM | 2637 | CE2 | TYR | 272 | 13.287 | 58.256 | 117.312 | 1.00 | 15.43 | 0 |
| ATOM | 2638 | CZ | TYR | 272 | 12.243 | 57.813 | 116.529 | 1.00 | 9.40 | 0 |
| ATOM | 2639 | OH | TYR | 272 | 11.143 | 58.636 | 116.375 | 1.00 | 17.38 | 0 |
| ATOM | 2641 | C | TYR | 272 | 17.332 | 56.132 | 115.299 | 1.00 | 2.00 | 0 |
| ATOM | 2642 | O | TYR | 272 | 18.356 | 56.471 | 115.888 | 1.00 | 29.84 | 0 |
| ATOM | 2643 | N | CYS | 273 | 16.860 | 56.731 | 114.201 | 1.00 | 7.24 | 0 |
| ATOM | 2645 | CA | CYS | 273 | 17.490 | 57.875 | 113.553 | 1.00 | 6.82 | 0 |
| ATOM | 2646 | CB | CYS | 273 | 17.203 | 59.167 | 114.331 | 1.00 | 11.61 | 0 |

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|---|---|---|---|---|---|---|---|---|---|---|
| ATOM | 2647 | SG | CYS | 273 | 15.496 | 59.459 | 114.843 | 1.00 | 10.42 | 0 |
| ATOM | 2648 | C | CYS | 273 | 19.010 | 57.724 | 113.411 | 1.00 | 8.43 | 0 |
| ATOM | 2649 | O | CYS | 273 | 19.738 | 58.717 | 113.512 | 1.00 | 9.04 | 0 |
| ATOM | 2650 | N | GLY | 274 | 19.498 | 56.502 | 113.185 | 1.00 | 13.82 | 0 |
| ATOM | 2652 | CA | GLY | 274 | 20.934 | 56.303 | 113.044 | 1.00 | 13.82 | 0 |
| ATOM | 2653 | C | GLY | 274 | 21.710 | 57.029 | 114.134 | 1.00 | 13.82 | 0 |
| ATOM | 2654 | O | GLY | 274 | 22.817 | 57.515 | 113.906 | 1.00 | 39.65 | 0 |
| ATOM | 2655 | N | GLU | 275 | 21.120 | 57.085 | 115.326 | 1.00 | 92.80 | 0 |
| ATOM | 2657 | CA | GLU | 275 | 21.719 | 57.764 | 116.467 | 1.00 | 91.32 | 0 |
| ATOM | 2658 | CB | GLU | 275 | 21.479 | 59.276 | 116.340 | 1.00 | 25.01 | 0 |
| ATOM | 2659 | CG | GLU | 275 | 19.994 | 59.656 | 116.224 | 1.00 | 31.82 | 0 |
| ATOM | 2660 | CD | GLU | 275 | 19.730 | 61.158 | 116.060 | 1.00 | 30.92 | 0 |
| ATOM | 2661 | OE1 | GLU | 275 | 18.951 | 61.713 | 116.868 | 1.00 | 38.31 | 0 |
| ATOM | 2662 | OE2 | GLU | 275 | 20.276 | 61.787 | 115.125 | 1.00 | 34.18 | 0 |
| ATOM | 2663 | C | GLU | 275 | 21.137 | 57.260 | 117.794 | 1.00 | 90.32 | 0 |
| ATOM | 2664 | O | GLU | 275 | 20.941 | 58.047 | 118.716 | 1.00 | 23.69 | 0 |
| ATOM | 2665 | N | PHE | 276 | 20.868 | 55.958 | 117.901 | 1.00 | 18.78 | 0 |
| ATOM | 2667 | CA | PHE | 276 | 20.303 | 55.412 | 119.134 | 1.00 | 17.07 | 0 |
| ATOM | 2668 | CB | PHE | 276 | 18.774 | 55.551 | 119.125 | 1.00 | 37.20 | 0 |
| ATOM | 2669 | CG | PHE | 276 | 18.280 | 56.876 | 119.652 | 1.00 | 35.89 | 0 |
| ATOM | 2670 | CD1 | PHE | 276 | 17.522 | 57.726 | 118.849 | 1.00 | 35.53 | 0 |
| ATOM | 2671 | CD2 | PHE | 276 | 18.572 | 57.273 | 120.949 | 1.00 | 39.17 | 0 |
| ATOM | 2672 | CE1 | PHE | 276 | 17.067 | 58.945 | 119.329 | 1.00 | 31.45 | 0 |
| ATOM | 2673 | CE2 | PHE | 276 | 18.123 | 58.485 | 121.434 | 1.00 | 36.03 | 0 |
| ATOM | 2674 | CZ | PHE | 276 | 17.367 | 59.324 | 120.621 | 1.00 | 39.75 | 0 |
| ATOM | 2675 | C | PHE | 276 | 20.681 | 53.992 | 119.597 | 1.00 | 17.79 | 0 |
| ATOM | 2676 | O | PHE | 276 | 20.463 | 53.669 | 120.772 | 1.00 | 38.38 | 0 |
| ATOM | 2677 | N | ASP | 277 | 21.213 | 53.140 | 118.712 | 1.00 | 27.69 | 0 |
| ATOM | 2679 | CA | ASP | 277 | 21.638 | 51.772 | 119.093 | 1.00 | 27.89 | 0 |
| ATOM | 2680 | CB | ASP | 277 | 22.884 | 51.848 | 120.018 | 1.00 | 0.27 | 0 |
| ATOM | 2681 | CG | ASP | 277 | 23.231 | 50.508 | 120.716 | 1.00 | 39.20 | 0 |
| ATOM | 2682 | OD1 | ASP | 277 | 23.163 | 50.470 | 121.964 | 1.00 | 39.20 | 0 |
| ATOM | 2683 | OD2 | ASP | 277 | 23.576 | 49.508 | 120.036 | 1.00 | 39.20 | 0 |
| ATOM | 2684 | C | ASP | 277 | 20.560 | 50.892 | 119.742 | 1.00 | 26.41 | 0 |
| ATOM | 2685 | O | ASP | 277 | 20.761 | 49.675 | 119.918 | 1.00 | 0.76 | 0 |
| ATOM | 2686 | N | ASN | 278 | 19.428 | 51.491 | 120.101 | 1.00 | 2.00 | 0 |
| ATOM | 2688 | CA | ASN | 278 | 18.344 | 50.758 | 120.722 | 1.00 | 2.00 | 0 |
| ATOM | 2689 | CB | ASN | 278 | 17.142 | 51.676 | 120.920 | 1.00 | 2.00 | 0 |
| ATOM | 2690 | CG | ASN | 278 | 16.394 | 51.930 | 119.639 | 1.00 | 2.00 | 0 |
| ATOM | 2691 | OD1 | ASN | 278 | 16.867 | 52.643 | 118.765 | 1.00 | 2.00 | 0 |
| ATOM | 2692 | ND2 | ASN | 278 | 15.225 | 51.324 | 119.510 | 1.00 | 2.00 | 0 |
| ATOM | 2695 | C | ASN | 278 | 17.938 | 49.602 | 119.829 | 1.00 | 2.00 | 0 |
| ATOM | 2696 | O | ASN | 278 | 17.970 | 49.710 | 118.600 | 1.00 | 2.00 | 0 |
| ATOM | 2697 | N | ALA | 279 | 17.603 | 48.487 | 120.454 | 1.00 | 14.31 | 0 |
| ATOM | 2699 | CA | ALA | 279 | 17.133 | 47.320 | 119.734 | 1.00 | 14.31 | 0 |
| ATOM | 2700 | CB | ALA | 279 | 17.281 | 46.081 | 120.594 | 1.00 | 2.00 | 0 |
| ATOM | 2701 | C | ALA | 279 | 15.655 | 47.631 | 119.498 | 1.00 | 14.31 | 0 |
| ATOM | 2702 | O | ALA | 279 | 15.155 | 48.645 | 119.996 | 1.00 | 2.00 | 0 |
| ATOM | 2703 | N | GLY | 280 | 14.959 | 46.788 | 118.743 | 1.00 | 2.00 | 0 |
| ATOM | 2705 | CA | GLY | 280 | 13.549 | 47.014 | 118.484 | 1.00 | 2.00 | 0 |
| ATOM | 2706 | C | GLY | 280 | 12.864 | 45.783 | 118.992 | 1.00 | 2.00 | 0 |
| ATOM | 2707 | O | GLY | 280 | 13.381 | 44.698 | 118.799 | 1.00 | 9.35 | 0 |
| ATOM | 2708 | N | ALA | 281 | 11.725 | 45.906 | 119.643 | 1.00 | 2.00 | 0 |
| ATOM | 2710 | CA | ALA | 281 | 11.082 | 44.702 | 120.167 | 1.00 | 2.00 | 0 |
| ATOM | 2711 | CB | ALA | 281 | 10.799 | 44.850 | 121.658 | 1.00 | 2.00 | 0 |
| ATOM | 2712 | C | ALA | 281 | 9.815 | 44.345 | 119.437 | 1.00 | 2.00 | 0 |
| ATOM | 2713 | O | ALA | 281 | 9.451 | 44.992 | 118.473 | 1.00 | 2.00 | 0 |
| ATOM | 2714 | N | MET | 282 | 9.140 | 43.312 | 119.918 | 1.00 | 14.19 | 0 |
| ATOM | 2716 | CA | MET | 282 | 7.907 | 42.833 | 119.315 | 1.00 | 14.19 | 0 |
| ATOM | 2717 | CB | MET | 282 | 8.232 | 42.115 | 117.995 | 1.00 | 25.98 | 0 |
| ATOM | 2718 | CG | MET | 282 | 7.056 | 41.885 | 117.060 | 1.00 | 24.91 | 0 |
| ATOM | 2719 | SD | MET | 282 | 7.304 | 40.449 | 115.980 | 1.00 | 25.45 | 0 |
| ATOM | 2720 | CE | MET | 282 | 9.044 | 40.644 | 115.525 | 1.00 | 21.20 | 0 |
| ATOM | 2721 | C | MET | 282 | 7.397 | 41.851 | 120.363 | 1.00 | 14.19 | 0 |
| ATOM | 2722 | O | MET | 282 | 8.142 | 40.972 | 120.790 | 1.00 | 24.98 | 0 |
| ATOM | 2723 | N | MET | 283 | 6.148 | 42.004 | 120.788 | 1.00 | 2.00 | 0 |
| ATOM | 2725 | CA | MET | 283 | 5.592 | 41.143 | 121.825 | 1.00 | 2.00 | 0 |
| ATOM | 2726 | CB | MET | 283 | 4.940 | 41.991 | 122.925 | 1.00 | 19.29 | 0 |

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|---|---|---|---|---|---|---|---|---|---|---|
| ATOM | 2727 | CG | MET | 283 | 4.481 | 41.205 | 124.142 | 1.00 | 19.76 | 0 |
| ATOM | 2728 | SD | MET | 283 | 3.228 | 42.077 | 125.116 | 1.00 | 20.92 | 0 |
| ATOM | 2729 | CE | MET | 283 | 4.204 | 43.235 | 125.966 | 1.00 | 17.38 | 0 |
| ATOM | 2730 | C | MET | 283 | 4.592 | 40.125 | 121.339 | 1.00 | 2.00 | 0 |
| ATOM | 2731 | O | MET | 283 | 3.456 | 40.470 | 121.036 | 1.00 | 16.17 | 0 |
| ATOM | 2732 | N | SER | 284 | 5.012 | 38.871 | 121.291 | 1.00 | 2.00 | 0 |
| ATOM | 2734 | CA | SER | 284 | 4.148 | 37.777 | 120.869 | 1.00 | 2.00 | 0 |
| ATOM | 2735 | CB | SER | 284 | 4.991 | 36.664 | 120.220 | 1.00 | 20.90 | 0 |
| ATOM | 2736 | OG | SER | 284 | 6.376 | 36.771 | 120.528 | 1.00 | 23.67 | 0 |
| ATOM | 2738 | C | SER | 284 | 3.275 | 37.202 | 122.018 | 1.00 | 2.00 | 0 |
| ATOM | 2739 | O | SER | 284 | 3.777 | 36.595 | 122.978 | 1.00 | 26.24 | 0 |
| ATOM | 2740 | N | VAL | 285 | 1.967 | 37.402 | 121.894 | 1.00 | 2.00 | 0 |
| ATOM | 2742 | CA | VAL | 285 | 0.979 | 36.940 | 122.859 | 1.00 | 2.00 | 0 |
| ATOM | 2743 | CB | VAL | 285 | -0.091 | 38.026 | 123.056 | 1.00 | 2.00 | 0 |
| ATOM | 2744 | CG1 | VAL | 285 | -0.952 | 37.714 | 124.262 | 1.00 | 2.00 | 0 |
| ATOM | 2745 | CG2 | VAL | 285 | 0.572 | 39.381 | 123.171 | 1.00 | 2.00 | 0 |
| ATOM | 2746 | C | VAL | 285 | 0.274 | 35.644 | 122.417 | 1.00 | 2.00 | 0 |
| ATOM | 2747 | O | VAL | 285 | -0.572 | 35.672 | 121.532 | 1.00 | 2.00 | 0 |
| ATOM | 2748 | N | ASP | 286 | 0.609 | 34.512 | 123.026 | 1.00 | 2.00 | 0 |
| ATOM | 2750 | CA | ASP | 286 | -0.056 | 33.258 | 122.663 | 1.00 | 2.00 | 0 |
| ATOM | 2751 | CB | ASP | 286 | 0.771 | 32.019 | 123.071 | 1.00 | 22.05 | 0 |
| ATOM | 2752 | CG | ASP | 286 | 1.192 | 32.020 | 124.531 | 1.00 | 24.93 | 0 |
| ATOM | 2753 | OD1 | ASP | 286 | 0.578 | 32.742 | 125.344 | 1.00 | 32.49 | 0 |
| ATOM | 2754 | OD2 | ASP | 286 | 2.152 | 31.285 | 124.866 | 1.00 | 28.80 | 0 |
| ATOM | 2755 | C | ASP | 286 | -1.494 | 33.141 | 123.181 | 1.00 | 2.00 | 0 |
| ATOM | 2756 | O | ASP | 286 | -1.993 | 34.023 | 123.881 | 1.00 | 12.72 | 0 |
| ATOM | 2757 | N | GLU | 287 | -2.144 | 32.036 | 122.817 | 1.00 | 28.94 | 0 |
| ATOM | 2759 | CA | GLU | 287 | -3.543 | 31.744 | 123.153 | 1.00 | 28.07 | 0 |
| ATOM | 2760 | CB | GLU | 287 | -3.912 | 30.340 | 122.657 | 1.00 | 59.96 | 0 |
| ATOM | 2761 | CG | GLU | 287 | -3.610 | 30.049 | 121.177 | 1.00 | 66.13 | 0 |
| ATOM | 2762 | CD | GLU | 287 | -2.139 | 29.730 | 120.890 | 1.00 | 70.85 | 0 |
| ATOM | 2763 | OE1 | GLU | 287 | -1.712 | 29.890 | 119.723 | 1.00 | 75.38 | 0 |
| ATOM | 2764 | OE2 | GLU | 287 | -1.412 | 29.315 | 121.822 | 1.00 | 73.00 | 0 |
| ATOM | 2765 | C | GLU | 287 | -3.876 | 31.836 | 124.638 | 1.00 | 30.16 | 0 |
| ATOM | 2766 | O | GLU | 287 | -5.017 | 32.074 | 125.029 | 1.00 | 62.37 | 0 |
| ATOM | 2767 | N | THR | 288 | -2.852 | 31.654 | 125.455 | 1.00 | 41.83 | 0 |
| ATOM | 2769 | CA | THR | 288 | -2.995 | 31.665 | 126.894 | 1.00 | 36.69 | 0 |
| ATOM | 2770 | CB | THR | 288 | -2.269 | 30.449 | 127.457 | 1.00 | 11.26 | 0 |
| ATOM | 2771 | OG1 | THR | 288 | -0.865 | 30.552 | 127.171 | 1.00 | 11.65 | 0 |
| ATOM | 2773 | CG2 | THR | 288 | -2.827 | 29.171 | 126.800 | 1.00 | 11.00 | 0 |
| ATOM | 2774 | C | THR | 288 | -2.461 | 32.947 | 127.533 | 1.00 | 36.73 | 0 |
| ATOM | 2775 | O | THR | 288 | -2.015 | 32.948 | 128.675 | 1.00 | 18.83 | 0 |
| ATOM | 2776 | N | LEU | 289 | -2.492 | 34.034 | 126.776 | 1.00 | 6.34 | 0 |
| ATOM | 2778 | CA | LEU | 289 | -2.027 | 35.334 | 127.232 | 1.00 | 2.00 | 0 |
| ATOM | 2779 | CB | LEU | 289 | -3.081 | 35.946 | 128.155 | 1.00 | 2.00 | 0 |
| ATOM | 2780 | CG | LEU | 289 | -4.282 | 36.465 | 127.346 | 1.00 | 2.00 | 0 |
| ATOM | 2781 | CD1 | LEU | 289 | -5.390 | 36.973 | 128.263 | 1.00 | 2.00 | 0 |
| ATOM | 2782 | CD2 | LEU | 289 | -3.817 | 37.593 | 126.412 | 1.00 | 2.00 | 0 |
| ATOM | 2783 | C | LEU | 289 | -0.615 | 35.454 | 127.826 | 1.00 | 2.00 | 0 |
| ATOM | 2784 | O | LEU | 289 | -0.299 | 36.445 | 128.493 | 1.00 | 2.00 | 0 |
| ATOM | 2785 | N | MET | 290 | 0.244 | 34.475 | 127.566 | 1.00 | 20.85 | 0 |
| ATOM | 2787 | CA | MET | 290 | 1.619 | 34.548 | 128.046 | 1.00 | 23.75 | 0 |
| ATOM | 2788 | CB | MET | 290 | 2.238 | 33.156 | 128.212 | 1.00 | 24.81 | 0 |
| ATOM | 2789 | CG | MET | 290 | 3.717 | 33.200 | 128.623 | 1.00 | 23.46 | 0 |
| ATOM | 2790 | SD | MET | 290 | 4.726 | 31.867 | 127.935 | 1.00 | 26.75 | 0 |
| ATOM | 2791 | CE | MET | 290 | 5.196 | 32.555 | 126.310 | 1.00 | 29.16 | 0 |
| ATOM | 2792 | C | MET | 290 | 2.430 | 35.332 | 127.015 | 1.00 | 19.20 | 0 |
| ATOM | 2793 | O | MET | 290 | 2.545 | 34.910 | 125.858 | 1.00 | 29.26 | 0 |
| ATOM | 2794 | N | CYS | 291 | 3.003 | 36.454 | 127.449 | 1.00 | 2.00 | 0 |
| ATOM | 2796 | CA | CYS | 291 | 3.797 | 37.336 | 126.590 | 1.00 | 2.00 | 0 |
| ATOM | 2797 | CB | CYS | 291 | 3.624 | 38.773 | 127.062 | 1.00 | 17.87 | 0 |
| ATOM | 2798 | SG | CYS | 291 | 1.913 | 39.123 | 127.404 | 1.00 | 13.14 | 0 |
| ATOM | 2799 | C | CYS | 291 | 5.293 | 37.034 | 126.465 | 1.00 | 2.00 | 0 |
| ATOM | 2800 | O | CYS | 291 | 5.958 | 36.694 | 127.448 | 1.00 | 23.09 | 0 |
| ATOM | 2801 | N | SER | 292 | 5.808 | 37.187 | 125.244 | 1.00 | 5.71 | 0 |
| ATOM | 2803 | CA | SER | 292 | 7.223 | 36.977 | 124.928 | 1.00 | 9.30 | 0 |
| ATOM | 2804 | CB | SER | 292 | 7.385 | 35.709 | 124.098 | 1.00 | 12.57 | 0 |
| ATOM | 2805 | OG | SER | 292 | 6.548 | 34.675 | 124.593 | 1.00 | 20.05 | 0 |

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|---|---|---|---|---|---|---|---|---|---|---|
| ATOM | 2807 | C | SER | 292 | 7.691 | 38.195 | 124.113 | 1.00 | 4.04 | 0 |
| ATOM | 2808 | O | SER | 292 | 6.867 | 38.867 | 123.485 | 1.00 | 14.24 | 0 |
| ATOM | 2809 | N | PHE | 293 | 8.993 | 38.487 | 124.128 | 1.00 | 2.00 | 0 |
| ATOM | 2811 | CA | PHE | 293 | 9.526 | 39.623 | 123.385 | 1.00 | 2.00 | 0 |
| ATOM | 2812 | CB | PHE | 293 | 10.077 | 40.676 | 124.337 | 1.00 | 17.01 | 0 |
| ATOM | 2813 | CG | PHE | 293 | 9.063 | 41.244 | 125.270 | 1.00 | 19.48 | 0 |
| ATOM | 2814 | CD1 | PHE | 293 | 8.772 | 40.611 | 126.466 | 1.00 | 23.05 | 0 |
| ATOM | 2815 | CD2 | PHE | 293 | 8.414 | 42.426 | 124.967 | 1.00 | 21.44 | 0 |
| ATOM | 2816 | CE1 | PHE | 293 | 7.852 | 41.146 | 127.352 | 1.00 | 24.82 | 0 |
| ATOM | 2817 | CE2 | PHE | 293 | 7.494 | 42.968 | 125.845 | 1.00 | 20.24 | 0 |
| ATOM | 2818 | CZ | PHE | 293 | 7.213 | 42.325 | 127.044 | 1.00 | 22.28 | 0 |
| ATOM | 2819 | C | PHE | 293 | 10.641 | 39.259 | 122.412 | 1.00 | 2.00 | 0 |
| ATOM | 2820 | O | PHE | 293 | 11.715 | 38.839 | 122.853 | 1.00 | 17.14 | 0 |
| ATOM | 2821 | N | GLN | 294 | 10.390 | 39.418 | 121.104 | 1.00 | 2.00 | 0 |
| ATOM | 2823 | CA | GLN | 294 | 11.404 | 39.162 | 120.060 | 1.00 | 2.00 | 0 |
| ATOM | 2824 | CB | GLN | 294 | 10.748 | 38.742 | 118.743 | 1.00 | 14.58 | 0 |
| ATOM | 2825 | CG | GLN | 294 | 10.074 | 37.383 | 118.798 | 1.00 | 22.67 | 0 |
| ATOM | 2826 | CD | GLN | 294 | 8.684 | 37.387 | 118.179 | 1.00 | 24.62 | 0 |
| ATOM | 2827 | OE1 | GLN | 294 | 7.835 | 38.206 | 118.535 | 1.00 | 27.17 | 0 |
| ATOM | 2828 | NE2 | GLN | 294 | 8.441 | 36.456 | 117.258 | 1.00 | 25.84 | 0 |
| ATOM | 2831 | C | GLN | 294 | 12.182 | 40.464 | 119.855 | 1.00 | 2.00 | 0 |
| ATOM | 2832 | O | GLN | 294 | 11.587 | 41.528 | 119.660 | 1.00 | 20.63 | 0 |
| ATOM | 2833 | N | ILE | 295 | 13.507 | 40.379 | 119.893 | 1.00 | 11.23 | 0 |
| ATOM | 2835 | CA | ILE | 295 | 14.356 | 41.569 | 119.772 | 1.00 | 12.32 | 0 |
| ATOM | 2836 | CB | ILE | 295 | 15.400 | 41.624 | 120.968 | 1.00 | 10.45 | 0 |
| ATOM | 2837 | CG2 | ILE | 295 | 16.277 | 42.875 | 120.886 | 1.00 | 10.45 | 0 |
| ATOM | 2838 | CG1 | ILE | 295 | 14.674 | 41.607 | 122.324 | 1.00 | 10.45 | 0 |
| ATOM | 2839 | CD1 | ILE | 295 | 13.756 | 42.807 | 122.580 | 1.00 | 10.45 | 0 |
| ATOM | 2840 | C | ILE | 295 | 15.126 | 41.703 | 118.453 | 1.00 | 7.79 | 0 |
| ATOM | 2841 | O | ILE | 295 | 15.723 | 40.741 | 117.974 | 1.00 | 10.45 | 0 |
| ATOM | 2842 | N | LEU | 296 | 15.087 | 42.900 | 117.873 | 1.00 | 11.71 | 0 |
| ATOM | 2844 | CA | LEU | 296 | 15.824 | 43.235 | 116.658 | 1.00 | 13.33 | 0 |
| ATOM | 2845 | CB | LEU | 296 | 14.987 | 44.102 | 115.717 | 1.00 | 24.46 | 0 |
| ATOM | 2846 | CG | LEU | 296 | 13.835 | 43.467 | 114.946 | 1.00 | 22.89 | 0 |
| ATOM | 2847 | CD1 | LEU | 296 | 12.626 | 43.340 | 115.862 | 1.00 | 22.12 | 0 |
| ATOM | 2848 | CD2 | LEU | 296 | 13.499 | 44.331 | 113.732 | 1.00 | 19.71 | 0 |
| ATOM | 2849 | C | LEU | 296 | 16.965 | 44.070 | 117.224 | 1.00 | 13.82 | 0 |
| ATOM | 2850 | O | LEU | 296 | 16.785 | 45.260 | 117.485 | 1.00 | 13.73 | 0 |
| ATOM | 2851 | N | LYS | 297 | 18.135 | 43.454 | 117.381 | 1.00 | 2.00 | 0 |
| ATOM | 2853 | CA | LYS | 297 | 19.319 | 44.087 | 117.997 | 1.00 | 2.00 | 0 |
| ATOM | 2854 | CB | LYS | 297 | 20.224 | 42.971 | 118.527 | 1.00 | 79.20 | 0 |
| ATOM | 2855 | CG | LYS | 297 | 20.792 | 42.094 | 117.419 | 1.00 | 79.65 | 0 |
| ATOM | 2856 | CD | LYS | 297 | 21.898 | 41.187 | 117.915 | 1.00 | 76.76 | 0 |
| ATOM | 2857 | CE | LYS | 297 | 22.543 | 40.430 | 116.762 | 1.00 | 71.01 | 0 |
| ATOM | 2858 | NZ | LYS | 297 | 23.644 | 39.543 | 117.232 | 1.00 | 68.76 | 0 |
| ATOM | 2862 | C | LYS | 297 | 20.259 | 45.149 | 117.376 | 1.00 | 2.00 | 0 |
| ATOM | 2863 | O | LYS | 297 | 21.255 | 45.501 | 118.013 | 1.00 | 94.11 | 0 |
| ATOM | 2864 | N | PRO | 298 | 19.995 | 45.656 | 116.152 | 1.00 | 40.11 | 0 |
| ATOM | 2865 | CD | PRO | 298 | 18.942 | 45.297 | 115.188 | 1.00 | 2.00 | 0 |
| ATOM | 2866 | CA | PRO | 298 | 20.900 | 46.658 | 115.553 | 1.00 | 40.11 | 0 |
| ATOM | 2867 | CB | PRO | 298 | 20.220 | 46.981 | 114.227 | 1.00 | 2.00 | 0 |
| ATOM | 2868 | CG | PRO | 298 | 19.570 | 45.700 | 113.886 | 1.00 | 2.00 | 0 |
| ATOM | 2869 | C | PRO | 298 | 21.264 | 47.935 | 116.312 | 1.00 | 40.11 | 0 |
| ATOM | 2870 | O | PRO | 298 | 21.041 | 48.056 | 117.514 | 1.00 | 2.00 | 0 |
| ATOM | 2871 | N | ALA | 299 | 21.854 | 48.878 | 115.574 | 1.00 | 61.74 | 0 |
| ATOM | 2873 | CA | ALA | 299 | 22.276 | 50.176 | 116.101 | 1.00 | 61.74 | 0 |
| ATOM | 2874 | CB | ALA | 299 | 23.627 | 50.063 | 116.799 | 1.00 | 2.00 | 0 |
| ATOM | 2875 | C | ALA | 299 | 22.373 | 51.193 | 114.973 | 1.00 | 61.74 | 0 |
| ATOM | 2876 | O | ALA | 299 | 21.893 | 52.319 | 115.105 | 1.00 | 2.00 | 0 |
| ATOM | 2877 | N | ASN | 508 | 41.191 | 29.848 | 91.500 | 1.00 | 48.97 | 0 |
| ATOM | 2879 | CA | ASN | 508 | 39.902 | 30.150 | 90.896 | 1.00 | 48.97 | 0 |
| ATOM | 2880 | CB | ASN | 508 | 38.951 | 30.831 | 91.887 | 1.00 | 0.74 | 0 |
| ATOM | 2881 | CG | ASN | 508 | 37.666 | 31.359 | 91.203 | 1.00 | 0.74 | 0 |
| ATOM | 2882 | OD1 | ASN | 508 | 36.879 | 30.587 | 90.592 | 1.00 | 0.74 | 0 |
| ATOM | 2883 | ND2 | ASN | 508 | 37.453 | 32.682 | 91.290 | 1.00 | 0.74 | 0 |
| ATOM | 2886 | C | ASN | 508 | 40.096 | 31.041 | 89.687 | 1.00 | 48.97 | 0 |
| ATOM | 2887 | O | ASN | 508 | 40.274 | 32.266 | 89.798 | 1.00 | 0.74 | 0 |
| ATOM | 2888 | N | ILE | 509 | 40.006 | 30.387 | 88.533 | 1.00 | 17.27 | 0 |

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|---|---|---|---|---|---|---|---|---|---|
| ATOM | 2890 | CA | ILE | 509 | 40.188 | 30.983 | 87.224 | 1.00 | 18.75 | 0 |
| ATOM | 2891 | CB | ILE | 509 | 40.088 | 29.889 | 86.127 | 1.00 | 44.37 | 0 |
| ATOM | 2892 | CG2 | ILE | 509 | 38.650 | 29.700 | 85.673 | 1.00 | 52.59 | 0 |
| ATOM | 2893 | CG1 | ILE | 509 | 41.013 | 30.238 | 84.966 | 1.00 | 44.31 | 0 |
| ATOM | 2894 | CD1 | ILE | 509 | 42.489 | 30.093 | 85.305 | 1.00 | 44.07 | 0 |
| ATOM | 2895 | C | ILE | 509 | 39.196 | 32.089 | 86.957 | 1.00 | 18.83 | 0 |
| ATOM | 2896 | O | ILE | 509 | 39.463 | 32.956 | 86.131 | 1.00 | 44.94 | 0 |
| ATOM | 2897 | N | ASP | 510 | 38.070 | 32.071 | 87.670 | 1.00 | 2.00 | 0 |
| ATOM | 2899 | CA | ASP | 510 | 37.048 | 33.088 | 87.485 | 1.00 | 2.00 | 0 |
| ATOM | 2900 | CB | ASP | 510 | 35.711 | 32.605 | 88.031 | 1.00 | 52.76 | 0 |
| ATOM | 2901 | CG | ASP | 510 | 35.029 | 31.634 | 87.089 | 1.00 | 54.58 | 0 |
| ATOM | 2902 | OD1 | ASP | 510 | 34.008 | 32.015 | 86.483 | 1.00 | 54.54 | 0 |
| ATOM | 2903 | OD2 | ASP | 510 | 35.521 | 30.497 | 86.944 | 1.00 | 58.16 | 0 |
| ATOM | 2904 | C | ASP | 510 | 37.403 | 34.442 | 88.056 | 1.00 | 2.00 | 0 |
| ATOM | 2905 | O | ASP | 510 | 37.016 | 35.464 | 87.490 | 1.00 | 52.34 | 0 |
| ATOM | 2906 | N | SER | 511 | 38.143 | 34.471 | 89.160 | 1.00 | 2.00 | 0 |
| ATOM | 2908 | CA | SER | 511 | 38.548 | 35.763 | 89.739 | 1.00 | 2.00 | 0 |
| ATOM | 2909 | CB | SER | 511 | 39.372 | 35.570 | 91.015 | 1.00 | 53.95 | 0 |
| ATOM | 2910 | OG | SER | 511 | 38.631 | 34.907 | 92.020 | 1.00 | 50.17 | 0 |
| ATOM | 2912 | C | SER | 511 | 39.447 | 36.379 | 88.690 | 1.00 | 2.00 | 0 |
| ATOM | 2913 | O | SER | 511 | 39.228 | 37.488 | 88.203 | 1.00 | 59.62 | 0 |
| ATOM | 2914 | N | ILE | 512 | 40.453 | 35.584 | 88.349 | 1.00 | 45.56 | 0 |
| ATOM | 2916 | CA | ILE | 512 | 41.462 | 35.892 | 87.361 | 1.00 | 40.32 | 0 |
| ATOM | 2917 | CB | ILE | 512 | 42.224 | 34.598 | 87.035 | 1.00 | 2.00 | 0 |
| ATOM | 2918 | CG2 | ILE | 512 | 43.250 | 34.842 | 85.943 | 1.00 | 2.00 | 0 |
| ATOM | 2919 | CG1 | ILE | 512 | 42.897 | 34.092 | 88.316 | 1.00 | 2.00 | 0 |
| ATOM | 2920 | CD1 | ILE | 512 | 43.635 | 32.772 | 88.174 | 1.00 | 2.00 | 0 |
| ATOM | 2921 | C | ILE | 512 | 40.843 | 36.514 | 86.105 | 1.00 | 41.22 | 0 |
| ATOM | 2922 | O | ILE | 512 | 41.051 | 37.700 | 85.848 | 1.00 | 2.00 | 0 |
| ATOM | 2923 | N | ILE | 513 | 40.061 | 35.728 | 85.358 | 1.00 | 2.00 | 0 |
| ATOM | 2925 | CA | ILE | 513 | 39.408 | 36.195 | 84.136 | 1.00 | 2.00 | 0 |
| ATOM | 2926 | CB | ILE | 513 | 38.435 | 35.123 | 83.529 | 1.00 | 2.00 | 0 |
| ATOM | 2927 | CG2 | ILE | 513 | 37.560 | 35.757 | 82.455 | 1.00 | 2.00 | 0 |
| ATOM | 2928 | CG1 | ILE | 513 | 39.227 | 33.963 | 82.890 | 1.00 | 2.00 | 0 |
| ATOM | 2929 | CD1 | ILE | 513 | 38.365 | 32.796 | 82.367 | 1.00 | 2.00 | 0 |
| ATOM | 2930 | C | ILE | 513 | 38.640 | 37.493 | 84.335 | 1.00 | 2.00 | 0 |
| ATOM | 2931 | O | ILE | 513 | 38.764 | 38.403 | 83.519 | 1.00 | 2.00 | 0 |
| ATOM | 2932 | N | GLN | 514 | 37.858 | 37.611 | 85.402 | 1.00 | 12.46 | 0 |
| ATOM | 2934 | CA | GLN | 514 | 37.117 | 38.853 | 85.581 | 1.00 | 12.46 | 0 |
| ATOM | 2935 | CB | GLN | 514 | 35.985 | 38.678 | 86.591 | 1.00 | 26.62 | 0 |
| ATOM | 2936 | CG | GLN | 514 | 36.384 | 38.251 | 87.972 | 1.00 | 26.62 | 0 |
| ATOM | 2937 | CD | GLN | 514 | 35.195 | 38.279 | 88.929 | 1.00 | 26.62 | 0 |
| ATOM | 2938 | OE1 | GLN | 514 | 34.582 | 39.337 | 89.140 | 1.00 | 26.62 | 0 |
| ATOM | 2939 | NE2 | GLN | 514 | 34.851 | 37.116 | 89.502 | 1.00 | 26.62 | 0 |
| ATOM | 2942 | C | GLN | 514 | 38.009 | 40.055 | 85.936 | 1.00 | 12.46 | 0 |
| ATOM | 2943 | O | GLN | 514 | 37.686 | 41.205 | 85.613 | 1.00 | 26.62 | 0 |
| ATOM | 2944 | N | ARG | 515 | 39.147 | 39.773 | 86.564 | 1.00 | 6.50 | 0 |
| ATOM | 2946 | CA | ARG | 515 | 40.090 | 40.810 | 86.937 | 1.00 | 7.53 | 0 |
| ATOM | 2947 | CB | ARG | 515 | 41.125 | 40.251 | 87.917 | 1.00 | 8.04 | 0 |
| ATOM | 2948 | CG | ARG | 515 | 40.626 | 40.257 | 89.362 | 1.00 | 8.04 | 0 |
| ATOM | 2949 | CD | ARG | 515 | 41.182 | 39.117 | 90.212 | 1.00 | 8.04 | 0 |
| ATOM | 2950 | NE | ARG | 515 | 42.609 | 39.250 | 90.490 | 1.00 | 8.04 | 0 |
| ATOM | 2952 | CZ | ARG | 515 | 43.355 | 38.276 | 90.998 | 1.00 | 8.04 | 0 |
| ATOM | 2953 | NH1 | ARG | 515 | 42.805 | 37.103 | 91.275 | 1.00 | 8.04 | 0 |
| ATOM | 2956 | NH2 | ARG | 515 | 44.646 | 38.478 | 91.228 | 1.00 | 8.04 | 0 |
| ATOM | 2959 | C | ARG | 515 | 40.745 | 41.325 | 85.669 | 1.00 | 12.92 | 0 |
| ATOM | 2960 | O | ARG | 515 | 40.840 | 42.537 | 85.464 | 1.00 | 8.04 | 0 |
| ATOM | 2961 | N | LEU | 516 | 41.167 | 40.398 | 84.810 | 1.00 | 8.93 | 0 |
| ATOM | 2963 | CA | LEU | 516 | 41.788 | 40.727 | 83.525 | 1.00 | 6.71 | 0 |
| ATOM | 2964 | CB | LEU | 516 | 42.172 | 39.431 | 82.786 | 1.00 | 2.00 | 0 |
| ATOM | 2965 | CG | LEU | 516 | 43.298 | 38.561 | 83.385 | 1.00 | 2.00 | 0 |
| ATOM | 2966 | CD1 | LEU | 516 | 43.057 | 37.096 | 83.083 | 1.00 | 2.00 | 0 |
| ATOM | 2967 | CD2 | LEU | 516 | 44.650 | 38.986 | 82.843 | 1.00 | 2.00 | 0 |
| ATOM | 2968 | C | LEU | 516 | 40.809 | 41.562 | 82.675 | 1.00 | 5.82 | 0 |
| ATOM | 2969 | O | LEU | 516 | 41.187 | 42.516 | 82.002 | 1.00 | 2.00 | 0 |
| ATOM | 2970 | N | LEU | 517 | 39.534 | 41.228 | 82.755 | 1.00 | 2.00 | 0 |
| ATOM | 2972 | CA | LEU | 517 | 38.519 | 41.928 | 81.993 | 1.00 | 2.73 | 0 |
| ATOM | 2973 | CB | LEU | 517 | 37.336 | 40.993 | 81.752 | 1.00 | 7.08 | 0 |

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|---|---|---|---|---|---|---|---|---|---|---|
| ATOM | 2974 | CG | LEU | 517 | 37.203 | 40.297 | 80.398 | 1.00 | 3.18 | 0 |
| ATOM | 2975 | CD1 | LEU | 517 | 38.524 | 39.694 | 79.950 | 1.00 | 12.86 | 0 |
| ATOM | 2976 | CD2 | LEU | 517 | 36.133 | 39.227 | 80.518 | 1.00 | 9.89 | 0 |
| ATOM | 2977 | C | LEU | 517 | 37.989 | 43.262 | 82.536 | 1.00 | 9.79 | 0 |
| ATOM | 2978 | O | LEU | 517 | 37.169 | 43.908 | 81.858 | 1.00 | 16.46 | 0 |
| ATOM | 2979 | N | GLU | 518 | 38.409 | 43.708 | 83.722 | 1.00 | 2.00 | 0 |
| ATOM | 2981 | CA | GLU | 518 | 37.845 | 44.981 | 84.178 | 1.00 | 2.00 | 0 |
| ATOM | 2982 | CB | GLU | 518 | 37.621 | 45.015 | 85.699 | 1.00 | 2.00 | 0 |
| ATOM | 2983 | CG | GLU | 518 | 36.908 | 46.315 | 86.231 | 1.00 | 2.00 | 0 |
| ATOM | 2984 | CD | GLU | 518 | 35.550 | 46.705 | 85.526 | 1.00 | 2.00 | 0 |
| ATOM | 2985 | OE1 | GLU | 518 | 34.554 | 47.001 | 86.262 | 1.00 | 2.00 | 0 |
| ATOM | 2986 | OE2 | GLU | 518 | 35.481 | 46.748 | 84.252 | 1.00 | 2.00 | 0 |
| ATOM | 2987 | C | GLU | 518 | 38.618 | 46.200 | 83.677 | 1.00 | 2.00 | 0 |
| ATOM | 2988 | O | GLU | 518 | 38.121 | 47.335 | 83.729 | 1.00 | 2.00 | 0 |
| ATOM | 2989 | N | VAL | 519 | 39.828 | 45.978 | 83.166 | 1.00 | 21.94 | 0 |
| ATOM | 2991 | CA | VAL | 519 | 40.582 | 47.094 | 82.589 | 1.00 | 19.66 | 0 |
| ATOM | 2992 | CB | VAL | 519 | 42.078 | 46.804 | 82.428 | 1.00 | 40.73 | 0 |
| ATOM | 2993 | CG1 | VAL | 519 | 42.759 | 46.806 | 83.771 | 1.00 | 42.53 | 0 |
| ATOM | 2994 | CG2 | VAL | 519 | 42.272 | 45.488 | 81.684 | 1.00 | 37.62 | 0 |
| ATOM | 2995 | C | VAL | 519 | 40.007 | 47.307 | 81.196 | 1.00 | 22.58 | 0 |
| ATOM | 2996 | O | VAL | 519 | 40.402 | 48.229 | 80.493 | 1.00 | 48.07 | 0 |
| ATOM | 2997 | N | ARG | 520 | 39.066 | 46.442 | 80.815 | 1.00 | 26.87 | 0 |
| ATOM | 2999 | CA | ARG | 520 | 38.410 | 46.495 | 79.515 | 1.00 | 28.58 | 0 |
| ATOM | 3000 | CB | ARG | 520 | 37.216 | 45.534 | 79.480 | 1.00 | 40.18 | 0 |
| ATOM | 3001 | CG | ARG | 520 | 36.878 | 45.043 | 78.086 | 1.00 | 44.14 | 0 |
| ATOM | 3002 | CD | ARG | 520 | 35.994 | 43.814 | 78.116 | 1.00 | 47.95 | 0 |
| ATOM | 3003 | NE | ARG | 520 | 34.592 | 44.131 | 77.872 | 1.00 | 44.40 | 0 |
| ATOM | 3005 | CZ | ARG | 520 | 33.565 | 43.402 | 78.308 | 1.00 | 51.11 | 0 |
| ATOM | 3006 | NH1 | ARG | 520 | 33.767 | 42.298 | 79.022 | 1.00 | 48.24 | 0 |
| ATOM | 3009 | NH2 | ARG | 520 | 32.325 | 43.778 | 78.026 | 1.00 | 49.03 | 0 |
| ATOM | 3012 | C | ARG | 520 | 37.946 | 47.899 | 79.147 | 1.00 | 28.36 | 0 |
| ATOM | 3013 | O | ARG | 520 | 37.881 | 48.247 | 77.964 | 1.00 | 46.63 | 0 |
| ATOM | 3014 | N | GLY | 521 | 37.639 | 48.703 | 80.158 | 1.00 | 27.79 | 0 |
| ATOM | 3016 | CA | GLY | 521 | 37.186 | 50.056 | 79.905 | 1.00 | 30.97 | 0 |
| ATOM | 3017 | C | GLY | 521 | 38.158 | 51.099 | 80.400 | 1.00 | 32.39 | 0 |
| ATOM | 3018 | O | GLY | 521 | 37.739 | 52.124 | 80.940 | 1.00 | 54.55 | 0 |
| ATOM | 3019 | N | SER | 522 | 39.451 | 50.840 | 80.225 | 1.00 | 46.95 | 0 |
| ATOM | 3021 | CA | SER | 522 | 40.495 | 51.761 | 80.663 | 1.00 | 47.91 | 0 |
| ATOM | 3022 | CB | SER | 522 | 41.300 | 51.146 | 81.801 | 1.00 | 33.41 | 0 |
| ATOM | 3023 | OG | SER | 522 | 40.459 | 50.694 | 82.844 | 1.00 | 32.38 | 0 |
| ATOM | 3025 | C | SER | 522 | 41.436 | 52.094 | 79.517 | 1.00 | 49.38 | 0 |
| ATOM | 3026 | O | SER | 522 | 41.495 | 51.378 | 78.513 | 1.00 | 34.02 | 0 |
| ATOM | 3027 | N | LYS | 523 | 42.174 | 53.184 | 79.679 | 1.00 | 84.47 | 0 |
| ATOM | 3029 | CA | LYS | 523 | 43.127 | 53.640 | 78.674 | 1.00 | 81.24 | 0 |
| ATOM | 3030 | CB | LYS | 523 | 44.035 | 54.715 | 79.274 | 1.00 | 43.78 | 0 |
| ATOM | 3031 | CG | LYS | 523 | 43.307 | 55.987 | 79.619 | 1.00 | 44.40 | 0 |
| ATOM | 3032 | CD | LYS | 523 | 44.206 | 56.990 | 80.322 | 1.00 | 68.84 | 0 |
| ATOM | 3033 | CE | LYS | 523 | 43.493 | 58.336 | 80.458 | 1.00 | 44.38 | 0 |
| ATOM | 3034 | NZ | LYS | 523 | 42.092 | 58.186 | 80.983 | 1.00 | 44.06 | 0 |
| ATOM | 3038 | C | LYS | 523 | 44.000 | 52.501 | 78.173 | 1.00 | 80.03 | 0 |
| ATOM | 3039 | O | LYS | 523 | 44.314 | 51.584 | 78.937 | 1.00 | 43.77 | 0 |
| ATOM | 3040 | N | PRO | 524 | 44.360 | 52.514 | 76.873 | 1.00 | 2.00 | 0 |
| ATOM | 3041 | CD | PRO | 524 | 43.901 | 53.427 | 75.811 | 1.00 | 84.06 | 0 |
| ATOM | 3042 | CA | PRO | 524 | 45.218 | 51.459 | 76.316 | 1.00 | 2.00 | 0 |
| ATOM | 3043 | CB | PRO | 524 | 45.357 | 51.871 | 74.850 | 1.00 | 82.26 | 0 |
| ATOM | 3044 | CG | PRO | 524 | 44.057 | 52.574 | 74.576 | 1.00 | 78.74 | 0 |
| ATOM | 3045 | C | PRO | 524 | 46.576 | 51.489 | 77.063 | 1.00 | 2.00 | 0 |
| ATOM | 3046 | O | PRO | 524 | 47.510 | 52.190 | 76.653 | 1.00 | 76.15 | 0 |
| ATOM | 3047 | N | GLY | 525 | 46.647 | 50.742 | 78.166 | 1.00 | 33.80 | 0 |
| ATOM | 3049 | CA | GLY | 525 | 47.846 | 50.682 | 78.984 | 1.00 | 98.68 | 0 |
| ATOM | 3050 | C | GLY | 525 | 47.575 | 50.197 | 80.403 | 1.00 | 99.00 | 0 |
| ATOM | 3051 | O | GLY | 525 | 48.427 | 49.555 | 81.013 | 1.00 | 2.00 | 0 |
| ATOM | 3052 | N | LYS | 526 | 46.397 | 50.496 | 80.942 | 1.00 | 49.37 | 0 |
| ATOM | 3054 | CA | LYS | 526 | 46.047 | 50.070 | 82.297 | 1.00 | 44.35 | 0 |
| ATOM | 3055 | CB | LYS | 526 | 44.537 | 50.226 | 82.505 | 1.00 | 0.79 | 0 |
| ATOM | 3056 | CG | LYS | 526 | 44.013 | 49.851 | 83.911 | 1.00 | 0.82 | 0 |
| ATOM | 3057 | CD | LYS | 526 | 44.370 | 50.915 | 84.950 | 1.00 | 0.29 | 0 |
| ATOM | 3058 | CE | LYS | 526 | 44.413 | 50.312 | 86.354 | 1.00 | 28.48 | 0 |

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|---|---|---|---|---|---|---|---|---|---|---|
| ATOM | 3059 | NZ | LYS | 526 | 45.166 | 51.143 | 87.348 | 1.00 | 28.16 | 0 |
| ATOM | 3063 | C | LYS | 526 | 46.461 | 48.602 | 82.479 | 1.00 | 41.81 | 0 |
| ATOM | 3064 | O | LYS | 526 | 45.984 | 47.727 | 81.760 | 1.00 | 0.75 | 0 |
| ATOM | 3065 | N | ASN | 527 | 47.372 | 48.337 | 83.412 | 1.00 | 6.60 | 0 |
| ATOM | 3067 | CA | ASN | 527 | 47.861 | 46.972 | 83.639 | 1.00 | 6.60 | 0 |
| ATOM | 3068 | CB | ASN | 527 | 49.208 | 46.977 | 84.381 | 1.00 | 20.38 | 0 |
| ATOM | 3069 | CG | ASN | 527 | 50.300 | 47.733 | 83.645 | 1.00 | 30.42 | 0 |
| ATOM | 3070 | OD1 | ASN | 527 | 50.695 | 48.820 | 84.068 | 1.00 | 29.99 | 0 |
| ATOM | 3071 | ND2 | ASN | 527 | 50.818 | 47.148 | 82.561 | 1.00 | 30.17 | 0 |
| ATOM | 3074 | C | ASN | 527 | 46.895 | 46.135 | 84.463 | 1.00 | 6.60 | 0 |
| ATOM | 3075 | O | ASN | 527 | 45.866 | 46.628 | 84.924 | 1.00 | 23.47 | 0 |
| ATOM | 3076 | N | VAL | 528 | 47.271 | 44.866 | 84.647 | 1.00 | 26.67 | 0 |
| ATOM | 3078 | CA | VAL | 528 | 46.541 | 43.874 | 85.443 | 1.00 | 26.67 | 0 |
| ATOM | 3079 | CB | VAL | 528 | 45.575 | 43.004 | 84.603 | 1.00 | 33.44 | 0 |
| ATOM | 3080 | CG1 | VAL | 528 | 44.909 | 41.956 | 85.488 | 1.00 | 33.01 | 0 |
| ATOM | 3081 | CG2 | VAL | 528 | 44.524 | 43.858 | 83.956 | 1.00 | 35.61 | 0 |
| ATOM | 3082 | C | VAL | 528 | 47.607 | 42.940 | 86.018 | 1.00 | 26.67 | 0 |
| ATOM | 3083 | O | VAL | 528 | 48.054 | 42.003 | 85.348 | 1.00 | 36.85 | 0 |
| ATOM | 3084 | N | GLN | 529 | 48.048 | 43.231 | 87.239 | 1.00 | 2.00 | 0 |
| ATOM | 3086 | CA | GLN | 529 | 49.061 | 42.407 | 87.920 | 1.00 | 2.00 | 0 |
| ATOM | 3087 | CB | GLN | 529 | 49.968 | 43.297 | 88.787 | 1.00 | 30.41 | 0 |
| ATOM | 3088 | CG | GLN | 529 | 51.142 | 42.569 | 89.428 | 1.00 | 32.34 | 0 |
| ATOM | 3089 | CD | GLN | 529 | 52.380 | 42.558 | 88.558 | 1.00 | 31.37 | 0 |
| ATOM | 3090 | OE1 | GLN | 529 | 53.436 | 43.035 | 88.962 | 1.00 | 35.47 | 0 |
| ATOM | 3091 | NE2 | GLN | 529 | 52.259 | 42.014 | 87.361 | 1.00 | 30.69 | 0 |
| ATOM | 3094 | C | GLN | 529 | 48.350 | 41.347 | 88.792 | 1.00 | 2.00 | 0 |
| ATOM | 3095 | O | GLN | 529 | 47.545 | 41.689 | 89.663 | 1.00 | 32.29 | 0 |
| ATOM | 3096 | N | LEU | 530 | 48.624 | 40.072 | 88.536 | 1.00 | 2.00 | 0 |
| ATOM | 3098 | CA | LEU | 530 | 47.994 | 39.002 | 89.303 | 1.00 | 2.00 | 0 |
| ATOM | 3099 | CB | LEU | 530 | 47.462 | 37.911 | 88.381 | 1.00 | 12.99 | 0 |
| ATOM | 3100 | CG | LEU | 530 | 46.535 | 38.302 | 87.248 | 1.00 | 12.99 | 0 |
| ATOM | 3101 | CD1 | LEU | 530 | 47.297 | 38.159 | 85.956 | 1.00 | 12.99 | 0 |
| ATOM | 3102 | CD2 | LEU | 530 | 45.313 | 37.403 | 87.243 | 1.00 | 12.99 | 0 |
| ATOM | 3103 | C | LEU | 530 | 49.002 | 38.365 | 90.236 | 1.00 | 2.00 | 0 |
| ATOM | 3104 | O | LEU | 530 | 50.207 | 38.543 | 90.067 | 1.00 | 12.99 | 0 |
| ATOM | 3105 | N | GLN | 531 | 48.516 | 37.622 | 91.221 | 1.00 | 2.00 | 0 |
| ATOM | 3107 | CA | GLN | 531 | 49.418 | 36.932 | 92.117 | 1.00 | 2.00 | 0 |
| ATOM | 3108 | CB | GLN | 531 | 48.634 | 36.051 | 93.090 | 1.00 | 61.54 | 0 |
| ATOM | 3109 | CG | GLN | 531 | 48.376 | 36.639 | 94.465 | 1.00 | 62.91 | 0 |
| ATOM | 3110 | CD | GLN | 531 | 47.221 | 37.603 | 94.487 | 1.00 | 63.71 | 0 |
| ATOM | 3111 | OE1 | GLN | 531 | 47.322 | 38.684 | 95.053 | 1.00 | 59.60 | 0 |
| ATOM | 3112 | NE2 | GLN | 531 | 46.111 | 37.219 | 93.876 | 1.00 | 61.96 | 0 |
| ATOM | 3115 | C | GLN | 531 | 50.337 | 36.040 | 91.266 | 1.00 | 2.00 | 0 |
| ATOM | 3116 | O | GLN | 531 | 49.859 | 35.276 | 90.422 | 1.00 | 67.15 | 0 |
| ATOM | 3117 | N | GLU | 532 | 51.647 | 36.153 | 91.480 | 1.00 | 2.00 | 0 |
| ATOM | 3119 | CA | GLU | 532 | 52.655 | 35.349 | 90.766 | 1.00 | 2.00 | 0 |
| ATOM | 3120 | CB | GLU | 532 | 54.056 | 35.623 | 91.336 | 1.00 | 19.01 | 0 |
| ATOM | 3121 | CG | GLU | 532 | 55.176 | 34.623 | 90.966 | 1.00 | 22.74 | 0 |
| ATOM | 3122 | CD | GLU | 532 | 56.496 | 34.871 | 91.746 | 1.00 | 25.50 | 0 |
| ATOM | 3123 | OE1 | GLU | 532 | 56.845 | 36.042 | 92.058 | 1.00 | 20.16 | 0 |
| ATOM | 3124 | OE2 | GLU | 532 | 57.195 | 33.879 | 92.051 | 1.00 | 20.82 | 0 |
| ATOM | 3125 | C | GLU | 532 | 52.345 | 33.866 | 90.900 | 1.00 | 2.00 | 0 |
| ATOM | 3126 | O | GLU | 532 | 52.833 | 33.059 | 90.116 | 1.00 | 17.28 | 0 |
| ATOM | 3127 | N | ASN | 533 | 51.568 | 33.509 | 91.918 | 1.00 | 26.78 | 0 |
| ATOM | 3129 | CA | ASN | 533 | 51.181 | 32.120 | 92.127 | 1.00 | 27.69 | 0 |
| ATOM | 3130 | CB | ASN | 533 | 50.751 | 31.857 | 93.587 | 1.00 | 42.65 | 0 |
| ATOM | 3131 | CG | ASN | 533 | 49.834 | 32.944 | 94.154 | 1.00 | 49.17 | 0 |
| ATOM | 3132 | OD1 | ASN | 533 | 50.274 | 34.070 | 94.392 | 1.00 | 50.06 | 0 |
| ATOM | 3133 | ND2 | ASN | 533 | 48.568 | 32.605 | 94.387 | 1.00 | 50.92 | 0 |
| ATOM | 3136 | C | ASN | 533 | 50.053 | 31.770 | 91.165 | 1.00 | 26.24 | 0 |
| ATOM | 3137 | O | ASN | 533 | 49.918 | 30.615 | 90.747 | 1.00 | 41.80 | 0 |
| ATOM | 3138 | N | GLU | 534 | 49.253 | 32.777 | 90.815 | 1.00 | 24.76 | 0 |
| ATOM | 3140 | CA | GLU | 534 | 48.146 | 32.592 | 89.893 | 1.00 | 19.83 | 0 |
| ATOM | 3141 | CB | GLU | 534 | 47.228 | 33.801 | 89.918 | 1.00 | 17.15 | 0 |
| ATOM | 3142 | CG | GLU | 534 | 46.509 | 33.924 | 91.239 | 1.00 | 23.75 | 0 |
| ATOM | 3143 | CD | GLU | 534 | 45.598 | 35.132 | 91.323 | 1.00 | 25.22 | 0 |
| ATOM | 3144 | OE1 | GLU | 534 | 44.490 | 34.997 | 91.890 | 1.00 | 24.06 | 0 |
| ATOM | 3145 | OE2 | GLU | 534 | 45.991 | 36.215 | 90.837 | 1.00 | 29.17 | 0 |

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|---|---|---|---|---|---|---|---|---|---|---|
| ATOM | 3146 | C | GLU | 534 | 48.712 | 32.365 | 88.510 | 1.00 | 21.16 | 0 |
| ATOM | 3147 | O | GLU | 534 | 48.235 | 31.500 | 87.779 | 1.00 | 14.12 | 0 |
| ATOM | 3148 | N | ILE | 535 | 49.747 | 33.122 | 88.156 | 1.00 | 2.00 | 0 |
| ATOM | 3150 | CA | ILE | 535 | 50.389 | 32.942 | 86.859 | 1.00 | 2.00 | 0 |
| ATOM | 3151 | CB | ILE | 535 | 51.442 | 34.023 | 86.570 | 1.00 | 2.00 | 0 |
| ATOM | 3152 | CG2 | ILE | 535 | 52.050 | 33.784 | 85.190 | 1.00 | 2.00 | 0 |
| ATOM | 3153 | CG1 | ILE | 535 | 50.793 | 35.411 | 86.641 | 1.00 | 2.00 | 0 |
| ATOM | 3154 | CD1 | ILE | 535 | 51.537 | 36.488 | 85.849 | 1.00 | 2.00 | 0 |
| ATOM | 3155 | C | ILE | 535 | 51.060 | 31.565 | 86.797 | 1.00 | 2.00 | 0 |
| ATOM | 3156 | O | ILE | 535 | 50.788 | 30.780 | 85.876 | 1.00 | 2.00 | 0 |
| ATOM | 3157 | N | ARG | 536 | 51.914 | 31.256 | 87.778 | 1.00 | 2.00 | 0 |
| ATOM | 3159 | CA | ARG | 536 | 52.583 | 29.951 | 87.793 | 1.00 | 2.00 | 0 |
| ATOM | 3160 | CB | ARG | 536 | 53.495 | 29.818 | 89.011 | 1.00 | 39.13 | 0 |
| ATOM | 3161 | CG | ARG | 536 | 52.808 | 29.604 | 90.341 | 1.00 | 45.43 | 0 |
| ATOM | 3162 | CD | ARG | 536 | 53.839 | 29.648 | 91.474 | 1.00 | 49.26 | 0 |
| ATOM | 3163 | NE | ARG | 536 | 55.059 | 28.910 | 91.132 | 1.00 | 56.04 | 0 |
| ATOM | 3165 | CZ | ARG | 536 | 55.110 | 27.603 | 90.876 | 1.00 | 55.24 | 0 |
| ATOM | 3166 | NH1 | ARG | 536 | 54.011 | 26.860 | 90.920 | 1.00 | 53.92 | 0 |
| ATOM | 3169 | NH2 | ARG | 536 | 56.267 | 27.032 | 90.576 | 1.00 | 44.45 | 0 |
| ATOM | 3172 | C | ARG | 536 | 51.562 | 28.811 | 87.742 | 1.00 | 2.00 | 0 |
| ATOM | 3173 | O | ARG | 536 | 51.806 | 27.778 | 87.126 | 1.00 | 37.01 | 0 |
| ATOM | 3174 | N | GLY | 537 | 50.406 | 29.033 | 88.363 | 1.00 | 2.00 | 0 |
| ATOM | 3176 | CA | GLY | 537 | 49.345 | 28.046 | 88.340 | 1.00 | 2.00 | 0 |
| ATOM | 3177 | C | GLY | 537 | 48.690 | 28.000 | 86.970 | 1.00 | 2.00 | 0 |
| ATOM | 3178 | O | GLY | 537 | 48.292 | 26.924 | 86.512 | 1.00 | 2.00 | 0 |
| ATOM | 3179 | N | LEU | 538 | 48.574 | 29.164 | 86.319 | 1.00 | 9.51 | 0 |
| ATOM | 3181 | CA | LEU | 538 | 47.979 | 29.276 | 84.977 | 1.00 | 7.63 | 0 |
| ATOM | 3182 | CB | LEU | 538 | 47.930 | 30.736 | 84.513 | 1.00 | 2.00 | 0 |
| ATOM | 3183 | CG | LEU | 538 | 46.654 | 31.524 | 84.772 | 1.00 | 2.00 | 0 |
| ATOM | 3184 | CD1 | LEU | 538 | 46.865 | 32.966 | 84.408 | 1.00 | 2.00 | 0 |
| ATOM | 3185 | CD2 | LEU | 538 | 45.531 | 30.940 | 83.972 | 1.00 | 2.00 | 0 |
| ATOM | 3186 | C | LEU | 538 | 48.816 | 28.472 | 84.000 | 1.00 | 12.73 | 0 |
| ATOM | 3187 | O | LEU | 538 | 48.295 | 27.635 | 83.271 | 1.00 | 2.00 | 0 |
| ATOM | 3188 | N | CYS | 539 | 50.120 | 28.724 | 84.000 | 1.00 | 2.00 | 0 |
| ATOM | 3190 | CA | CYS | 539 | 51.036 | 28.001 | 83.132 | 1.00 | 2.00 | 0 |
| ATOM | 3191 | CB | CYS | 539 | 52.473 | 28.494 | 83.337 | 1.00 | 20.52 | 0 |
| ATOM | 3192 | SG | CYS | 539 | 52.713 | 30.280 | 83.567 | 1.00 | 19.48 | 0 |
| ATOM | 3193 | C | CYS | 539 | 50.957 | 26.501 | 83.474 | 1.00 | 2.00 | 0 |
| ATOM | 3194 | O | CYS | 539 | 50.854 | 25.658 | 82.588 | 1.00 | 29.69 | 0 |
| ATOM | 3195 | N | LEU | 540 | 50.984 | 26.191 | 84.769 | 1.00 | 26.60 | 0 |
| ATOM | 3197 | CA | LEU | 540 | 50.919 | 24.819 | 85.265 | 1.00 | 26.60 | 0 |
| ATOM | 3198 | CB | LEU | 540 | 51.106 | 24.818 | 86.786 | 1.00 | 2.00 | 0 |
| ATOM | 3199 | CG | LEU | 540 | 52.539 | 24.770 | 87.339 | 1.00 | 2.00 | 0 |
| ATOM | 3200 | CD1 | LEU | 540 | 53.001 | 23.360 | 87.385 | 1.00 | 2.00 | 0 |
| ATOM | 3201 | CD2 | LEU | 540 | 53.492 | 25.577 | 86.497 | 1.00 | 2.00 | 0 |
| ATOM | 3202 | C | LEU | 540 | 49.635 | 24.061 | 84.899 | 1.00 | 26.60 | 0 |
| ATOM | 3203 | O | LEU | 540 | 49.677 | 22.856 | 84.619 | 1.00 | 2.00 | 0 |
| ATOM | 3204 | N | LYS | 541 | 48.500 | 24.756 | 84.901 | 1.00 | 13.81 | 0 |
| ATOM | 3206 | CA | LYS | 541 | 47.219 | 24.126 | 84.561 | 1.00 | 17.46 | 0 |
| ATOM | 3207 | CB | LYS | 541 | 46.046 | 24.964 | 85.108 | 1.00 | 14.61 | 0 |
| ATOM | 3208 | CG | LYS | 541 | 45.844 | 24.880 | 86.624 | 1.00 | 22.53 | 0 |
| ATOM | 3209 | CD | LYS | 541 | 44.709 | 25.777 | 87.150 | 1.00 | 31.64 | 0 |
| ATOM | 3210 | CE | LYS | 541 | 45.175 | 27.201 | 87.517 | 1.00 | 37.15 | 0 |
| ATOM | 3211 | NZ | LYS | 541 | 44.147 | 28.010 | 88.284 | 1.00 | 27.95 | 0 |
| ATOM | 3215 | C | LYS | 541 | 47.047 | 23.891 | 83.046 | 1.00 | 16.97 | 0 |
| ATOM | 3216 | O | LYS | 541 | 46.862 | 22.745 | 82.608 | 1.00 | 8.92 | 0 |
| ATOM | 3217 | N | SER | 542 | 47.131 | 24.963 | 82.253 | 1.00 | 2.00 | 0 |
| ATOM | 3219 | CA | SER | 542 | 46.975 | 24.877 | 80.791 | 1.00 | 2.00 | 0 |
| ATOM | 3220 | CB | SER | 542 | 47.165 | 26.256 | 80.150 | 1.00 | 2.00 | 0 |
| ATOM | 3221 | OG | SER | 542 | 48.499 | 26.703 | 80.298 | 1.00 | 2.00 | 0 |
| ATOM | 3223 | C | SER | 542 | 47.915 | 23.870 | 80.107 | 1.00 | 2.00 | 0 |
| ATOM | 3224 | O | SER | 542 | 47.450 | 22.991 | 79.377 | 1.00 | 2.00 | 0 |
| ATOM | 3225 | N | ARG | 543 | 49.223 | 24.016 | 80.338 | 1.00 | 8.64 | 0 |
| ATOM | 3227 | CA | ARG | 543 | 50.244 | 23.128 | 79.772 | 1.00 | 8.64 | 0 |
| ATOM | 3228 | CB | ARG | 543 | 51.607 | 23.381 | 80.434 | 1.00 | 2.00 | 0 |
| ATOM | 3229 | CG | ARG | 543 | 52.676 | 22.339 | 80.116 | 1.00 | 4.46 | 0 |
| ATOM | 3230 | CD | ARG | 543 | 53.757 | 22.313 | 81.173 | 1.00 | 2.00 | 0 |
| ATOM | 3231 | NE | ARG | 543 | 54.989 | 21.663 | 80.708 | 1.00 | 2.00 | 0 |

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|---|---|---|---|---|---|---|---|---|---|---|
| ATOM | 3233 | CZ | ARG | 543 | 55.326 | 20.395 | 80.952 | 1.00 | 2.00 | 0 |
| ATOM | 3234 | NH1 | ARG | 543 | 54.523 | 19.606 | 81.656 | 1.00 | 3.99 | 0 |
| ATOM | 3237 | NH2 | ARG | 543 | 56.483 | 19.915 | 80.508 | 1.00 | 2.00 | 0 |
| ATOM | 3240 | C | ARG | 543 | 49.873 | 21.660 | 79.981 | 1.00 | 8.64 | 0 |
| ATOM | 3241 | O | ARG | 543 | 50.187 | 20.806 | 79.148 | 1.00 | 5.52 | 0 |
| ATOM | 3242 | N | GLU | 544 | 49.227 | 21.352 | 81.098 | 1.00 | 42.94 | 0 |
| ATOM | 3244 | CA | GLU | 544 | 48.834 | 19.978 | 81.355 | 1.00 | 44.22 | 0 |
| ATOM | 3245 | CB | GLU | 544 | 48.308 | 19.841 | 82.778 | 1.00 | 37.01 | 0 |
| ATOM | 3246 | CG | GLU | 544 | 48.175 | 18.415 | 83.249 | 1.00 | 41.48 | 0 |
| ATOM | 3247 | CD | GLU | 544 | 47.561 | 18.341 | 84.626 | 1.00 | 46.37 | 0 |
| ATOM | 3248 | OE1 | GLU | 544 | 46.433 | 18.858 | 84.791 | 1.00 | 53.09 | 0 |
| ATOM | 3249 | OE2 | GLU | 544 | 48.202 | 17.777 | 85.543 | 1.00 | 47.19 | 0 |
| ATOM | 3250 | C | GLU | 544 | 47.763 | 19.584 | 80.339 | 1.00 | 40.49 | 0 |
| ATOM | 3251 | O | GLU | 544 | 47.742 | 18.450 | 79.867 | 1.00 | 34.80 | 0 |
| ATOM | 3252 | N | ILE | 545 | 46.898 | 20.538 | 79.994 | 1.00 | 2.00 | 0 |
| ATOM | 3254 | CA | ILE | 545 | 45.823 | 20.315 | 79.017 | 1.00 | 2.00 | 0 |
| ATOM | 3255 | CB | ILE | 545 | 44.805 | 21.487 | 78.959 | 1.00 | 11.87 | 0 |
| ATOM | 3256 | CG2 | ILE | 545 | 43.645 | 21.102 | 78.064 | 1.00 | 6.53 | 0 |
| ATOM | 3257 | CG1 | ILE | 545 | 44.288 | 21.836 | 80.353 | 1.00 | 16.65 | 0 |
| ATOM | 3258 | CD1 | ILE | 545 | 43.267 | 22.955 | 80.361 | 1.00 | 13.01 | 0 |
| ATOM | 3259 | C | ILE | 545 | 46.377 | 20.149 | 77.605 | 1.00 | 2.00 | 0 |
| ATOM | 3260 | O | ILE | 545 | 45.960 | 19.267 | 76.868 | 1.00 | 9.05 | 0 |
| ATOM | 3261 | N | PHE | 546 | 47.302 | 21.018 | 77.227 | 1.00 | 2.00 | 0 |
| ATOM | 3263 | CA | PHE | 546 | 47.895 | 20.945 | 75.918 | 1.00 | 2.00 | 0 |
| ATOM | 3264 | CB | PHE | 546 | 49.058 | 21.906 | 75.816 | 1.00 | 2.00 | 0 |
| ATOM | 3265 | CG | PHE | 546 | 48.653 | 23.335 | 75.875 | 1.00 | 2.00 | 0 |
| ATOM | 3266 | CD1 | PHE | 546 | 49.512 | 24.293 | 76.399 | 1.00 | 2.00 | 0 |
| ATOM | 3267 | CD2 | PHE | 546 | 47.411 | 23.730 | 75.426 | 1.00 | 2.00 | 0 |
| ATOM | 3268 | CE1 | PHE | 546 | 49.127 | 25.630 | 76.473 | 1.00 | 2.00 | 0 |
| ATOM | 3269 | CE2 | PHE | 546 | 47.023 | 25.050 | 75.496 | 1.00 | 2.00 | 0 |
| ATOM | 3270 | CZ | PHE | 546 | 47.881 | 26.006 | 76.020 | 1.00 | 2.00 | 0 |
| ATOM | 3271 | C | PHE | 546 | 48.374 | 19.538 | 75.658 | 1.00 | 2.00 | 0 |
| ATOM | 3272 | O | PHE | 546 | 48.141 | 18.990 | 74.596 | 1.00 | 2.00 | 0 |
| ATOM | 3273 | N | LEU | 547 | 49.012 | 18.935 | 76.647 | 1.00 | 2.00 | 0 |
| ATOM | 3275 | CA | LEU | 547 | 49.527 | 17.582 | 76.506 | 1.00 | 2.00 | 0 |
| ATOM | 3276 | CB | LEU | 547 | 50.499 | 17.289 | 77.654 | 1.00 | 6.91 | 0 |
| ATOM | 3277 | CG | LEU | 547 | 51.754 | 18.159 | 77.582 | 1.00 | 8.40 | 0 |
| ATOM | 3278 | CD1 | LEU | 547 | 52.096 | 18.701 | 78.934 | 1.00 | 16.17 | 0 |
| ATOM | 3279 | CD2 | LEU | 547 | 52.905 | 17.363 | 77.029 | 1.00 | 11.72 | 0 |
| ATOM | 3280 | C | LEU | 547 | 48.422 | 16.526 | 76.434 | 1.00 | 2.00 | 0 |
| ATOM | 3281 | O | LEU | 547 | 48.642 | 15.414 | 75.946 | 1.00 | 6.91 | 0 |
| ATOM | 3282 | N | SER | 548 | 47.230 | 16.881 | 76.903 | 1.00 | 5.34 | 0 |
| ATOM | 3284 | CA | SER | 548 | 46.091 | 15.964 | 76.898 | 1.00 | 5.34 | 0 |
| ATOM | 3285 | CB | SER | 548 | 45.099 | 16.356 | 77.993 | 1.00 | 36.19 | 0 |
| ATOM | 3286 | OG | SER | 548 | 45.611 | 17.389 | 78.821 | 1.00 | 39.64 | 0 |
| ATOM | 3288 | C | SER | 548 | 45.374 | 15.975 | 75.552 | 1.00 | 5.34 | 0 |
| ATOM | 3289 | O | SER | 548 | 44.299 | 15.381 | 75.406 | 1.00 | 36.66 | 0 |
| ATOM | 3290 | N | GLN | 549 | 45.968 | 16.649 | 74.569 | 1.00 | 23.79 | 0 |
| ATOM | 3292 | CA | GLN | 549 | 45.384 | 16.754 | 73.242 | 1.00 | 23.94 | 0 |
| ATOM | 3293 | CB | GLN | 549 | 44.751 | 18.128 | 73.084 | 1.00 | 46.80 | 0 |
| ATOM | 3294 | CG | GLN | 549 | 43.567 | 18.354 | 73.990 | 1.00 | 38.43 | 0 |
| ATOM | 3295 | CD | GLN | 549 | 43.180 | 19.800 | 74.054 | 1.00 | 38.53 | 0 |
| ATOM | 3296 | OE1 | GLN | 549 | 43.934 | 20.672 | 73.624 | 1.00 | 46.42 | 0 |
| ATOM | 3297 | NE2 | GLN | 549 | 42.002 | 20.074 | 74.595 | 1.00 | 39.54 | 0 |
| ATOM | 3300 | C | GLN | 549 | 46.456 | 16.547 | 72.182 | 1.00 | 25.87 | 0 |
| ATOM | 3301 | O | GLN | 549 | 47.634 | 16.766 | 72.451 | 1.00 | 42.01 | 0 |
| ATOM | 3302 | N | PRO | 550 | 46.068 | 16.105 | 70.963 | 1.00 | 2.00 | 0 |
| ATOM | 3303 | CD | PRO | 550 | 44.729 | 15.738 | 70.469 | 1.00 | 36.68 | 0 |
| ATOM | 3304 | CA | PRO | 550 | 47.075 | 15.894 | 69.921 | 1.00 | 2.00 | 0 |
| ATOM | 3305 | CB | PRO | 550 | 46.253 | 15.350 | 68.750 | 1.00 | 36.68 | 0 |
| ATOM | 3306 | CG | PRO | 550 | 44.886 | 15.915 | 68.988 | 1.00 | 36.68 | 0 |
| ATOM | 3307 | C | PRO | 550 | 47.816 | 17.184 | 69.580 | 1.00 | 2.00 | 0 |
| ATOM | 3308 | O | PRO | 550 | 47.318 | 18.280 | 69.840 | 1.00 | 36.68 | 0 |
| ATOM | 3309 | N | ILE | 551 | 49.013 | 17.046 | 69.015 | 1.00 | 2.00 | 0 |
| ATOM | 3311 | CA | ILE | 551 | 49.824 | 18.198 | 68.626 | 1.00 | 2.00 | 0 |
| ATOM | 3312 | CB | ILE | 551 | 51.293 | 17.788 | 68.510 | 1.00 | 2.00 | 0 |
| ATOM | 3313 | CG2 | ILE | 551 | 51.490 | 16.914 | 67.292 | 1.00 | 2.00 | 0 |
| ATOM | 3314 | CG1 | ILE | 551 | 52.182 | 19.021 | 68.475 | 1.00 | 2.00 | 0 |

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|---|---|---|---|---|---|---|---|---|---|---|
| ATOM | 3315 | CD1 | ILE | 551 | 53.648 | 18.701 | 68.468 | 1.00 | 2.00 | 0 |
| ATOM | 3316 | C | ILE | 551 | 49.295 | 18.705 | 67.281 | 1.00 | 2.00 | 0 |
| ATOM | 3317 | O | ILE | 551 | 49.596 | 19.807 | 66.840 | 1.00 | 2.00 | 0 |
| ATOM | 3318 | N | LEU | 552 | 48.514 | 17.863 | 66.627 | 1.00 | 2.00 | 0 |
| ATOM | 3320 | CA | LEU | 552 | 47.896 | 18.202 | 65.369 | 1.00 | 2.00 | 0 |
| ATOM | 3321 | CB | LEU | 552 | 48.287 | 17.148 | 64.320 | 1.00 | 2.00 | 0 |
| ATOM | 3322 | CG | LEU | 552 | 47.809 | 17.215 | 62.867 | 1.00 | 2.00 | 0 |
| ATOM | 3323 | CD1 | LEU | 552 | 48.082 | 18.532 | 62.209 | 1.00 | 2.00 | 0 |
| ATOM | 3324 | CD2 | LEU | 552 | 48.544 | 16.174 | 62.131 | 1.00 | 2.00 | 0 |
| ATOM | 3325 | C | LEU | 552 | 46.397 | 18.180 | 65.728 | 1.00 | 2.00 | 0 |
| ATOM | 3326 | O | LEU | 552 | 45.753 | 17.124 | 65.734 | 1.00 | 2.00 | 0 |
| ATOM | 3327 | N | LEU | 553 | 45.881 | 19.352 | 66.100 | 1.00 | 20.15 | 0 |
| ATOM | 3329 | CA | LEU | 553 | 44.485 | 19.512 | 66.517 | 1.00 | 20.15 | 0 |
| ATOM | 3330 | CB | LEU | 553 | 44.240 | 20.926 | 67.055 | 1.00 | 2.00 | 0 |
| ATOM | 3331 | CG | LEU | 553 | 44.374 | 21.262 | 68.543 | 1.00 | 2.00 | 0 |
| ATOM | 3332 | CD1 | LEU | 553 | 45.224 | 20.282 | 69.290 | 1.00 | 2.00 | 0 |
| ATOM | 3333 | CD2 | LEU | 553 | 44.942 | 22.639 | 68.638 | 1.00 | 2.00 | 0 |
| ATOM | 3334 | C | LEU | 553 | 43.495 | 19.229 | 65.410 | 1.00 | 20.15 | 0 |
| ATOM | 3335 | O | LEU | 553 | 43.604 | 19.780 | 64.309 | 1.00 | 2.00 | 0 |
| ATOM | 3336 | N | GLU | 554 | 42.524 | 18.375 | 65.724 | 1.00 | 14.62 | 0 |
| ATOM | 3338 | CA | GLU | 554 | 41.476 | 17.983 | 64.786 | 1.00 | 13.80 | 0 |
| ATOM | 3339 | CB | GLU | 554 | 41.135 | 16.492 | 64.956 | 1.00 | 57.31 | 0 |
| ATOM | 3340 | CG | GLU | 554 | 42.326 | 15.550 | 65.177 | 1.00 | 69.83 | 0 |
| ATOM | 3341 | CD | GLU | 554 | 43.168 | 15.310 | 63.927 | 1.00 | 73.58 | 0 |
| ATOM | 3342 | OE1 | GLU | 554 | 42.918 | 15.957 | 62.887 | 1.00 | 82.45 | 0 |
| ATOM | 3343 | OE2 | GLU | 554 | 44.090 | 14.465 | 63.988 | 1.00 | 79.54 | 0 |
| ATOM | 3344 | C | GLU | 554 | 40.241 | 18.823 | 65.105 | 1.00 | 12.33 | 0 |
| ATOM | 3345 | O | GLU | 554 | 39.253 | 18.311 | 65.638 | 1.00 | 51.99 | 0 |
| ATOM | 3346 | N | LEU | 555 | 40.296 | 20.112 | 64.792 | 1.00 | 2.00 | 0 |
| ATOM | 3348 | CA | LEU | 555 | 39.176 | 21.007 | 65.077 | 1.00 | 2.00 | 0 |
| ATOM | 3349 | CB | LEU | 555 | 39.628 | 22.456 | 64.911 | 1.00 | 2.00 | 0 |
| ATOM | 3350 | CG | LEU | 555 | 40.660 | 22.840 | 65.972 | 1.00 | 2.00 | 0 |
| ATOM | 3351 | CD1 | LEU | 555 | 41.274 | 24.194 | 65.697 | 1.00 | 2.00 | 0 |
| ATOM | 3352 | CD2 | LEU | 555 | 39.959 | 22.839 | 67.294 | 1.00 | 2.00 | 0 |
| ATOM | 3353 | C | LEU | 555 | 37.932 | 20.734 | 64.237 | 1.00 | 2.00 | 0 |
| ATOM | 3354 | O | LEU | 555 | 37.862 | 19.731 | 63.537 | 1.00 | 2.00 | 0 |
| ATOM | 3355 | N | GLU | 556 | 36.933 | 21.603 | 64.345 | 1.00 | 2.00 | 0 |
| ATOM | 3357 | CA | GLU | 556 | 35.716 | 21.460 | 63.569 | 1.00 | 2.00 | 0 |
| ATOM | 3358 | CB | GLU | 556 | 35.028 | 20.115 | 63.846 | 1.00 | 32.90 | 0 |
| ATOM | 3359 | CG | GLU | 556 | 34.175 | 20.063 | 65.100 | 1.00 | 48.42 | 0 |
| ATOM | 3360 | CD | GLU | 556 | 32.935 | 19.176 | 64.941 | 1.00 | 58.49 | 0 |
| ATOM | 3361 | OE1 | GLU | 556 | 32.792 | 18.188 | 65.711 | 1.00 | 60.59 | 0 |
| ATOM | 3362 | OE2 | GLU | 556 | 32.101 | 19.477 | 64.047 | 1.00 | 59.64 | 0 |
| ATOM | 3363 | C | GLU | 556 | 34.736 | 22.583 | 63.826 | 1.00 | 2.00 | 0 |
| ATOM | 3364 | O | GLU | 556 | 35.067 | 23.580 | 64.446 | 1.00 | 16.83 | 0 |
| ATOM | 3365 | N | ALA | 557 | 33.544 | 22.423 | 63.257 | 1.00 | 2.00 | 0 |
| ATOM | 3367 | CA | ALA | 557 | 32.398 | 23.330 | 63.427 | 1.00 | 2.00 | 0 |
| ATOM | 3368 | CB | ALA | 557 | 31.747 | 23.013 | 64.788 | 1.00 | 47.62 | 0 |
| ATOM | 3369 | C | ALA | 557 | 32.701 | 24.826 | 63.286 | 1.00 | 2.00 | 0 |
| ATOM | 3370 | O | ALA | 557 | 33.711 | 25.191 | 62.671 | 1.00 | 40.85 | 0 |
| ATOM | 3371 | N | PRO | 558 | 31.811 | 25.711 | 63.802 | 1.00 | 2.00 | 0 |
| ATOM | 3372 | CD | PRO | 558 | 30.459 | 25.558 | 64.353 | 1.00 | 2.44 | 0 |
| ATOM | 3373 | CA | PRO | 558 | 32.123 | 27.139 | 63.658 | 1.00 | 2.00 | 0 |
| ATOM | 3374 | CB | PRO | 558 | 30.786 | 27.826 | 63.951 | 1.00 | 2.53 | 0 |
| ATOM | 3375 | CG | PRO | 558 | 29.798 | 26.759 | 63.843 | 1.00 | 2.44 | 0 |
| ATOM | 3376 | C | PRO | 558 | 33.190 | 27.648 | 64.627 | 1.00 | 2.00 | 0 |
| ATOM | 3377 | O | PRO | 558 | 32.975 | 27.616 | 65.844 | 1.00 | 7.53 | 0 |
| ATOM | 3378 | N | LEU | 559 | 34.325 | 28.119 | 64.112 | 1.00 | 2.00 | 0 |
| ATOM | 3380 | CA | LEU | 559 | 35.349 | 28.689 | 64.982 | 1.00 | 2.00 | 0 |
| ATOM | 3381 | CB | LEU | 559 | 36.568 | 27.769 | 65.148 | 1.00 | 2.00 | 0 |
| ATOM | 3382 | CG | LEU | 559 | 37.592 | 27.571 | 64.050 | 1.00 | 2.00 | 0 |
| ATOM | 3383 | CD1 | LEU | 559 | 38.620 | 26.563 | 64.476 | 1.00 | 2.00 | 0 |
| ATOM | 3384 | CD2 | LEU | 559 | 36.885 | 27.083 | 62.830 | 1.00 | 2.00 | 0 |
| ATOM | 3385 | C | LEU | 559 | 35.769 | 30.038 | 64.435 | 1.00 | 2.00 | 0 |
| ATOM | 3386 | O | LEU | 559 | 35.444 | 30.389 | 63.311 | 1.00 | 2.00 | 0 |
| ATOM | 3387 | N | LYS | 560 | 36.461 | 30.804 | 65.260 | 1.00 | 2.00 | 0 |
| ATOM | 3389 | CA | LYS | 560 | 36.932 | 32.115 | 64.889 | 1.00 | 2.00 | 0 |
| ATOM | 3390 | CB | LYS | 560 | 36.359 | 33.143 | 65.843 | 1.00 | 20.44 | 0 |

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|---|---|---|---|---|---|---|---|---|---|---|
| ATOM | 3391 | CG | LYS | 560 | 36.612 | 34.562 | 65.427 | 1.00 | 20.44 | 0 |
| ATOM | 3392 | CD | LYS | 560 | 35.574 | 35.512 | 66.018 | 1.00 | 20.44 | 0 |
| ATOM | 3393 | CE | LYS | 560 | 34.253 | 35.452 | 65.278 | 1.00 | 20.44 | 0 |
| ATOM | 3394 | NZ | LYS | 560 | 33.706 | 34.083 | 65.225 | 1.00 | 20.44 | 0 |
| ATOM | 3398 | C | LYS | 560 | 38.426 | 31.990 | 65.052 | 1.00 | 2.00 | 0 |
| ATOM | 3399 | O | LYS | 560 | 38.908 | 31.624 | 66.117 | 1.00 | 20.44 | 0 |
| ATOM | 3400 | N | ILE | 561 | 39.164 | 32.244 | 63.986 | 1.00 | 2.00 | 0 |
| ATOM | 3402 | CA | ILE | 561 | 40.606 | 32.106 | 64.017 | 1.00 | 2.00 | 0 |
| ATOM | 3403 | CB | ILE | 561 | 41.095 | 31.318 | 62.750 | 1.00 | 2.00 | 0 |
| ATOM | 3404 | CG2 | ILE | 561 | 42.566 | 30.913 | 62.891 | 1.00 | 2.00 | 0 |
| ATOM | 3405 | CG1 | ILE | 561 | 40.204 | 30.076 | 62.558 | 1.00 | 2.00 | 0 |
| ATOM | 3406 | CD1 | ILE | 561 | 40.806 | 28.940 | 61.761 | 1.00 | 2.00 | 0 |
| ATOM | 3407 | C | ILE | 561 | 41.247 | 33.488 | 64.102 | 1.00 | 2.00 | 0 |
| ATOM | 3408 | O | ILE | 561 | 40.703 | 34.450 | 63.543 | 1.00 | 2.00 | 0 |
| ATOM | 3409 | N | CYS | 562 | 42.365 | 33.586 | 64.833 | 1.00 | 2.00 | 0 |
| ATOM | 3411 | CA | CYS | 562 | 43.124 | 34.829 | 65.001 | 1.00 | 2.00 | 0 |
| ATOM | 3412 | CB | CYS | 562 | 42.793 | 35.464 | 66.339 | 1.00 | 13.31 | 0 |
| ATOM | 3413 | SG | CYS | 562 | 41.073 | 35.733 | 66.574 | 1.00 | 13.31 | 0 |
| ATOM | 3414 | C | CYS | 562 | 44.642 | 34.589 | 64.928 | 1.00 | 2.00 | 0 |
| ATOM | 3415 | O | CYS | 562 | 45.151 | 33.551 | 65.373 | 1.00 | 13.31 | 0 |
| ATOM | 3416 | N | GLY | 563 | 45.362 | 35.540 | 64.348 | 1.00 | 2.00 | 0 |
| ATOM | 3418 | CA | GLY | 563 | 46.805 | 35.424 | 64.252 | 1.00 | 2.00 | 0 |
| ATOM | 3419 | C | GLY | 563 | 47.546 | 36.260 | 65.291 | 1.00 | 2.00 | 0 |
| ATOM | 3420 | O | GLY | 563 | 46.997 | 36.556 | 66.351 | 1.00 | 5.66 | 0 |
| ATOM | 3421 | N | ASP | 564 | 48.780 | 36.649 | 64.958 | 1.00 | 2.00 | 0 |
| ATOM | 3423 | CA | ASP | 564 | 49.657 | 37.452 | 65.811 | 1.00 | 2.00 | 0 |
| ATOM | 3424 | CB | ASP | 564 | 50.705 | 38.191 | 64.964 | 1.00 | 2.00 | 0 |
| ATOM | 3425 | CG | ASP | 564 | 51.724 | 37.270 | 64.321 | 1.00 | 2.00 | 0 |
| ATOM | 3426 | OD1 | ASP | 564 | 51.390 | 36.585 | 63.334 | 1.00 | 2.00 | 0 |
| ATOM | 3427 | OD2 | ASP | 564 | 52.876 | 37.249 | 64.786 | 1.00 | 2.00 | 0 |
| ATOM | 3428 | C | ASP | 564 | 48.981 | 38.497 | 66.693 | 1.00 | 2.00 | 0 |
| ATOM | 3429 | O | ASP | 564 | 48.395 | 39.442 | 66.189 | 1.00 | 2.00 | 0 |
| ATOM | 3430 | N | ILE | 565 | 49.094 | 38.327 | 68.009 | 1.00 | 31.53 | 0 |
| ATOM | 3432 | CA | ILE | 565 | 48.537 | 39.294 | 68.953 | 1.00 | 35.54 | 0 |
| ATOM | 3433 | CB | ILE | 565 | 47.810 | 38.612 | 70.135 | 1.00 | 9.39 | 0 |
| ATOM | 3434 | CG2 | ILE | 565 | 47.139 | 39.664 | 70.996 | 1.00 | 9.39 | 0 |
| ATOM | 3435 | CG1 | ILE | 565 | 46.710 | 37.685 | 69.622 | 1.00 | 9.39 | 0 |
| ATOM | 3436 | CD1 | ILE | 565 | 45.611 | 38.424 | 68.906 | 1.00 | 9.39 | 0 |
| ATOM | 3437 | C | ILE | 565 | 49.681 | 40.168 | 69.489 | 1.00 | 32.16 | 0 |
| ATOM | 3438 | O | ILE | 565 | 49.491 | 41.356 | 69.756 | 1.00 | 9.39 | 0 |
| ATOM | 3439 | N | HIS | 566 | 50.859 | 39.560 | 69.637 | 1.00 | 14.33 | 0 |
| ATOM | 3441 | CA | HIS | 566 | 52.082 | 40.219 | 70.111 | 1.00 | 15.67 | 0 |
| ATOM | 3442 | C | HIS | 566 | 51.958 | 41.227 | 71.245 | 1.00 | 16.54 | 0 |
| ATOM | 3443 | O | HIS | 566 | 52.427 | 42.359 | 71.127 | 1.00 | 15.89 | 0 |
| ATOM | 3444 | CB | HIS | 566 | 52.811 | 40.882 | 68.943 | 1.00 | 9.53 | 0 |
| ATOM | 3445 | CG | HIS | 566 | 53.652 | 39.936 | 68.153 | 1.00 | 9.53 | 0 |
| ATOM | 3446 | ND1 | HIS | 566 | 54.829 | 39.391 | 68.605 | 1.00 | 9.53 | 0 |
| ATOM | 3448 | CD2 | HIS | 566 | 53.470 | 39.432 | 66.910 | 1.00 | 9.53 | 0 |
| ATOM | 3449 | NE2 | HIS | 566 | 54.525 | 38.582 | 66.589 | 1.00 | 9.53 | 0 |
| ATOM | 3450 | CE1 | HIS | 566 | 55.312 | 38.600 | 67.652 | 1.00 | 9.53 | 0 |
| ATOM | 3451 | N | GLY | 567 | 51.337 | 40.808 | 72.345 | 1.00 | 2.00 | 0 |
| ATOM | 3453 | CA | GLY | 567 | 51.170 | 41.686 | 73.490 | 1.00 | 2.00 | 0 |
| ATOM | 3454 | C | GLY | 567 | 50.249 | 42.894 | 73.375 | 1.00 | 2.00 | 0 |
| ATOM | 3455 | O | GLY | 567 | 50.269 | 43.764 | 74.254 | 1.00 | 3.59 | 0 |
| ATOM | 3456 | N | GLN | 568 | 49.455 | 42.973 | 72.314 | 1.00 | 36.66 | 0 |
| ATOM | 3458 | CA | GLN | 568 | 48.527 | 44.086 | 72.141 | 1.00 | 34.60 | 0 |
| ATOM | 3459 | CB | GLN | 568 | 48.164 | 44.236 | 70.667 | 1.00 | 2.50 | 0 |
| ATOM | 3460 | CG | GLN | 568 | 49.345 | 44.164 | 69.715 | 1.00 | 3.37 | 0 |
| ATOM | 3461 | CD | GLN | 568 | 49.768 | 45.507 | 69.144 | 1.00 | 3.10 | 0 |
| ATOM | 3462 | OE1 | GLN | 568 | 50.958 | 45.769 | 68.974 | 1.00 | 4.87 | 0 |
| ATOM | 3463 | NE2 | GLN | 568 | 48.800 | 46.349 | 68.813 | 1.00 | 18.91 | 0 |
| ATOM | 3466 | C | GLN | 568 | 47.280 | 43.730 | 72.950 | 1.00 | 34.26 | 0 |
| ATOM | 3467 | O | GLN | 568 | 46.253 | 43.365 | 72.380 | 1.00 | 7.33 | 0 |
| ATOM | 3468 | N | TYR | 569 | 47.363 | 43.864 | 74.272 | 1.00 | 2.00 | 0 |
| ATOM | 3470 | CA | TYR | 569 | 46.263 | 43.485 | 75.161 | 1.00 | 2.00 | 0 |
| ATOM | 3471 | CB | TYR | 569 | 46.664 | 43.687 | 76.626 | 1.00 | 26.93 | 0 |
| ATOM | 3472 | CG | TYR | 569 | 45.692 | 43.048 | 77.600 | 1.00 | 27.02 | 0 |
| ATOM | 3473 | CD1 | TYR | 569 | 45.401 | 41.684 | 77.526 | 1.00 | 22.43 | 0 |

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|---|---|---|---|---|---|---|---|---|---|---|
| ATOM | 3474 | CE1 | TYR | 569 | 44.496 | 41.097 | 78.393 | 1.00 | 24.12 | 0 |
| ATOM | 3475 | CD2 | TYR | 569 | 45.049 | 43.807 | 78.575 | 1.00 | 24.68 | 0 |
| ATOM | 3476 | CE2 | TYR | 569 | 44.139 | 43.223 | 79.449 | 1.00 | 24.01 | 0 |
| ATOM | 3477 | CZ | TYR | 569 | 43.866 | 41.869 | 79.352 | 1.00 | 28.35 | 0 |
| ATOM | 3478 | OH | TYR | 569 | 42.950 | 41.282 | 80.197 | 1.00 | 35.43 | 0 |
| ATOM | 3480 | C | TYR | 569 | 44.888 | 44.085 | 74.946 | 1.00 | 2.00 | 0 |
| ATOM | 3481 | O | TYR | 569 | 43.885 | 43.374 | 75.015 | 1.00 | 29.07 | 0 |
| ATOM | 3482 | N | TYR | 570 | 44.817 | 45.384 | 74.710 | 1.00 | 11.04 | 0 |
| ATOM | 3484 | CA | TYR | 570 | 43.515 | 45.999 | 74.510 | 1.00 | 14.25 | 0 |
| ATOM | 3485 | CB | TYR | 570 | 43.599 | 47.505 | 74.766 | 1.00 | 46.12 | 0 |
| ATOM | 3486 | CG | TYR | 570 | 43.577 | 47.792 | 76.261 | 1.00 | 51.43 | 0 |
| ATOM | 3487 | CD1 | TYR | 570 | 44.749 | 47.743 | 77.025 | 1.00 | 48.11 | 0 |
| ATOM | 3488 | CE1 | TYR | 570 | 44.715 | 47.952 | 78.398 | 1.00 | 52.04 | 0 |
| ATOM | 3489 | CD2 | TYR | 570 | 42.375 | 48.063 | 76.917 | 1.00 | 49.50 | 0 |
| ATOM | 3490 | CE2 | TYR | 570 | 42.340 | 48.272 | 78.277 | 1.00 | 51.48 | 0 |
| ATOM | 3491 | CZ | TYR | 570 | 43.507 | 48.215 | 79.010 | 1.00 | 53.24 | 0 |
| ATOM | 3492 | OH | TYR | 570 | 43.452 | 48.426 | 80.359 | 1.00 | 54.97 | 0 |
| ATOM | 3494 | C | TYR | 570 | 42.929 | 45.653 | 73.152 | 1.00 | 13.58 | 0 |
| ATOM | 3495 | O | TYR | 570 | 41.708 | 45.654 | 72.967 | 1.00 | 43.14 | 0 |
| ATOM | 3496 | N | ASP | 571 | 43.813 | 45.311 | 72.217 | 1.00 | 12.28 | 0 |
| ATOM | 3498 | CA | ASP | 571 | 43.402 | 44.903 | 70.891 | 1.00 | 11.58 | 0 |
| ATOM | 3499 | CB | ASP | 571 | 44.590 | 44.870 | 69.975 | 1.00 | 6.85 | 0 |
| ATOM | 3500 | CG | ASP | 571 | 45.128 | 46.237 | 69.733 | 1.00 | 12.88 | 0 |
| ATOM | 3501 | OD1 | ASP | 571 | 46.254 | 46.522 | 70.185 | 1.00 | 19.21 | 0 |
| ATOM | 3502 | OD2 | ASP | 571 | 44.402 | 47.044 | 69.110 | 1.00 | 16.01 | 0 |
| ATOM | 3503 | C | ASP | 571 | 42.818 | 43.539 | 71.062 | 1.00 | 14.93 | 0 |
| ATOM | 3504 | O | ASP | 571 | 41.775 | 43.247 | 70.507 | 1.00 | 19.59 | 0 |
| ATOM | 3505 | N | LEU | 572 | 43.487 | 42.707 | 71.853 | 1.00 | 2.00 | 0 |
| ATOM | 3507 | CA | LEU | 572 | 42.977 | 41.378 | 72.147 | 1.00 | 2.00 | 0 |
| ATOM | 3508 | CB | LEU | 572 | 43.909 | 40.641 | 73.110 | 1.00 | 2.00 | 0 |
| ATOM | 3509 | CG | LEU | 572 | 43.302 | 39.416 | 73.820 | 1.00 | 2.00 | 0 |
| ATOM | 3510 | CD1 | LEU | 572 | 43.061 | 38.267 | 72.832 | 1.00 | 2.00 | 0 |
| ATOM | 3511 | CD2 | LEU | 572 | 44.227 | 38.982 | 74.955 | 1.00 | 2.00 | 0 |
| ATOM | 3512 | C | LEU | 572 | 41.579 | 41.554 | 72.771 | 1.00 | 2.00 | 0 |
| ATOM | 3513 | O | LEU | 572 | 40.678 | 40.758 | 72.512 | 1.00 | 2.00 | 0 |
| ATOM | 3514 | N | LEU | 573 | 41.395 | 42.604 | 73.572 | 1.00 | 9.95 | 0 |
| ATOM | 3516 | CA | LEU | 573 | 40.092 | 42.874 | 74.195 | 1.00 | 6.25 | 0 |
| ATOM | 3517 | CB | LEU | 573 | 40.224 | 43.910 | 75.317 | 1.00 | 2.00 | 0 |
| ATOM | 3518 | CG | LEU | 573 | 40.807 | 43.360 | 76.625 | 1.00 | 2.00 | 0 |
| ATOM | 3519 | CD1 | LEU | 573 | 40.667 | 44.416 | 77.717 | 1.00 | 2.00 | 0 |
| ATOM | 3520 | CD2 | LEU | 573 | 40.079 | 42.053 | 77.033 | 1.00 | 2.00 | 0 |
| ATOM | 3521 | C | LEU | 573 | 39.055 | 43.344 | 73.170 | 1.00 | 4.08 | 0 |
| ATOM | 3522 | O | LEU | 573 | 37.865 | 42.974 | 73.260 | 1.00 | 2.00 | 0 |
| ATOM | 3523 | N | ARG | 574 | 39.518 | 44.153 | 72.203 | 1.00 | 13.12 | 0 |
| ATOM | 3525 | CA | ARG | 574 | 38.682 | 44.665 | 71.115 | 1.00 | 12.30 | 0 |
| ATOM | 3526 | CB | ARG | 574 | 39.491 | 45.598 | 70.212 | 1.00 | 30.04 | 0 |
| ATOM | 3527 | CG | ARG | 574 | 39.704 | 46.994 | 70.757 | 1.00 | 31.00 | 0 |
| ATOM | 3528 | CD | ARG | 574 | 40.697 | 47.811 | 69.915 | 1.00 | 35.07 | 0 |
| ATOM | 3529 | NE | ARG | 574 | 40.294 | 47.989 | 68.514 | 1.00 | 36.10 | 0 |
| ATOM | 3531 | CZ | ARG | 574 | 41.018 | 48.625 | 67.587 | 1.00 | 36.14 | 0 |
| ATOM | 3532 | NH1 | ARG | 574 | 42.198 | 49.162 | 67.890 | 1.00 | 35.84 | 0 |
| ATOM | 3535 | NH2 | ARG | 574 | 40.565 | 48.713 | 66.341 | 1.00 | 40.46 | 0 |
| ATOM | 3538 | C | ARG | 574 | 38.265 | 43.440 | 70.324 | 1.00 | 10.99 | 0 |
| ATOM | 3539 | O | ARG | 574 | 37.092 | 43.253 | 70.004 | 1.00 | 30.16 | 0 |
| ATOM | 3540 | N | LEU | 575 | 39.260 | 42.591 | 70.066 | 1.00 | 2.00 | 0 |
| ATOM | 3542 | CA | LEU | 575 | 39.156 | 41.339 | 69.323 | 1.00 | 2.00 | 0 |
| ATOM | 3543 | CB | LEU | 575 | 40.471 | 40.578 | 69.502 | 1.00 | 18.14 | 0 |
| ATOM | 3544 | CG | LEU | 575 | 41.058 | 39.569 | 68.514 | 1.00 | 18.14 | 0 |
| ATOM | 3545 | CD1 | LEU | 575 | 40.112 | 38.378 | 68.370 | 1.00 | 18.14 | 0 |
| ATOM | 3546 | CD2 | LEU | 575 | 41.355 | 40.249 | 67.176 | 1.00 | 18.14 | 0 |
| ATOM | 3547 | C | LEU | 575 | 37.970 | 40.494 | 69.801 | 1.00 | 2.00 | 0 |
| ATOM | 3548 | O | LEU | 575 | 37.121 | 40.081 | 69.001 | 1.00 | 18.14 | 0 |
| ATOM | 3549 | N | PHE | 576 | 37.908 | 40.247 | 71.103 | 1.00 | 29.25 | 0 |
| ATOM | 3551 | CA | PHE | 576 | 36.823 | 39.459 | 71.664 | 1.00 | 32.60 | 0 |
| ATOM | 3552 | CB | PHE | 576 | 37.115 | 39.098 | 73.119 | 1.00 | 2.00 | 0 |
| ATOM | 3553 | CG | PHE | 576 | 38.116 | 38.001 | 73.270 | 1.00 | 2.00 | 0 |
| ATOM | 3554 | CD1 | PHE | 576 | 39.158 | 38.111 | 74.184 | 1.00 | 2.00 | 0 |
| ATOM | 3555 | CD2 | PHE | 576 | 38.022 | 36.855 | 72.491 | 1.00 | 2.00 | 0 |

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|---|---|---|---|---|---|---|---|---|---|---|
| ATOM | 3556 | CE1 | PHE | 576 | 40.097 | 37.098 | 74.324 | 1.00 | 2.00 | 0 |
| ATOM | 3557 | CE2 | PHE | 576 | 38.960 | 35.828 | 72.621 | 1.00 | 2.00 | 0 |
| ATOM | 3558 | CZ | PHE | 576 | 40.000 | 35.953 | 73.540 | 1.00 | 2.00 | 0 |
| ATOM | 3559 | C | PHE | 576 | 35.479 | 40.164 | 71.573 | 1.00 | 29.95 | 0 |
| ATOM | 3560 | O | PHE | 576 | 34.433 | 39.517 | 71.648 | 1.00 | 2.00 | 0 |
| ATOM | 3561 | N | GLU | 577 | 35.504 | 41.484 | 71.421 | 1.00 | 21.04 | 0 |
| ATOM | 3563 | CA | GLU | 577 | 34.273 | 42.259 | 71.307 | 1.00 | 23.58 | 0 |
| ATOM | 3564 | CB | GLU | 577 | 34.561 | 43.731 | 71.566 | 1.00 | 40.21 | 0 |
| ATOM | 3565 | CG | GLU | 577 | 35.032 | 44.001 | 72.971 | 1.00 | 50.88 | 0 |
| ATOM | 3566 | CD | GLU | 577 | 35.688 | 45.347 | 73.113 | 1.00 | 55.67 | 0 |
| ATOM | 3567 | OE1 | GLU | 577 | 36.439 | 45.522 | 74.099 | 1.00 | 60.01 | 0 |
| ATOM | 3568 | OE2 | GLU | 577 | 35.461 | 46.224 | 72.245 | 1.00 | 63.14 | 0 |
| ATOM | 3569 | C | GLU | 577 | 33.654 | 42.091 | 69.928 | 1.00 | 25.67 | 0 |
| ATOM | 3570 | O | GLU | 577 | 32.435 | 42.156 | 69.772 | 1.00 | 44.83 | 0 |
| ATOM | 3571 | N | TYR | 578 | 34.509 | 41.901 | 68.928 | 1.00 | 51.92 | 0 |
| ATOM | 3573 | CA | TYR | 578 | 34.052 | 41.700 | 67.561 | 1.00 | 48.79 | 0 |
| ATOM | 3574 | CB | TYR | 578 | 35.208 | 41.834 | 66.564 | 1.00 | 35.56 | 0 |
| ATOM | 3575 | CG | TYR | 578 | 35.703 | 43.245 | 66.356 | 1.00 | 40.25 | 0 |
| ATOM | 3576 | CD1 | TYR | 578 | 35.598 | 43.865 | 65.111 | 1.00 | 40.27 | 0 |
| ATOM | 3577 | CE1 | TYR | 578 | 36.062 | 45.168 | 64.917 | 1.00 | 44.74 | 0 |
| ATOM | 3578 | CD2 | TYR | 578 | 36.281 | 43.960 | 67.399 | 1.00 | 45.71 | 0 |
| ATOM | 3579 | CE2 | TYR | 578 | 36.747 | 45.258 | 67.217 | 1.00 | 42.53 | 0 |
| ATOM | 3580 | CZ | TYR | 578 | 36.636 | 45.853 | 65.979 | 1.00 | 49.98 | 0 |
| ATOM | 3581 | OH | TYR | 578 | 37.106 | 47.131 | 65.812 | 1.00 | 54.82 | 0 |
| ATOM | 3583 | C | TYR | 578 | 33.467 | 40.303 | 67.458 | 1.00 | 49.18 | 0 |
| ATOM | 3584 | O | TYR | 578 | 32.316 | 40.124 | 67.081 | 1.00 | 35.27 | 0 |
| ATOM | 3585 | N | GLY | 579 | 34.271 | 39.307 | 67.797 | 1.00 | 2.60 | 0 |
| ATOM | 3587 | CA | GLY | 579 | 33.787 | 37.949 | 67.713 | 1.00 | 6.22 | 0 |
| ATOM | 3588 | C | GLY | 579 | 32.737 | 37.628 | 68.755 | 1.00 | 8.52 | 0 |
| ATOM | 3589 | O | GLY | 579 | 31.555 | 37.446 | 68.437 | 1.00 | 39.88 | 0 |
| ATOM | 3590 | N | GLY | 580 | 33.194 | 37.557 | 70.006 | 1.00 | 2.00 | 0 |
| ATOM | 3592 | CA | GLY | 580 | 32.342 | 37.236 | 71.140 | 1.00 | 2.00 | 0 |
| ATOM | 3593 | C | GLY | 580 | 33.191 | 36.491 | 72.151 | 1.00 | 2.00 | 0 |
| ATOM | 3594 | O | GLY | 580 | 33.725 | 35.415 | 71.853 | 1.00 | 44.94 | 0 |
| ATOM | 3595 | N | PHE | 581 | 33.307 | 37.067 | 73.348 | 1.00 | 15.06 | 0 |
| ATOM | 3597 | CA | PHE | 581 | 34.116 | 36.500 | 74.432 | 1.00 | 12.63 | 0 |
| ATOM | 3598 | CB | PHE | 581 | 33.857 | 37.263 | 75.744 | 1.00 | 2.00 | 0 |
| ATOM | 3599 | CG | PHE | 581 | 34.679 | 38.542 | 75.885 | 1.00 | 2.00 | 0 |
| ATOM | 3600 | CD1 | PHE | 581 | 34.136 | 39.783 | 75.557 | 1.00 | 2.00 | 0 |
| ATOM | 3601 | CD2 | PHE | 581 | 35.999 | 38.495 | 76.346 | 1.00 | 2.00 | 0 |
| ATOM | 3602 | CE1 | PHE | 581 | 34.894 | 40.941 | 75.687 | 1.00 | 2.00 | 0 |
| ATOM | 3603 | CE2 | PHE | 581 | 36.757 | 39.659 | 76.475 | 1.00 | 2.00 | 0 |
| ATOM | 3604 | CZ | PHE | 581 | 36.204 | 40.875 | 76.146 | 1.00 | 2.00 | 0 |
| ATOM | 3605 | C | PHE | 581 | 33.913 | 34.999 | 74.611 | 1.00 | 12.63 | 0 |
| ATOM | 3606 | O | PHE | 581 | 32.782 | 34.521 | 74.647 | 1.00 | 2.00 | 0 |
| ATOM | 3607 | N | PRO | 582 | 35.021 | 34.243 | 74.737 | 1.00 | 21.81 | 0 |
| ATOM | 3608 | CD | PRO | 582 | 36.360 | 34.852 | 74.820 | 1.00 | 85.20 | 0 |
| ATOM | 3609 | CA | PRO | 582 | 35.141 | 32.795 | 74.910 | 1.00 | 24.62 | 0 |
| ATOM | 3610 | CB | PRO | 582 | 36.398 | 32.675 | 75.737 | 1.00 | 86.40 | 0 |
| ATOM | 3611 | CG | PRO | 582 | 37.266 | 33.636 | 75.008 | 1.00 | 87.84 | 0 |
| ATOM | 3612 | C | PRO | 582 | 33.966 | 31.958 | 75.425 | 1.00 | 28.53 | 0 |
| ATOM | 3613 | O | PRO | 582 | 33.816 | 30.796 | 75.012 | 1.00 | 0.58 | 0 |
| ATOM | 3614 | N | PRO | 583 | 33.160 | 32.466 | 76.374 | 1.00 | 13.00 | 0 |
| ATOM | 3615 | CD | PRO | 583 | 33.090 | 33.632 | 77.269 | 1.00 | 51.24 | 0 |
| ATOM | 3616 | CA | PRO | 583 | 32.099 | 31.500 | 76.681 | 1.00 | 13.55 | 0 |
| ATOM | 3617 | CB | PRO | 583 | 31.281 | 32.215 | 77.759 | 1.00 | 53.59 | 0 |
| ATOM | 3618 | CG | PRO | 583 | 31.616 | 33.699 | 77.550 | 1.00 | 50.46 | 0 |
| ATOM | 3619 | C | PRO | 583 | 31.296 | 31.283 | 75.389 | 1.00 | 14.03 | 0 |
| ATOM | 3620 | O | PRO | 583 | 30.950 | 30.152 | 75.043 | 1.00 | 48.29 | 0 |
| ATOM | 3621 | N | GLU | 584 | 31.089 | 32.383 | 74.663 | 1.00 | 35.81 | 0 |
| ATOM | 3623 | CA | GLU | 584 | 30.333 | 32.439 | 73.412 | 1.00 | 39.44 | 0 |
| ATOM | 3624 | CB | GLU | 584 | 30.122 | 33.913 | 73.043 | 1.00 | 78.69 | 0 |
| ATOM | 3625 | CG | GLU | 584 | 28.955 | 34.213 | 72.117 | 1.00 | 90.10 | 0 |
| ATOM | 3626 | CD | GLU | 584 | 28.662 | 35.712 | 72.022 | 1.00 | 95.41 | 0 |
| ATOM | 3627 | OE1 | GLU | 584 | 28.313 | 36.190 | 70.918 | 1.00 | 90.41 | 0 |
| ATOM | 3628 | OE2 | GLU | 584 | 28.782 | 36.418 | 73.053 | 1.00 | 95.81 | 0 |
| ATOM | 3629 | C | GLU | 584 | 30.975 | 31.676 | 72.244 | 1.00 | 36.17 | 0 |
| ATOM | 3630 | O | GLU | 584 | 30.780 | 30.466 | 72.106 | 1.00 | 78.35 | 0 |

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|---|---|---|---|---|---|---|---|---|---|---|
| ATOM | 3631 | N | SER | 585 | 31.737 | 32.381 | 71.406 | 1.00 | 12.28 | 0 |
| ATOM | 3633 | CA | SER | 585 | 32.394 | 31.779 | 70.245 | 1.00 | 8.77 | 0 |
| ATOM | 3634 | CB | SER | 585 | 32.720 | 32.857 | 69.209 | 1.00 | 31.98 | 0 |
| ATOM | 3635 | OG | SER | 585 | 31.558 | 33.556 | 68.809 | 1.00 | 27.38 | 0 |
| ATOM | 3637 | C | SER | 585 | 33.669 | 30.995 | 70.539 | 1.00 | 9.84 | 0 |
| ATOM | 3638 | O | SER | 585 | 34.382 | 31.258 | 71.502 | 1.00 | 35.35 | 0 |
| ATOM | 3639 | N | ASN | 586 | 33.947 | 30.037 | 69.664 | 1.00 | 2.00 | 0 |
| ATOM | 3641 | CA | ASN | 586 | 35.136 | 29.197 | 69.749 | 1.00 | 2.00 | 0 |
| ATOM | 3642 | CB | ASN | 586 | 34.909 | 27.854 | 69.068 | 1.00 | 2.87 | 0 |
| ATOM | 3643 | CG | ASN | 586 | 33.728 | 27.107 | 69.625 | 1.00 | 10.37 | 0 |
| ATOM | 3644 | OD1 | ASN | 586 | 33.497 | 25.960 | 69.265 | 1.00 | 11.13 | 0 |
| ATOM | 3645 | ND2 | ASN | 586 | 32.967 | 27.745 | 70.506 | 1.00 | 4.44 | 0 |
| ATOM | 3648 | C | ASN | 586 | 36.251 | 29.937 | 69.029 | 1.00 | 2.00 | 0 |
| ATOM | 3649 | O | ASN | 586 | 36.017 | 30.574 | 68.007 | 1.00 | 2.87 | 0 |
| ATOM | 3650 | N | TYR | 587 | 37.458 | 29.858 | 69.564 | 1.00 | 13.99 | 0 |
| ATOM | 3652 | CA | TYR | 587 | 38.571 | 30.554 | 68.966 | 1.00 | 13.99 | 0 |
| ATOM | 3653 | CB | TYR | 587 | 39.049 | 31.706 | 69.876 | 1.00 | 2.00 | 0 |
| ATOM | 3654 | CG | TYR | 587 | 38.177 | 32.946 | 69.873 | 1.00 | 2.00 | 0 |
| ATOM | 3655 | CD1 | TYR | 587 | 36.998 | 33.004 | 70.638 | 1.00 | 2.00 | 0 |
| ATOM | 3656 | CE1 | TYR | 587 | 36.177 | 34.138 | 70.624 | 1.00 | 2.00 | 0 |
| ATOM | 3657 | CD2 | TYR | 587 | 38.519 | 34.061 | 69.088 | 1.00 | 2.00 | 0 |
| ATOM | 3658 | CE2 | TYR | 587 | 37.701 | 35.205 | 69.065 | 1.00 | 2.00 | 0 |
| ATOM | 3659 | CZ | TYR | 587 | 36.532 | 35.231 | 69.840 | 1.00 | 2.00 | 0 |
| ATOM | 3660 | OH | TYR | 587 | 35.743 | 36.352 | 69.838 | 1.00 | 2.00 | 0 |
| ATOM | 3662 | C | TYR | 587 | 39.721 | 29.608 | 68.745 | 1.00 | 13.99 | 0 |
| ATOM | 3663 | O | TYR | 587 | 39.812 | 28.562 | 69.392 | 1.00 | 2.00 | 0 |
| ATOM | 3664 | N | LEU | 588 | 40.584 | 29.987 | 67.809 | 1.00 | 2.00 | 0 |
| ATOM | 3666 | CA | LEU | 588 | 41.803 | 29.261 | 67.493 | 1.00 | 2.00 | 0 |
| ATOM | 3667 | CB | LEU | 588 | 41.681 | 28.482 | 66.195 | 1.00 | 10.69 | 0 |
| ATOM | 3668 | CG | LEU | 588 | 43.032 | 27.907 | 65.781 | 1.00 | 10.69 | 0 |
| ATOM | 3669 | CD1 | LEU | 588 | 43.568 | 27.073 | 66.912 | 1.00 | 10.69 | 0 |
| ATOM | 3670 | CD2 | LEU | 588 | 42.912 | 27.079 | 64.533 | 1.00 | 10.69 | 0 |
| ATOM | 3671 | C | LEU | 588 | 42.809 | 30.375 | 67.301 | 1.00 | 2.00 | 0 |
| ATOM | 3672 | O | LEU | 588 | 42.547 | 31.301 | 66.532 | 1.00 | 10.69 | 0 |
| ATOM | 3673 | N | PHE | 589 | 43.924 | 30.333 | 68.026 | 1.00 | 2.00 | 0 |
| ATOM | 3675 | CA | PHE | 589 | 44.938 | 31.363 | 67.865 | 1.00 | 2.00 | 0 |
| ATOM | 3676 | CB | PHE | 589 | 45.289 | 32.013 | 69.200 | 1.00 | 2.00 | 0 |
| ATOM | 3677 | CG | PHE | 589 | 44.279 | 33.026 | 69.652 | 1.00 | 2.00 | 0 |
| ATOM | 3678 | CD1 | PHE | 589 | 43.136 | 32.633 | 70.326 | 1.00 | 2.00 | 0 |
| ATOM | 3679 | CD2 | PHE | 589 | 44.471 | 34.376 | 69.391 | 1.00 | 2.00 | 0 |
| ATOM | 3680 | CE1 | PHE | 589 | 42.203 | 33.567 | 70.732 | 1.00 | 2.00 | 0 |
| ATOM | 3681 | CE2 | PHE | 589 | 43.542 | 35.321 | 69.793 | 1.00 | 2.00 | 0 |
| ATOM | 3682 | CZ | PHE | 589 | 42.408 | 34.918 | 70.463 | 1.00 | 2.00 | 0 |
| ATOM | 3683 | C | PHE | 589 | 46.140 | 30.717 | 67.219 | 1.00 | 2.00 | 0 |
| ATOM | 3684 | O | PHE | 589 | 46.532 | 29.610 | 67.602 | 1.00 | 2.00 | 0 |
| ATOM | 3685 | N | LEU | 590 | 46.715 | 31.411 | 66.235 | 1.00 | 2.00 | 0 |
| ATOM | 3687 | CA | LEU | 590 | 47.845 | 30.892 | 65.459 | 1.00 | 2.00 | 0 |
| ATOM | 3688 | CB | LEU | 590 | 47.650 | 31.303 | 63.988 | 1.00 | 9.73 | 0 |
| ATOM | 3689 | CG | LEU | 590 | 46.273 | 31.022 | 63.356 | 1.00 | 9.73 | 0 |
| ATOM | 3690 | CD1 | LEU | 590 | 46.162 | 31.702 | 62.014 | 1.00 | 9.73 | 0 |
| ATOM | 3691 | CD2 | LEU | 590 | 46.056 | 29.529 | 63.211 | 1.00 | 9.73 | 0 |
| ATOM | 3692 | C | LEU | 590 | 49.277 | 31.221 | 65.947 | 1.00 | 2.00 | 0 |
| ATOM | 3693 | O | LEU | 590 | 50.263 | 30.856 | 65.296 | 1.00 | 9.73 | 0 |
| ATOM | 3694 | N | GLY | 591 | 49.389 | 31.929 | 67.071 | 1.00 | 2.00 | 0 |
| ATOM | 3696 | CA | GLY | 591 | 50.703 | 32.223 | 67.626 | 1.00 | 2.00 | 0 |
| ATOM | 3697 | C | GLY | 591 | 51.132 | 33.648 | 67.923 | 1.00 | 2.00 | 0 |
| ATOM | 3698 | O | GLY | 591 | 50.369 | 34.620 | 67.769 | 1.00 | 2.00 | 0 |
| ATOM | 3699 | N | ASP | 592 | 52.387 | 33.741 | 68.358 | 1.00 | 2.00 | 0 |
| ATOM | 3701 | CA | ASP | 592 | 53.033 | 35.000 | 68.707 | 1.00 | 2.00 | 0 |
| ATOM | 3702 | CB | ASP | 592 | 53.424 | 35.746 | 67.448 | 1.00 | 6.15 | 0 |
| ATOM | 3703 | CG | ASP | 592 | 54.521 | 35.051 | 66.686 | 1.00 | 16.84 | 0 |
| ATOM | 3704 | OD1 | ASP | 592 | 54.955 | 35.606 | 65.657 | 1.00 | 11.71 | 0 |
| ATOM | 3705 | OD2 | ASP | 592 | 54.943 | 33.949 | 67.114 | 1.00 | 18.80 | 0 |
| ATOM | 3706 | C | ASP | 592 | 52.194 | 35.887 | 69.598 | 1.00 | 2.00 | 0 |
| ATOM | 3707 | O | ASP | 592 | 51.813 | 36.995 | 69.211 | 1.00 | 6.68 | 0 |
| ATOM | 3708 | N | TYR | 593 | 51.927 | 35.370 | 70.800 | 1.00 | 12.61 | 0 |
| ATOM | 3710 | CA | TYR | 593 | 51.127 | 36.036 | 71.822 | 1.00 | 12.61 | 0 |
| ATOM | 3711 | CB | TYR | 593 | 50.602 | 35.017 | 72.827 | 1.00 | 2.00 | 0 |

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|---|---|---|---|---|---|---|---|---|---|---|
| ATOM | 3712 | CG | TYR | 593 | 49.994 | 33.790 | 72.200 | 1.00 | 2.00 | 0 |
| ATOM | 3713 | CD1 | TYR | 593 | 50.558 | 32.532 | 72.382 | 1.00 | 2.00 | 0 |
| ATOM | 3714 | CE1 | TYR | 593 | 49.995 | 31.401 | 71.793 | 1.00 | 2.00 | 0 |
| ATOM | 3715 | CD2 | TYR | 593 | 48.852 | 33.886 | 71.413 | 1.00 | 2.00 | 0 |
| ATOM | 3716 | CE2 | TYR | 593 | 48.284 | 32.772 | 70.822 | 1.00 | 2.00 | 0 |
| ATOM | 3717 | CZ | TYR | 593 | 48.856 | 31.540 | 71.013 | 1.00 | 2.00 | 0 |
| ATOM | 3718 | OH | TYR | 593 | 48.267 | 30.459 | 70.412 | 1.00 | 2.00 | 0 |
| ATOM | 3720 | C | TYR | 593 | 51.995 | 37.019 | 72.560 | 1.00 | 12.61 | 0 |
| ATOM | 3721 | O | TYR | 593 | 51.526 | 38.079 | 72.981 | 1.00 | 2.00 | 0 |
| ATOM | 3722 | N | VAL | 594 | 53.270 | 36.660 | 72.692 | 1.00 | 2.00 | 0 |
| ATOM | 3724 | CA | VAL | 594 | 54.238 | 37.463 | 73.420 | 1.00 | 2.00 | 0 |
| ATOM | 3725 | CB | VAL | 594 | 54.913 | 36.599 | 74.501 | 1.00 | 30.06 | 0 |
| ATOM | 3726 | CG1 | VAL | 594 | 53.855 | 35.785 | 75.241 | 1.00 | 30.06 | 0 |
| ATOM | 3727 | CG2 | VAL | 594 | 55.950 | 35.684 | 73.875 | 1.00 | 30.06 | 0 |
| ATOM | 3728 | C | VAL | 594 | 55.309 | 38.154 | 72.563 | 1.00 | 2.00 | 0 |
| ATOM | 3729 | O | VAL | 594 | 55.408 | 37.919 | 71.356 | 1.00 | 30.06 | 0 |
| ATOM | 3730 | N | ASP | 595 | 56.112 | 38.991 | 73.218 | 1.00 | 2.00 | 0 |
| ATOM | 3732 | CA | ASP | 595 | 57.184 | 39.776 | 72.601 | 1.00 | 2.00 | 0 |
| ATOM | 3733 | CB | ASP | 595 | 58.073 | 38.903 | 71.705 | 1.00 | 33.25 | 0 |
| ATOM | 3734 | CG | ASP | 595 | 58.911 | 37.890 | 72.502 | 1.00 | 42.03 | 0 |
| ATOM | 3735 | OD1 | ASP | 595 | 59.240 | 38.147 | 73.679 | 1.00 | 40.72 | 0 |
| ATOM | 3736 | OD2 | ASP | 595 | 59.256 | 36.831 | 71.941 | 1.00 | 46.45 | 0 |
| ATOM | 3737 | C | ASP | 595 | 56.547 | 40.920 | 71.818 | 1.00 | 2.00 | 0 |
| ATOM | 3738 | O | ASP | 595 | 55.335 | 40.901 | 71.575 | 1.00 | 29.29 | 0 |
| ATOM | 3739 | N | ARG | 596 | 57.342 | 41.927 | 71.460 | 1.00 | 2.00 | 0 |
| ATOM | 3741 | CA | ARG | 596 | 56.843 | 43.096 | 70.716 | 1.00 | 2.00 | 0 |
| ATOM | 3742 | CB | ARG | 596 | 56.146 | 42.658 | 69.416 | 1.00 | 7.10 | 0 |
| ATOM | 3743 | CG | ARG | 596 | 57.043 | 41.863 | 68.457 | 1.00 | 13.06 | 0 |
| ATOM | 3744 | CD | ARG | 596 | 58.035 | 42.755 | 67.729 | 1.00 | 17.94 | 0 |
| ATOM | 3745 | NE | ARG | 596 | 59.293 | 42.081 | 67.407 | 1.00 | 25.56 | 0 |
| ATOM | 3747 | CZ | ARG | 596 | 59.402 | 40.954 | 66.709 | 1.00 | 35.06 | 0 |
| ATOM | 3748 | NH1 | ARG | 596 | 58.325 | 40.338 | 66.236 | 1.00 | 31.67 | 0 |
| ATOM | 3751 | NH2 | ARG | 596 | 60.604 | 40.438 | 66.486 | 1.00 | 31.81 | 0 |
| ATOM | 3754 | C | ARG | 596 | 55.898 | 43.996 | 71.547 | 1.00 | 2.00 | 0 |
| ATOM | 3755 | O | ARG | 596 | 56.269 | 45.112 | 71.922 | 1.00 | 7.10 | 0 |
| ATOM | 3756 | N | GLY | 597 | 54.692 | 43.521 | 71.847 | 1.00 | 32.20 | 0 |
| ATOM | 3758 | CA | GLY | 597 | 53.763 | 44.323 | 72.632 | 1.00 | 30.86 | 0 |
| ATOM | 3759 | C | GLY | 597 | 54.199 | 44.603 | 74.062 | 1.00 | 35.68 | 0 |
| ATOM | 3760 | O | GLY | 597 | 55.120 | 43.976 | 74.570 | 1.00 | 2.00 | 0 |
| ATOM | 3761 | N | LYS | 598 | 53.520 | 45.539 | 74.720 | 1.00 | 20.71 | 0 |
| ATOM | 3763 | CA | LYS | 598 | 53.845 | 45.911 | 76.097 | 1.00 | 17.90 | 0 |
| ATOM | 3764 | CB | LYS | 598 | 53.686 | 47.427 | 76.271 | 1.00 | 54.79 | 0 |
| ATOM | 3765 | CG | LYS | 598 | 54.813 | 48.259 | 75.655 | 1.00 | 53.06 | 0 |
| ATOM | 3766 | CD | LYS | 598 | 56.159 | 48.031 | 76.359 | 1.00 | 56.27 | 0 |
| ATOM | 3767 | CE | LYS | 598 | 56.120 | 48.441 | 77.838 | 1.00 | 53.59 | 0 |
| ATOM | 3768 | NZ | LYS | 598 | 57.407 | 48.186 | 78.548 | 1.00 | 56.50 | 0 |
| ATOM | 3772 | C | LYS | 598 | 53.064 | 45.179 | 77.210 | 1.00 | 18.19 | 0 |
| ATOM | 3773 | O | LYS | 598 | 53.384 | 45.314 | 78.395 | 1.00 | 55.50 | 0 |
| ATOM | 3774 | N | GLN | 599 | 52.053 | 44.400 | 76.832 | 1.00 | 2.00 | 0 |
| ATOM | 3776 | CA | GLN | 599 | 51.244 | 43.666 | 77.795 | 1.00 | 2.00 | 0 |
| ATOM | 3777 | CB | GLN | 599 | 49.820 | 44.244 | 77.839 | 1.00 | 24.44 | 0 |
| ATOM | 3778 | CG | GLN | 599 | 49.780 | 45.701 | 78.304 | 1.00 | 31.08 | 0 |
| ATOM | 3779 | CD | GLN | 599 | 48.398 | 46.169 | 78.728 | 1.00 | 27.33 | 0 |
| ATOM | 3780 | OE1 | GLN | 599 | 47.537 | 46.449 | 77.895 | 1.00 | 26.31 | 0 |
| ATOM | 3781 | NE2 | GLN | 599 | 48.188 | 46.277 | 80.029 | 1.00 | 27.77 | 0 |
| ATOM | 3784 | C | GLN | 599 | 51.215 | 42.163 | 77.514 | 1.00 | 2.00 | 0 |
| ATOM | 3785 | O | GLN | 599 | 50.183 | 41.515 | 77.626 | 1.00 | 24.92 | 0 |
| ATOM | 3786 | N | SER | 600 | 52.371 | 41.602 | 77.198 | 1.00 | 2.00 | 0 |
| ATOM | 3788 | CA | SER | 600 | 52.445 | 40.180 | 76.921 | 1.00 | 2.00 | 0 |
| ATOM | 3789 | CB | SER | 600 | 53.875 | 39.781 | 76.547 | 1.00 | 2.00 | 0 |
| ATOM | 3790 | OG | SER | 600 | 54.381 | 40.577 | 75.480 | 1.00 | 2.00 | 0 |
| ATOM | 3792 | C | SER | 600 | 51.968 | 39.304 | 78.078 | 1.00 | 2.00 | 0 |
| ATOM | 3793 | O | SER | 600 | 51.589 | 38.153 | 77.856 | 1.00 | 2.00 | 0 |
| ATOM | 3794 | N | LEU | 601 | 51.990 | 39.830 | 79.306 | 1.00 | 2.00 | 0 |
| ATOM | 3796 | CA | LEU | 601 | 51.566 | 39.055 | 80.486 | 1.00 | 2.00 | 0 |
| ATOM | 3797 | CB | LEU | 601 | 52.120 | 39.628 | 81.801 | 1.00 | 2.00 | 0 |
| ATOM | 3798 | CG | LEU | 601 | 53.573 | 39.753 | 82.260 | 1.00 | 2.00 | 0 |
| ATOM | 3799 | CD1 | LEU | 601 | 54.290 | 38.405 | 82.228 | 1.00 | 2.00 | 0 |

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|---|---|---|---|---|---|---|---|---|---|---|
| ATOM | 3800 | CD2 | LEU | 601 | 54.244 | 40.799 | 81.399 | 1.00 | 2.00 | 0 |
| ATOM | 3801 | C | LEU | 601 | 50.058 | 39.002 | 80.635 | 1.00 | 2.00 | 0 |
| ATOM | 3802 | O | LEU | 601 | 49.498 | 37.949 | 80.921 | 1.00 | 4.13 | 0 |
| ATOM | 3803 | N | GLU | 602 | 49.412 | 40.154 | 80.490 | 1.00 | 2.00 | 0 |
| ATOM | 3805 | CA | GLU | 602 | 47.969 | 40.227 | 80.608 | 1.00 | 2.00 | 0 |
| ATOM | 3806 | CB | GLU | 602 | 47.486 | 41.676 | 80.495 | 1.00 | 5.18 | 0 |
| ATOM | 3807 | CG | GLU | 602 | 47.752 | 42.552 | 81.739 | 1.00 | 5.18 | 0 |
| ATOM | 3808 | CD | GLU | 602 | 49.152 | 43.180 | 81.773 | 1.00 | 5.18 | 0 |
| ATOM | 3809 | OE1 | GLU | 602 | 50.146 | 42.439 | 81.854 | 1.00 | 5.18 | 0 |
| ATOM | 3810 | OE2 | GLU | 602 | 49.266 | 44.424 | 81.732 | 1.00 | 5.18 | 0 |
| ATOM | 3811 | C | GLU | 602 | 47.413 | 39.391 | 79.479 | 1.00 | 2.00 | 0 |
| ATOM | 3812 | O | GLU | 602 | 46.452 | 38.661 | 79.661 | 1.00 | 5.18 | 0 |
| ATOM | 3813 | N | THR | 603 | 48.072 | 39.477 | 78.323 | 1.00 | 56.10 | 0 |
| ATOM | 3815 | CA | THR | 603 | 47.705 | 38.748 | 77.110 | 1.00 | 56.10 | 0 |
| ATOM | 3816 | CB | THR | 603 | 48.585 | 39.206 | 75.941 | 1.00 | 8.67 | 0 |
| ATOM | 3817 | OG1 | THR | 603 | 48.197 | 40.527 | 75.557 | 1.00 | 8.67 | 0 |
| ATOM | 3819 | CG2 | THR | 603 | 48.437 | 38.272 | 74.748 | 1.00 | 8.67 | 0 |
| ATOM | 3820 | C | THR | 603 | 47.794 | 37.228 | 77.228 | 1.00 | 56.10 | 0 |
| ATOM | 3821 | O | THR | 603 | 46.804 | 36.522 | 77.060 | 1.00 | 8.67 | 0 |
| ATOM | 3822 | N | ILE | 604 | 48.980 | 36.713 | 77.505 | 1.00 | 2.00 | 0 |
| ATOM | 3824 | CA | ILE | 604 | 49.137 | 35.273 | 77.630 | 1.00 | 2.00 | 0 |
| ATOM | 3825 | CB | ILE | 604 | 50.643 | 34.900 | 77.738 | 1.00 | 2.00 | 0 |
| ATOM | 3826 | CG2 | ILE | 604 | 51.244 | 35.475 | 79.009 | 1.00 | 2.00 | 0 |
| ATOM | 3827 | CG1 | ILE | 604 | 50.812 | 33.382 | 77.627 | 1.00 | 2.00 | 0 |
| ATOM | 3828 | CD1 | ILE | 604 | 50.177 | 32.766 | 76.369 | 1.00 | 2.00 | 0 |
| ATOM | 3829 | C | ILE | 604 | 48.314 | 34.710 | 78.808 | 1.00 | 2.00 | 0 |
| ATOM | 3830 | O | ILE | 604 | 47.886 | 33.565 | 78.779 | 1.00 | 2.00 | 0 |
| ATOM | 3831 | N | CYS | 605 | 48.057 | 35.526 | 79.821 | 1.00 | 17.68 | 0 |
| ATOM | 3833 | CA | CYS | 605 | 47.283 | 35.072 | 80.962 | 1.00 | 16.48 | 0 |
| ATOM | 3834 | CB | CYS | 605 | 47.434 | 36.026 | 82.138 | 1.00 | 12.63 | 0 |
| ATOM | 3835 | SG | CYS | 605 | 48.994 | 35.843 | 82.980 | 1.00 | 18.12 | 0 |
| ATOM | 3836 | C | CYS | 605 | 45.824 | 34.923 | 80.630 | 1.00 | 10.22 | 0 |
| ATOM | 3837 | O | CYS | 605 | 45.185 | 33.963 | 81.068 | 1.00 | 8.59 | 0 |
| ATOM | 3838 | N | LEU | 606 | 45.280 | 35.856 | 79.861 | 1.00 | 2.00 | 0 |
| ATOM | 3840 | CA | LEU | 606 | 43.874 | 35.771 | 79.504 | 1.00 | 2.00 | 0 |
| ATOM | 3841 | CB | LEU | 606 | 43.396 | 37.087 | 78.881 | 1.00 | 2.00 | 0 |
| ATOM | 3842 | CG | LEU | 606 | 41.886 | 37.223 | 78.636 | 1.00 | 2.00 | 0 |
| ATOM | 3843 | CD1 | LEU | 606 | 41.081 | 36.716 | 79.867 | 1.00 | 2.00 | 0 |
| ATOM | 3844 | CD2 | LEU | 606 | 41.551 | 38.688 | 78.326 | 1.00 | 2.00 | 0 |
| ATOM | 3845 | C | LEU | 606 | 43.589 | 34.599 | 78.559 | 1.00 | 2.00 | 0 |
| ATOM | 3846 | O | LEU | 606 | 42.503 | 34.012 | 78.612 | 1.00 | 2.00 | 0 |
| ATOM | 3847 | N | LEU | 607 | 44.562 | 34.246 | 77.713 | 1.00 | 9.59 | 0 |
| ATOM | 3849 | CA | LEU | 607 | 44.392 | 33.137 | 76.772 | 1.00 | 9.59 | 0 |
| ATOM | 3850 | CB | LEU | 607 | 45.394 | 33.246 | 75.604 | 1.00 | 9.66 | 0 |
| ATOM | 3851 | CG | LEU | 607 | 45.302 | 34.531 | 74.755 | 1.00 | 9.66 | 0 |
| ATOM | 3852 | CD1 | LEU | 607 | 46.376 | 34.564 | 73.709 | 1.00 | 9.66 | 0 |
| ATOM | 3853 | CD2 | LEU | 607 | 43.951 | 34.634 | 74.114 | 1.00 | 9.66 | 0 |
| ATOM | 3854 | C | LEU | 607 | 44.509 | 31.781 | 77.476 | 1.00 | 9.59 | 0 |
| ATOM | 3855 | O | LEU | 607 | 43.772 | 30.841 | 77.148 | 1.00 | 9.66 | 0 |
| ATOM | 3856 | N | LEU | 608 | 45.412 | 31.688 | 78.452 | 1.00 | 67.56 | 0 |
| ATOM | 3858 | CA | LEU | 608 | 45.599 | 30.460 | 79.230 | 1.00 | 67.56 | 0 |
| ATOM | 3859 | CB | LEU | 608 | 46.872 | 30.529 | 80.054 | 1.00 | 2.00 | 0 |
| ATOM | 3860 | CG | LEU | 608 | 48.168 | 30.385 | 79.273 | 1.00 | 2.00 | 0 |
| ATOM | 3861 | CD1 | LEU | 608 | 49.357 | 30.366 | 80.234 | 1.00 | 2.00 | 0 |
| ATOM | 3862 | CD2 | LEU | 608 | 48.109 | 29.107 | 78.462 | 1.00 | 2.00 | 0 |
| ATOM | 3863 | C | LEU | 608 | 44.427 | 30.217 | 80.170 | 1.00 | 67.56 | 0 |
| ATOM | 3864 | O | LEU | 608 | 44.097 | 29.059 | 80.477 | 1.00 | 2.00 | 0 |
| ATOM | 3865 | N | ALA | 609 | 43.833 | 31.313 | 80.653 | 1.00 | 2.00 | 0 |
| ATOM | 3867 | CA | ALA | 609 | 42.667 | 31.250 | 81.531 | 1.00 | 2.00 | 0 |
| ATOM | 3868 | CB | ALA | 609 | 42.322 | 32.637 | 82.044 | 1.00 | 2.00 | 0 |
| ATOM | 3869 | C | ALA | 609 | 41.496 | 30.677 | 80.734 | 1.00 | 2.00 | 0 |
| ATOM | 3870 | O | ALA | 609 | 40.833 | 29.747 | 81.162 | 1.00 | 2.00 | 0 |
| ATOM | 3871 | N | TYR | 610 | 41.263 | 31.231 | 79.552 | 1.00 | 2.00 | 0 |
| ATOM | 3873 | CA | TYR | 610 | 40.186 | 30.771 | 78.686 | 1.00 | 2.00 | 0 |
| ATOM | 3874 | CB | TYR | 610 | 40.046 | 31.717 | 77.504 | 1.00 | 2.00 | 0 |
| ATOM | 3875 | CG | TYR | 610 | 39.274 | 32.974 | 77.820 | 1.00 | 2.00 | 0 |
| ATOM | 3876 | CD1 | TYR | 610 | 39.685 | 34.202 | 77.315 | 1.00 | 2.00 | 0 |
| ATOM | 3877 | CE1 | TYR | 610 | 38.952 | 35.359 | 77.558 | 1.00 | 2.00 | 0 |

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|---|---|---|---|---|---|---|---|---|---|---|
| ATOM | 3878 | CD2 | TYR | 610 | 38.108 | 32.933 | 78.589 | 1.00 | 2.00 | 0 |
| ATOM | 3879 | CE2 | TYR | 610 | 37.367 | 34.091 | 78.841 | 1.00 | 2.00 | 0 |
| ATOM | 3880 | CZ | TYR | 610 | 37.797 | 35.298 | 78.319 | 1.00 | 2.00 | 0 |
| ATOM | 3881 | OH | TYR | 610 | 37.086 | 36.452 | 78.533 | 1.00 | 2.00 | 0 |
| ATOM | 3883 | C | TYR | 610 | 40.431 | 29.342 | 78.205 | 1.00 | 2.00 | 0 |
| ATOM | 3884 | O | TYR | 610 | 39.481 | 28.575 | 78.006 | 1.00 | 2.00 | 0 |
| ATOM | 3885 | N | LYS | 611 | 41.703 | 28.991 | 78.017 | 1.00 | 2.00 | 0 |
| ATOM | 3887 | CA | LYS | 611 | 42.063 | 27.648 | 77.600 | 1.00 | 2.00 | 0 |
| ATOM | 3888 | CB | LYS | 611 | 43.551 | 27.532 | 77.308 | 1.00 | 3.53 | 0 |
| ATOM | 3889 | CG | LYS | 611 | 43.926 | 26.136 | 76.803 | 1.00 | 3.53 | 0 |
| ATOM | 3890 | CD | LYS | 611 | 43.240 | 25.837 | 75.467 | 1.00 | 3.53 | 0 |
| ATOM | 3891 | CE | LYS | 611 | 43.476 | 24.412 | 74.980 | 1.00 | 3.53 | 0 |
| ATOM | 3892 | NZ | LYS | 611 | 42.391 | 23.502 | 75.421 | 1.00 | 3.53 | 0 |
| ATOM | 3896 | C | LYS | 611 | 41.717 | 26.666 | 78.700 | 1.00 | 2.00 | 0 |
| ATOM | 3897 | O | LYS | 611 | 41.142 | 25.618 | 78.431 | 1.00 | 3.53 | 0 |
| ATOM | 3898 | N | ILE | 612 | 42.084 | 26.990 | 79.938 | 1.00 | 26.02 | 0 |
| ATOM | 3900 | CA | ILE | 612 | 41.780 | 26.115 | 81.069 | 1.00 | 26.02 | 0 |
| ATOM | 3901 | CB | ILE | 612 | 42.543 | 26.535 | 82.336 | 1.00 | 2.00 | 0 |
| ATOM | 3902 | CG2 | ILE | 612 | 42.232 | 25.576 | 83.475 | 1.00 | 2.00 | 0 |
| ATOM | 3903 | CG1 | ILE | 612 | 44.041 | 26.511 | 82.063 | 1.00 | 2.00 | 0 |
| ATOM | 3904 | CD1 | ILE | 612 | 44.860 | 27.144 | 83.135 | 1.00 | 2.00 | 0 |
| ATOM | 3905 | C | ILE | 612 | 40.284 | 26.149 | 81.365 | 1.00 | 26.02 | 0 |
| ATOM | 3906 | O | ILE | 612 | 39.698 | 25.131 | 81.739 | 1.00 | 2.00 | 0 |
| ATOM | 3907 | N | LYS | 613 | 39.683 | 27.326 | 81.181 | 1.00 | 2.00 | 0 |
| ATOM | 3909 | CA | LYS | 613 | 38.257 | 27.556 | 81.414 | 1.00 | 2.00 | 0 |
| ATOM | 3910 | CB | LYS | 613 | 37.966 | 29.058 | 81.402 | 1.00 | 10.53 | 0 |
| ATOM | 3911 | CG | LYS | 613 | 36.528 | 29.437 | 81.650 | 1.00 | 10.53 | 0 |
| ATOM | 3912 | CD | LYS | 613 | 36.070 | 29.072 | 83.035 | 1.00 | 10.53 | 0 |
| ATOM | 3913 | CE | LYS | 613 | 34.717 | 29.693 | 83.364 | 1.00 | 10.53 | 0 |
| ATOM | 3914 | NZ | LYS | 613 | 33.611 | 29.182 | 82.523 | 1.00 | 10.53 | 0 |
| ATOM | 3918 | C | LYS | 613 | 37.379 | 26.847 | 80.384 | 1.00 | 2.00 | 0 |
| ATOM | 3919 | O | LYS | 613 | 36.335 | 26.293 | 80.739 | 1.00 | 10.53 | 0 |
| ATOM | 3920 | N | TYR | 614 | 37.819 | 26.842 | 79.121 | 1.00 | 24.09 | 0 |
| ATOM | 3922 | CA | TYR | 614 | 37.079 | 26.214 | 78.016 | 1.00 | 27.84 | 0 |
| ATOM | 3923 | CB | TYR | 614 | 36.473 | 27.301 | 77.125 | 1.00 | 2.00 | 0 |
| ATOM | 3924 | CG | TYR | 614 | 35.679 | 28.363 | 77.855 | 1.00 | 2.00 | 0 |
| ATOM | 3925 | CD1 | TYR | 614 | 36.123 | 29.689 | 77.892 | 1.00 | 2.00 | 0 |
| ATOM | 3926 | CE1 | TYR | 614 | 35.409 | 30.671 | 78.567 | 1.00 | 2.00 | 0 |
| ATOM | 3927 | CD2 | TYR | 614 | 34.490 | 28.048 | 78.516 | 1.00 | 2.00 | 0 |
| ATOM | 3928 | CE2 | TYR | 614 | 33.766 | 29.020 | 79.199 | 1.00 | 2.00 | 0 |
| ATOM | 3929 | CZ | TYR | 614 | 34.232 | 30.330 | 79.227 | 1.00 | 2.00 | 0 |
| ATOM | 3930 | OH | TYR | 614 | 33.560 | 31.293 | 79.960 | 1.00 | 2.00 | 0 |
| ATOM | 3932 | C | TYR | 614 | 37.976 | 25.317 | 77.146 | 1.00 | 25.93 | 0 |
| ATOM | 3933 | O | TYR | 614 | 38.012 | 25.474 | 75.935 | 1.00 | 2.00 | 0 |
| ATOM | 3934 | N | PRO | 615 | 38.641 | 24.310 | 77.733 | 1.00 | 21.49 | 0 |
| ATOM | 3935 | CD | PRO | 615 | 38.494 | 23.854 | 79.123 | 1.00 | 11.83 | 0 |
| ATOM | 3936 | CA | PRO | 615 | 39.541 | 23.406 | 76.995 | 1.00 | 22.47 | 0 |
| ATOM | 3937 | CB | PRO | 615 | 39.950 | 22.384 | 78.055 | 1.00 | 11.83 | 0 |
| ATOM | 3938 | CG | PRO | 615 | 38.773 | 22.382 | 78.995 | 1.00 | 11.83 | 0 |
| ATOM | 3939 | C | PRO | 615 | 39.078 | 22.714 | 75.720 | 1.00 | 20.23 | 0 |
| ATOM | 3940 | O | PRO | 615 | 39.873 | 22.026 | 75.074 | 1.00 | 11.83 | 0 |
| ATOM | 3941 | N | GLU | 616 | 37.813 | 22.879 | 75.350 | 1.00 | 15.62 | 0 |
| ATOM | 3943 | CA | GLU | 616 | 37.296 | 22.213 | 74.159 | 1.00 | 16.61 | 0 |
| ATOM | 3944 | CB | GLU | 616 | 36.240 | 21.179 | 74.566 | 1.00 | 26.75 | 0 |
| ATOM | 3945 | CG | GLU | 616 | 36.644 | 20.253 | 75.695 | 1.00 | 30.68 | 0 |
| ATOM | 3946 | CD | GLU | 616 | 37.872 | 19.416 | 75.382 | 1.00 | 40.71 | 0 |
| ATOM | 3947 | OE1 | GLU | 616 | 38.747 | 19.294 | 76.273 | 1.00 | 39.65 | 0 |
| ATOM | 3948 | OE2 | GLU | 616 | 37.960 | 18.874 | 74.256 | 1.00 | 39.29 | 0 |
| ATOM | 3949 | C | GLU | 616 | 36.681 | 23.175 | 73.140 | 1.00 | 13.01 | 0 |
| ATOM | 3950 | O | GLU | 616 | 36.276 | 22.765 | 72.046 | 1.00 | 20.06 | 0 |
| ATOM | 3951 | N | ASN | 617 | 36.620 | 24.453 | 73.499 | 1.00 | 2.00 | 0 |
| ATOM | 3953 | CA | ASN | 617 | 36.027 | 25.467 | 72.636 | 1.00 | 2.00 | 0 |
| ATOM | 3954 | CB | ASN | 617 | 34.678 | 25.896 | 73.218 | 1.00 | 42.63 | 0 |
| ATOM | 3955 | CG | ASN | 617 | 33.743 | 24.720 | 73.456 | 1.00 | 47.29 | 0 |
| ATOM | 3956 | OD1 | ASN | 617 | 33.800 | 24.064 | 74.500 | 1.00 | 50.83 | 0 |
| ATOM | 3957 | ND2 | ASN | 617 | 32.883 | 24.443 | 72.485 | 1.00 | 53.65 | 0 |
| ATOM | 3960 | C | ASN | 617 | 36.941 | 26.686 | 72.476 | 1.00 | 2.00 | 0 |
| ATOM | 3961 | O | ASN | 617 | 36.505 | 27.747 | 72.032 | 1.00 | 45.01 | 0 |

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|---|---|---|---|---|---|---|---|---|---|---|
| ATOM | 3962 | N | PHE | 618 | 38.215 | 26.517 | 72.812 | 1.00 | 14.67 | 0 |
| ATOM | 3964 | CA | PHE | 618 | 39.192 | 27.596 | 72.736 | 1.00 | 14.67 | 0 |
| ATOM | 3965 | CB | PHE | 618 | 39.146 | 28.387 | 74.044 | 1.00 | 2.00 | 0 |
| ATOM | 3966 | CG | PHE | 618 | 40.042 | 29.585 | 74.073 | 1.00 | 2.00 | 0 |
| ATOM | 3967 | CD1 | PHE | 618 | 39.501 | 30.871 | 74.058 | 1.00 | 2.00 | 0 |
| ATOM | 3968 | CD2 | PHE | 618 | 41.422 | 29.441 | 74.147 | 1.00 | 2.00 | 0 |
| ATOM | 3969 | CE1 | PHE | 618 | 40.322 | 32.007 | 74.119 | 1.00 | 2.00 | 0 |
| ATOM | 3970 | CE2 | PHE | 618 | 42.254 | 30.562 | 74.209 | 1.00 | 2.00 | 0 |
| ATOM | 3971 | CZ | PHE | 618 | 41.696 | 31.854 | 74.195 | 1.00 | 2.00 | 0 |
| ATOM | 3972 | C | PHE | 618 | 40.540 | 26.907 | 72.570 | 1.00 | 14.67 | 0 |
| ATOM | 3973 | O | PHE | 618 | 40.893 | 26.066 | 73.394 | 1.00 | 2.00 | 0 |
| ATOM | 3974 | N | PHE | 619 | 41.285 | 27.239 | 71.514 | 1.00 | 2.00 | 0 |
| ATOM | 3976 | CA | PHE | 619 | 42.583 | 26.599 | 71.271 | 1.00 | 2.00 | 0 |
| ATOM | 3977 | CB | PHE | 619 | 42.468 | 25.622 | 70.111 | 1.00 | 2.00 | 0 |
| ATOM | 3978 | CG | PHE | 619 | 41.404 | 24.595 | 70.311 | 1.00 | 2.00 | 0 |
| ATOM | 3979 | CD1 | PHE | 619 | 40.063 | 24.936 | 70.159 | 1.00 | 2.00 | 0 |
| ATOM | 3980 | CD2 | PHE | 619 | 41.738 | 23.291 | 70.678 | 1.00 | 2.00 | 0 |
| ATOM | 3981 | CE1 | PHE | 619 | 39.068 | 23.997 | 70.370 | 1.00 | 2.00 | 0 |
| ATOM | 3982 | CE2 | PHE | 619 | 40.750 | 22.337 | 70.892 | 1.00 | 2.00 | 0 |
| ATOM | 3983 | CZ | PHE | 619 | 39.408 | 22.689 | 70.738 | 1.00 | 2.00 | 0 |
| ATOM | 3984 | C | PHE | 619 | 43.719 | 27.566 | 71.005 | 1.00 | 2.00 | 0 |
| ATOM | 3985 | O | PHE | 619 | 43.501 | 28.698 | 70.564 | 1.00 | 2.00 | 0 |
| ATOM | 3986 | N | LEU | 620 | 44.936 | 27.115 | 71.282 | 1.00 | 2.00 | 0 |
| ATOM | 3988 | CA | LEU | 620 | 46.118 | 27.933 | 71.073 | 1.00 | 2.00 | 0 |
| ATOM | 3989 | CB | LEU | 620 | 46.647 | 28.507 | 72.393 | 1.00 | 2.00 | 0 |
| ATOM | 3990 | CG | LEU | 620 | 45.826 | 29.389 | 73.321 | 1.00 | 2.00 | 0 |
| ATOM | 3991 | CD1 | LEU | 620 | 46.741 | 29.868 | 74.437 | 1.00 | 2.00 | 0 |
| ATOM | 3992 | CD2 | LEU | 620 | 45.247 | 30.563 | 72.565 | 1.00 | 2.00 | 0 |
| ATOM | 3993 | C | LEU | 620 | 47.225 | 27.093 | 70.438 | 1.00 | 2.00 | 0 |
| ATOM | 3994 | O | LEU | 620 | 47.548 | 25.987 | 70.910 | 1.00 | 2.00 | 0 |
| ATOM | 3995 | N | LEU | 621 | 47.805 | 27.634 | 69.376 | 1.00 | 2.00 | 0 |
| ATOM | 3997 | CA | LEU | 621 | 48.880 | 26.971 | 68.669 | 1.00 | 2.00 | 0 |
| ATOM | 3998 | CB | LEU | 621 | 48.577 | 26.929 | 67.162 | 1.00 | 2.00 | 0 |
| ATOM | 3999 | CG | LEU | 621 | 47.256 | 26.280 | 66.739 | 1.00 | 2.00 | 0 |
| ATOM | 4000 | CD1 | LEU | 621 | 47.021 | 26.511 | 65.253 | 1.00 | 2.00 | 0 |
| ATOM | 4001 | CD2 | LEU | 621 | 47.281 | 24.813 | 67.062 | 1.00 | 2.00 | 0 |
| ATOM | 4002 | C | LEU | 621 | 50.162 | 27.756 | 68.943 | 1.00 | 2.00 | 0 |
| ATOM | 4003 | O | LEU | 621 | 50.121 | 28.937 | 69.285 | 1.00 | 2.00 | 0 |
| ATOM | 4004 | N | ARG | 622 | 51.296 | 27.092 | 68.774 | 1.00 | 2.00 | 0 |
| ATOM | 4006 | CA | ARG | 622 | 52.593 | 27.690 | 69.013 | 1.00 | 2.00 | 0 |
| ATOM | 4007 | CB | ARG | 622 | 53.620 | 26.578 | 69.231 | 1.00 | 5.18 | 0 |
| ATOM | 4008 | CG | ARG | 622 | 54.967 | 27.052 | 69.716 | 1.00 | 5.18 | 0 |
| ATOM | 4009 | CD | ARG | 622 | 55.802 | 25.891 | 70.196 | 1.00 | 5.18 | 0 |
| ATOM | 4010 | NE | ARG | 622 | 56.969 | 26.357 | 70.941 | 1.00 | 5.18 | 0 |
| ATOM | 4012 | CZ | ARG | 622 | 57.830 | 25.553 | 71.557 | 1.00 | 5.18 | 0 |
| ATOM | 4013 | NH1 | ARG | 622 | 57.659 | 24.240 | 71.525 | 1.00 | 6.18 | 0 |
| ATOM | 4016 | NH2 | ARG | 622 | 58.870 | 26.056 | 72.199 | 1.00 | 5.18 | 0 |
| ATOM | 4019 | C | ARG | 622 | 53.070 | 28.615 | 67.894 | 1.00 | 2.00 | 0 |
| ATOM | 4020 | O | ARG | 622 | 53.032 | 28.270 | 66.702 | 1.00 | 16.40 | 0 |
| ATOM | 4021 | N | GLY | 623 | 53.508 | 29.805 | 68.286 | 1.00 | 19.04 | 0 |
| ATOM | 4023 | CA | GLY | 623 | 54.043 | 30.749 | 67.328 | 1.00 | 20.78 | 0 |
| ATOM | 4024 | C | GLY | 623 | 55.551 | 30.573 | 67.390 | 1.00 | 18.09 | 0 |
| ATOM | 4025 | O | GLY | 623 | 56.069 | 29.805 | 68.212 | 1.00 | 2.00 | 0 |
| ATOM | 4026 | N | ASN | 624 | 56.281 | 31.266 | 66.530 | 1.00 | 32.06 | 0 |
| ATOM | 4028 | CA | ASN | 624 | 57.728 | 31.144 | 66.566 | 1.00 | 32.95 | 0 |
| ATOM | 4029 | CB | ASN | 624 | 58.345 | 31.543 | 65.220 | 1.00 | 12.63 | 0 |
| ATOM | 4030 | CG | ASN | 624 | 58.120 | 33.002 | 64.857 | 1.00 | 8.84 | 0 |
| ATOM | 4031 | OD1 | ASN | 624 | 57.381 | 33.754 | 65.538 | 1.00 | 9.47 | 0 |
| ATOM | 4032 | ND2 | ASN | 624 | 58.721 | 33.411 | 63.757 | 1.00 | 8.50 | 0 |
| ATOM | 4035 | C | ASN | 624 | 58.260 | 31.988 | 67.721 | 1.00 | 32.42 | 0 |
| ATOM | 4036 | O | ASN | 624 | 59.442 | 31.926 | 68.066 | 1.00 | 7.81 | 0 |
| ATOM | 4037 | N | HIS | 625 | 57.359 | 32.757 | 68.335 | 1.00 | 7.73 | 0 |
| ATOM | 4039 | CA | HIS | 625 | 57.687 | 33.614 | 69.477 | 1.00 | 8.83 | 0 |
| ATOM | 4040 | CB | HIS | 625 | 57.030 | 34.987 | 69.320 | 1.00 | 2.00 | 0 |
| ATOM | 4041 | CG | HIS | 625 | 57.909 | 35.998 | 68.656 | 1.00 | 2.00 | 0 |
| ATOM | 4042 | CD2 | HIS | 625 | 59.042 | 35.854 | 67.933 | 1.00 | 2.00 | 0 |
| ATOM | 4043 | ND1 | HIS | 625 | 57.668 | 37.351 | 68.721 | 1.00 | 2.00 | 0 |
| ATOM | 4045 | CE1 | HIS | 625 | 58.618 | 37.999 | 68.069 | 1.00 | 2.00 | 0 |

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|---|---|---|---|---|---|---|---|---|---|---|
| ATOM | 4046 | NE2 | HIS | 625 | 59.464 | 37.113 | 67.582 | 1.00 | 2.00 | 0 |
| ATOM | 4048 | C | HIS | 625 | 57.278 | 32.980 | 70.807 | 1.00 | 8.94 | 0 |
| ATOM | 4049 | O | HIS | 625 | 57.188 | 33.644 | 71.825 | 1.00 | 2.00 | 0 |
| ATOM | 4050 | N | GLU | 626 | 56.984 | 31.691 | 70.767 | 1.00 | 2.00 | 0 |
| ATOM | 4052 | CA | GLU | 626 | 56.629 | 30.914 | 71.945 | 1.00 | 2.00 | 0 |
| ATOM | 4053 | CB | GLU | 626 | 55.404 | 30.026 | 71.666 | 1.00 | 23.06 | 0 |
| ATOM | 4054 | CG | GLU | 626 | 54.051 | 30.627 | 72.039 | 1.00 | 18.70 | 0 |
| ATOM | 4055 | CD | GLU | 626 | 53.812 | 31.997 | 71.445 | 1.00 | 17.00 | 0 |
| ATOM | 4056 | OE1 | GLU | 626 | 53.516 | 32.922 | 72.217 | 1.00 | 20.31 | 0 |
| ATOM | 4057 | OE2 | GLU | 626 | 53.911 | 32.165 | 70.214 | 1.00 | 23.26 | 0 |
| ATOM | 4058 | C | GLU | 626 | 57.888 | 30.068 | 72.029 | 1.00 | 2.00 | 0 |
| ATOM | 4059 | O | GLU | 626 | 57.851 | 28.841 | 71.921 | 1.00 | 23.50 | 0 |
| ATOM | 4060 | N | CYS | 627 | 59.015 | 30.748 | 72.184 | 1.00 | 2.00 | 0 |
| ATOM | 4062 | CA | CYS | 627 | 60.290 | 30.067 | 72.218 | 1.00 | 2.00 | 0 |
| ATOM | 4063 | CB | CYS | 627 | 60.832 | 29.957 | 70.789 | 1.00 | 7.85 | 0 |
| ATOM | 4064 | SG | CYS | 627 | 62.235 | 28.843 | 70.575 | 1.00 | 19.90 | 0 |
| ATOM | 4065 | C | CYS | 627 | 61.260 | 30.842 | 73.105 | 1.00 | 2.00 | 0 |
| ATOM | 4066 | O | CYS | 627 | 61.355 | 32.066 | 73.008 | 1.00 | 8.12 | 0 |
| ATOM | 4067 | N | ALA | 628 | 61.971 | 30.116 | 73.970 | 1.00 | 19.49 | 0 |
| ATOM | 4069 | CA | ALA | 628 | 62.934 | 30.702 | 74.900 | 1.00 | 19.49 | 0 |
| ATOM | 4070 | CB | ALA | 628 | 63.704 | 29.601 | 75.567 | 1.00 | 2.00 | 0 |
| ATOM | 4071 | C | ALA | 628 | 63.890 | 31.662 | 74.206 | 1.00 | 19.49 | 0 |
| ATOM | 4072 | O | ALA | 628 | 63.921 | 32.859 | 74.484 | 1.00 | 2.00 | 0 |
| ATOM | 4073 | N | SER | 629 | 64.660 | 31.101 | 73.291 | 1.00 | 10.83 | 0 |
| ATOM | 4075 | CA | SER | 629 | 65.637 | 31.813 | 72.478 | 1.00 | 14.60 | 0 |
| ATOM | 4076 | CB | SER | 629 | 66.057 | 30.877 | 71.355 | 1.00 | 15.99 | 0 |
| ATOM | 4077 | OG | SER | 629 | 65.846 | 29.522 | 71.762 | 1.00 | 20.43 | 0 |
| ATOM | 4079 | C | SER | 629 | 65.119 | 33.131 | 71.899 | 1.00 | 19.16 | 0 |
| ATOM | 4080 | O | SER | 629 | 65.869 | 34.085 | 71.759 | 1.00 | 13.43 | 0 |
| ATOM | 4081 | N | ILE | 630 | 63.834 | 33.167 | 71.566 | 1.00 | 2.00 | 0 |
| ATOM | 4083 | CA | ILE | 630 | 63.198 | 34.354 | 71.022 | 1.00 | 2.00 | 0 |
| ATOM | 4084 | CB | ILE | 630 | 62.076 | 33.973 | 70.017 | 1.00 | 2.00 | 0 |
| ATOM | 4085 | CG2 | ILE | 630 | 61.675 | 35.174 | 69.202 | 1.00 | 2.00 | 0 |
| ATOM | 4086 | CG1 | ILE | 630 | 62.604 | 32.998 | 68.980 | 1.00 | 2.00 | 0 |
| ATOM | 4087 | CD1 | ILE | 630 | 63.664 | 33.598 | 68.080 | 1.00 | 2.00 | 0 |
| ATOM | 4088 | C | ILE | 630 | 62.636 | 35.281 | 72.131 | 1.00 | 2.00 | 0 |
| ATOM | 4089 | O | ILE | 630 | 62.866 | 36.492 | 72.068 | 1.00 | 2.00 | 0 |
| ATOM | 4090 | N | ASN | 631 | 61.932 | 34.729 | 73.137 | 1.00 | 10.29 | 0 |
| ATOM | 4092 | CA | ASN | 631 | 61.350 | 35.504 | 74.272 | 1.00 | 9.61 | 0 |
| ATOM | 4093 | CB | ASN | 631 | 60.759 | 34.597 | 75.349 | 1.00 | 8.67 | 0 |
| ATOM | 4094 | CG | ASN | 631 | 59.555 | 33.848 | 74.891 | 1.00 | 17.37 | 0 |
| ATOM | 4095 | OD1 | ASN | 631 | 59.189 | 33.896 | 73.722 | 1.00 | 21.10 | 0 |
| ATOM | 4096 | ND2 | ASN | 631 | 58.926 | 33.124 | 75.815 | 1.00 | 15.25 | 0 |
| ATOM | 4099 | C | ASN | 631 | 62.367 | 36.370 | 75.003 | 1.00 | 6.75 | 0 |
| ATOM | 4100 | O | ASN | 631 | 62.059 | 37.486 | 75.438 | 1.00 | 6.80 | 0 |
| ATOM | 4101 | N | ARG | 632 | 63.555 | 35.810 | 75.189 | 1.00 | 2.00 | 0 |
| ATOM | 4103 | CA | ARG | 632 | 64.635 | 36.492 | 75.867 | 1.00 | 2.00 | 0 |
| ATOM | 4104 | CB | ARG | 632 | 65.873 | 35.595 | 75.909 | 1.00 | 6.06 | 0 |
| ATOM | 4105 | CG | ARG | 632 | 66.361 | 35.244 | 77.316 | 1.00 | 8.20 | 0 |
| ATOM | 4106 | CD | ARG | 632 | 67.436 | 36.202 | 77.839 | 1.00 | 8.31 | 0 |
| ATOM | 4107 | NE | ARG | 632 | 67.003 | 37.598 | 77.918 | 1.00 | 11.75 | 0 |
| ATOM | 4109 | CZ | ARG | 632 | 67.837 | 38.635 | 77.907 | 1.00 | 13.36 | 0 |
| ATOM | 4110 | NH1 | ARG | 632 | 69.144 | 38.423 | 77.811 | 1.00 | 13.50 | 0 |
| ATOM | 4113 | NH2 | ARG | 632 | 67.372 | 39.883 | 78.001 | 1.00 | 18.51 | 0 |
| ATOM | 4116 | C | ARG | 632 | 64.962 | 37.781 | 75.148 | 1.00 | 2.00 | 0 |
| ATOM | 4117 | O | ARG | 632 | 64.930 | 38.865 | 75.745 | 1.00 | 12.49 | 0 |
| ATOM | 4118 | N | ILE | 633 | 65.234 | 37.658 | 73.852 | 1.00 | 21.20 | 0 |
| ATOM | 4120 | CA | ILE | 633 | 65.608 | 38.788 | 73.014 | 1.00 | 19.86 | 0 |
| ATOM | 4121 | CB | ILE | 633 | 66.085 | 38.308 | 71.610 | 1.00 | 32.61 | 0 |
| ATOM | 4122 | CG2 | ILE | 633 | 66.132 | 39.471 | 70.625 | 1.00 | 29.80 | 0 |
| ATOM | 4123 | CG1 | ILE | 633 | 67.490 | 37.716 | 71.700 | 1.00 | 28.84 | 0 |
| ATOM | 4124 | CD1 | ILE | 633 | 67.619 | 36.496 | 72.594 | 1.00 | 35.23 | 0 |
| ATOM | 4125 | C | ILE | 633 | 64.550 | 39.866 | 72.815 | 1.00 | 22.19 | 0 |
| ATOM | 4126 | O | ILE | 633 | 64.864 | 41.053 | 72.878 | 1.00 | 30.44 | 0 |
| ATOM | 4127 | N | TYR | 634 | 63.303 | 39.473 | 72.588 | 1.00 | 32.62 | 0 |
| ATOM | 4129 | CA | TYR | 634 | 62.276 | 40.471 | 72.316 | 1.00 | 31.19 | 0 |
| ATOM | 4130 | CB | TYR | 634 | 61.395 | 40.006 | 71.147 | 1.00 | 13.98 | 0 |
| ATOM | 4131 | CG | TYR | 634 | 62.231 | 39.755 | 69.941 | 1.00 | 19.07 | 0 |

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|---|---|---|---|---|---|---|---|---|---|---|
| ATOM | 4132 | CD1 | TYR | 634 | 62.652 | 40.805 | 69.147 | 1.00 | 17.28 | 0 |
| ATOM | 4133 | CE1 | TYR | 634 | 63.498 | 40.587 | 68.074 | 1.00 | 16.13 | 0 |
| ATOM | 4134 | CD2 | TYR | 634 | 62.668 | 38.474 | 69.639 | 1.00 | 15.20 | 0 |
| ATOM | 4135 | CE2 | TYR | 634 | 63.515 | 38.236 | 68.571 | 1.00 | 18.14 | 0 |
| ATOM | 4136 | CZ | TYR | 634 | 63.935 | 39.296 | 67.786 | 1.00 | 21.41 | 0 |
| ATOM | 4137 | OH | TYR | 634 | 64.789 | 39.069 | 66.720 | 1.00 | 20.11 | 0 |
| ATOM | 4139 | C | TYR | 634 | 61.430 | 41.025 | 73.446 | 1.00 | 28.63 | 0 |
| ATOM | 4140 | O | TYR | 634 | 60.380 | 41.637 | 73.188 | 1.00 | 19.20 | 0 |
| ATOM | 4141 | N | GLY | 635 | 61.851 | 40.807 | 74.690 | 1.00 | 38.67 | 0 |
| ATOM | 4143 | CA | GLY | 635 | 61.114 | 41.407 | 75.786 | 1.00 | 39.39 | 0 |
| ATOM | 4144 | C | GLY | 635 | 60.270 | 40.658 | 76.780 | 1.00 | 41.31 | 0 |
| ATOM | 4145 | O | GLY | 635 | 60.103 | 41.155 | 77.892 | 1.00 | 69.69 | 0 |
| ATOM | 4146 | N | PHE | 636 | 59.725 | 39.502 | 76.431 | 1.00 | 54.49 | 0 |
| ATOM | 4148 | CA | PHE | 636 | 58.905 | 38.786 | 77.404 | 1.00 | 56.26 | 0 |
| ATOM | 4149 | CB | PHE | 636 | 58.386 | 37.461 | 76.831 | 1.00 | 2.00 | 0 |
| ATOM | 4150 | CG | PHE | 636 | 57.275 | 36.845 | 77.639 | 1.00 | 2.00 | 0 |
| ATOM | 4151 | CD1 | PHE | 636 | 56.293 | 37.638 | 78.208 | 1.00 | 2.00 | 0 |
| ATOM | 4152 | CD2 | PHE | 636 | 57.214 | 35.478 | 77.824 | 1.00 | 2.00 | 0 |
| ATOM | 4153 | CE1 | PHE | 636 | 55.276 | 37.076 | 78.942 | 1.00 | 2.00 | 0 |
| ATOM | 4154 | CE2 | PHE | 636 | 56.210 | 34.919 | 78.549 | 1.00 | 2.00 | 0 |
| ATOM | 4155 | CZ | PHE | 636 | 55.238 | 35.716 | 79.111 | 1.00 | 2.00 | 0 |
| ATOM | 4156 | C | PHE | 636 | 59.761 | 38.522 | 78.646 | 1.00 | 55.84 | 0 |
| ATOM | 4157 | O | PHE | 636 | 59.321 | 38.728 | 79.791 | 1.00 | 2.00 | 0 |
| ATOM | 4158 | N | TYR | 637 | 61.005 | 38.114 | 78.415 | 1.00 | 2.00 | 0 |
| ATOM | 4160 | CA | TYR | 637 | 61.918 | 37.836 | 79.506 | 1.00 | 2.00 | 0 |
| ATOM | 4161 | CB | TYR | 637 | 63.266 | 37.419 | 78.947 | 1.00 | 18.03 | 0 |
| ATOM | 4162 | CG | TYR | 637 | 64.345 | 37.308 | 79.986 | 1.00 | 13.39 | 0 |
| ATOM | 4163 | CD1 | TYR | 637 | 64.560 | 36.116 | 80.668 | 1.00 | 15.45 | 0 |
| ATOM | 4164 | CE1 | TYR | 637 | 65.563 | 36.007 | 81.603 | 1.00 | 14.13 | 0 |
| ATOM | 4165 | CD2 | TYR | 637 | 65.163 | 38.390 | 80.273 | 1.00 | 14.83 | 0 |
| ATOM | 4166 | CE2 | TYR | 637 | 66.163 | 38.292 | 81.200 | 1.00 | 13.98 | 0 |
| ATOM | 4167 | CZ | TYR | 637 | 66.363 | 37.101 | 81.863 | 1.00 | 14.88 | 0 |
| ATOM | 4168 | OH | TYR | 637 | 67.379 | 37.015 | 82.784 | 1.00 | 13.10 | 0 |
| ATOM | 4170 | C | TYR | 637 | 62.091 | 39.056 | 80.411 | 1.00 | 2.00 | 0 |
| ATOM | 4171 | O | TYR | 637 | 62.362 | 38.920 | 81.605 | 1.00 | 20.03 | 0 |
| ATOM | 4172 | N | ASP | 638 | 61.919 | 40.240 | 79.833 | 1.00 | 2.00 | 0 |
| ATOM | 4174 | CA | ASP | 638 | 62.086 | 41.484 | 80.554 | 1.00 | 2.00 | 0 |
| ATOM | 4175 | CB | ASP | 638 | 62.701 | 42.522 | 79.614 | 1.00 | 57.25 | 0 |
| ATOM | 4176 | CG | ASP | 638 | 64.049 | 42.053 | 79.046 | 1.00 | 66.80 | 0 |
| ATOM | 4177 | OD1 | ASP | 638 | 64.078 | 41.539 | 77.905 | 1.00 | 65.06 | 0 |
| ATOM | 4178 | OD2 | ASP | 638 | 65.077 | 42.175 | 79.750 | 1.00 | 69.12 | 0 |
| ATOM | 4179 | C | ASP | 638 | 60.816 | 41.961 | 81.245 | 1.00 | 2.00 | 0 |
| ATOM | 4180 | O | ASP | 638 | 60.884 | 42.531 | 82.331 | 1.00 | 55.83 | 0 |
| ATOM | 4181 | N | GLU | 639 | 59.656 | 41.724 | 80.644 | 1.00 | 2.00 | 0 |
| ATOM | 4183 | CA | GLU | 639 | 58.405 | 42.074 | 81.317 | 1.00 | 2.00 | 0 |
| ATOM | 4184 | CB | GLU | 639 | 57.210 | 41.774 | 80.419 | 1.00 | 64.74 | 0 |
| ATOM | 4185 | CG | GLU | 639 | 57.051 | 42.726 | 79.261 | 1.00 | 71.70 | 0 |
| ATOM | 4186 | CD | GLU | 639 | 55.900 | 42.349 | 78.355 | 1.00 | 66.55 | 0 |
| ATOM | 4187 | OE1 | GLU | 639 | 54.748 | 42.718 | 78.667 | 1.00 | 65.31 | 0 |
| ATOM | 4188 | OE2 | GLU | 639 | 56.152 | 41.684 | 77.329 | 1.00 | 72.66 | 0 |
| ATOM | 4189 | C | GLU | 639 | 58.372 | 41.145 | 82.547 | 1.00 | 2.00 | 0 |
| ATOM | 4190 | O | GLU | 639 | 58.009 | 41.550 | 83.654 | 1.00 | 65.95 | 0 |
| ATOM | 4191 | N | CYS | 640 | 58.787 | 39.895 | 82.314 | 1.00 | 15.74 | 0 |
| ATOM | 4193 | CA | CYS | 640 | 58.859 | 38.843 | 83.323 | 1.00 | 15.74 | 0 |
| ATOM | 4194 | CB | CYS | 640 | 59.187 | 37.504 | 82.684 | 1.00 | 4.35 | 0 |
| ATOM | 4195 | SG | CYS | 640 | 57.734 | 36.587 | 82.208 | 1.00 | 13.44 | 0 |
| ATOM | 4196 | C | CYS | 640 | 59.859 | 39.081 | 84.426 | 1.00 | 15.74 | 0 |
| ATOM | 4197 | O | CYS | 640 | 59.590 | 38.723 | 85.564 | 1.00 | 11.73 | 0 |
| ATOM | 4198 | N | LYS | 641 | 61.028 | 39.631 | 84.110 | 1.00 | 2.00 | 0 |
| ATOM | 4200 | CA | LYS | 641 | 62.009 | 39.890 | 85.153 | 1.00 | 2.00 | 0 |
| ATOM | 4201 | CB | LYS | 641 | 63.425 | 39.454 | 84.721 | 1.00 | 32.33 | 0 |
| ATOM | 4202 | CG | LYS | 641 | 64.225 | 40.436 | 83.869 | 1.00 | 32.55 | 0 |
| ATOM | 4203 | CD | LYS | 641 | 65.735 | 40.154 | 83.954 | 1.00 | 38.99 | 0 |
| ATOM | 4204 | CE | LYS | 641 | 66.281 | 40.198 | 85.386 | 1.00 | 41.14 | 0 |
| ATOM | 4205 | NZ | LYS | 641 | 66.228 | 41.554 | 86.007 | 1.00 | 38.23 | 0 |
| ATOM | 4209 | C | LYS | 641 | 61.950 | 41.371 | 85.568 | 1.00 | 2.00 | 0 |
| ATOM | 4210 | O | LYS | 641 | 62.948 | 42.106 | 85.548 | 1.00 | 35.25 | 0 |
| ATOM | 4211 | N | ARG | 642 | 60.750 | 41.801 | 85.945 | 1.00 | 17.38 | 0 |

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|---|---|---|---|---|---|---|---|---|---|
| ATOM | 4213 | CA | ARG | 642 | 60.502 | 43.168 | 86.384 | 1.00 | 17.38 | 0 |
| ATOM | 4214 | CB | ARG | 642 | 60.341 | 44.131 | 85.204 | 1.00 | 14.00 | 0 |
| ATOM | 4215 | CG | ARG | 642 | 61.636 | 44.613 | 84.561 | 1.00 | 23.15 | 0 |
| ATOM | 4216 | CD | ARG | 642 | 61.463 | 46.016 | 83.940 | 1.00 | 25.43 | 0 |
| ATOM | 4217 | NE | ARG | 642 | 60.488 | 46.077 | 82.846 | 1.00 | 33.87 | 0 |
| ATOM | 4219 | CZ | ARG | 642 | 60.816 | 46.208 | 81.560 | 1.00 | 39.98 | 0 |
| ATOM | 4220 | NH1 | ARG | 642 | 62.097 | 46.291 | 81.199 | 1.00 | 44.40 | 0 |
| ATOM | 4223 | NH2 | ARG | 642 | 59.867 | 46.253 | 80.631 | 1.00 | 41.77 | 0 |
| ATOM | 4226 | C | ARG | 642 | 59.200 | 43.098 | 87.126 | 1.00 | 17.38 | 0 |
| ATOM | 4227 | O | ARG | 642 | 59.114 | 43.455 | 88.288 | 1.00 | 26.01 | 0 |
| ATOM | 4228 | N | ARG | 643 | 58.180 | 42.630 | 86.427 | 1.00 | 11.54 | 0 |
| ATOM | 4230 | CA | ARG | 643 | 56.869 | 42.500 | 87.018 | 1.00 | 11.54 | 0 |
| ATOM | 4231 | CB | ARG | 643 | 55.804 | 42.392 | 85.924 | 1.00 | 8.38 | 0 |
| ATOM | 4232 | CG | ARG | 643 | 55.526 | 43.749 | 85.304 | 1.00 | 8.38 | 0 |
| ATOM | 4233 | CD | ARG | 643 | 54.377 | 43.745 | 84.341 | 1.00 | 8.38 | 0 |
| ATOM | 4234 | NE | ARG | 643 | 53.121 | 43.351 | 84.949 | 1.00 | 8.38 | 0 |
| ATOM | 4236 | CZ | ARG | 643 | 51.939 | 43.569 | 84.390 | 1.00 | 8.38 | 0 |
| ATOM | 4237 | NH1 | ARG | 643 | 51.869 | 44.187 | 83.218 | 1.00 | 8.38 | 0 |
| ATOM | 4240 | NH2 | ARG | 643 | 50.825 | 43.157 | 84.985 | 1.00 | 8.38 | 0 |
| ATOM | 4243 | C | ARG | 643 | 56.841 | 41.304 | 87.939 | 1.00 | 11.54 | 0 |
| ATOM | 4244 | O | ARG | 643 | 56.156 | 41.309 | 88.969 | 1.00 | 8.38 | 0 |
| ATOM | 4245 | N | TYR | 644 | 57.606 | 40.285 | 87.565 | 1.00 | 2.00 | 0 |
| ATOM | 4247 | CA | TYR | 644 | 57.703 | 39.052 | 88.333 | 1.00 | 2.00 | 0 |
| ATOM | 4248 | CB | TYR | 644 | 56.784 | 37.972 | 87.741 | 1.00 | 14.67 | 0 |
| ATOM | 4249 | CG | TYR | 644 | 55.338 | 38.378 | 87.740 | 1.00 | 14.67 | 0 |
| ATOM | 4250 | CD1 | TYR | 644 | 54.695 | 38.723 | 86.554 | 1.00 | 14.67 | 0 |
| ATOM | 4251 | CE1 | TYR | 644 | 53.359 | 39.140 | 86.548 | 1.00 | 14.67 | 0 |
| ATOM | 4252 | CD2 | TYR | 644 | 54.617 | 38.453 | 88.922 | 1.00 | 14.67 | 0 |
| ATOM | 4253 | CE2 | TYR | 644 | 53.289 | 38.866 | 88.929 | 1.00 | 14.67 | 0 |
| ATOM | 4254 | CZ | TYR | 644 | 52.665 | 39.209 | 87.739 | 1.00 | 14.67 | 0 |
| ATOM | 4255 | OH | TYR | 644 | 51.349 | 39.629 | 87.741 | 1.00 | 14.67 | 0 |
| ATOM | 4257 | C | TYR | 644 | 59.160 | 38.598 | 88.330 | 1.00 | 2.00 | 0 |
| ATOM | 4258 | O | TYR | 644 | 60.062 | 39.412 | 88.575 | 1.00 | 14.67 | 0 |
| ATOM | 4259 | N | ASN | 645 | 59.399 | 37.321 | 88.028 | 1.00 | 2.00 | 0 |
| ATOM | 4261 | CA | ASN | 645 | 60.753 | 36.794 | 88.021 | 1.00 | 2.00 | 0 |
| ATOM | 4262 | CB | ASN | 645 | 61.103 | 36.147 | 89.379 | 1.00 | 16.19 | 0 |
| ATOM | 4263 | CG | ASN | 645 | 60.081 | 35.097 | 89.846 | 1.00 | 16.19 | 0 |
| ATOM | 4264 | OD1 | ASN | 645 | 59.466 | 34.378 | 89.054 | 1.00 | 16.19 | 0 |
| ATOM | 4265 | ND2 | ASN | 645 | 59.916 | 35.009 | 91.150 | 1.00 | 16.19 | 0 |
| ATOM | 4268 | C | ASN | 645 | 61.051 | 35.809 | 86.927 | 1.00 | 2.00 | 0 |
| ATOM | 4269 | O | ASN | 645 | 60.156 | 35.217 | 86.333 | 1.00 | 16.19 | 0 |
| ATOM | 4270 | N | ILE | 646 | 62.342 | 35.648 | 86.678 | 1.00 | 2.00 | 0 |
| ATOM | 4272 | CA | ILE | 646 | 62.856 | 34.716 | 85.689 | 1.00 | 2.00 | 0 |
| ATOM | 4273 | CB | ILE | 646 | 64.390 | 34.593 | 85.830 | 1.00 | 2.81 | 0 |
| ATOM | 4274 | CG2 | ILE | 646 | 64.917 | 33.316 | 85.196 | 1.00 | 2.59 | 0 |
| ATOM | 4275 | CG1 | ILE | 646 | 65.054 | 35.814 | 85.221 | 1.00 | 2.59 | 0 |
| ATOM | 4276 | CD1 | ILE | 646 | 66.492 | 35.955 | 85.666 | 1.00 | 8.72 | 0 |
| ATOM | 4277 | C | ILE | 646 | 62.214 | 33.339 | 85.886 | 1.00 | 2.00 | 0 |
| ATOM | 4278 | O | ILE | 646 | 61.875 | 32.675 | 84.915 | 1.00 | 6.42 | 0 |
| ATOM | 4279 | N | LYS | 647 | 62.031 | 32.918 | 87.137 | 1.00 | 2.00 | 0 |
| ATOM | 4281 | CA | LYS | 647 | 61.441 | 31.614 | 87.411 | 1.00 | 2.00 | 0 |
| ATOM | 4282 | CB | LYS | 647 | 61.347 | 31.387 | 88.920 | 1.00 | 79.29 | 0 |
| ATOM | 4283 | CG | LYS | 647 | 62.714 | 31.450 | 89.594 | 1.00 | 84.06 | 0 |
| ATOM | 4284 | CD | LYS | 647 | 63.727 | 30.622 | 88.804 | 1.00 | 88.57 | 0 |
| ATOM | 4285 | CE | LYS | 647 | 65.157 | 31.090 | 89.028 | 1.00 | 86.67 | 0 |
| ATOM | 4286 | NZ | LYS | 647 | 66.029 | 30.668 | 87.886 | 1.00 | 91.44 | 0 |
| ATOM | 4290 | C | LYS | 647 | 60.083 | 31.478 | 86.738 | 1.00 | 2.00 | 0 |
| ATOM | 4291 | O | LYS | 647 | 59.751 | 30.426 | 86.187 | 1.00 | 74.01 | 0 |
| ATOM | 4292 | N | LEU | 648 | 59.322 | 32.563 | 86.763 | 1.00 | 25.02 | 0 |
| ATOM | 4294 | CA | LEU | 648 | 58.012 | 32.599 | 86.136 | 1.00 | 23.81 | 0 |
| ATOM | 4295 | CB | LEU | 648 | 57.300 | 33.918 | 86.460 | 1.00 | 2.00 | 0 |
| ATOM | 4296 | CG | LEU | 648 | 55.802 | 33.929 | 86.178 | 1.00 | 2.00 | 0 |
| ATOM | 4297 | CD1 | LEU | 648 | 55.145 | 32.777 | 86.951 | 1.00 | 2.00 | 0 |
| ATOM | 4298 | CD2 | LEU | 648 | 55.206 | 35.262 | 86.574 | 1.00 | 2.00 | 0 |
| ATOM | 4299 | C | LEU | 648 | 58.245 | 32.495 | 84.637 | 1.00 | 28.16 | 0 |
| ATOM | 4300 | O | LEU | 648 | 57.562 | 31.751 | 83.934 | 1.00 | 2.00 | 0 |
| ATOM | 4301 | N | TRP | 649 | 59.227 | 33.243 | 84.151 | 1.00 | 42.46 | 0 |
| ATOM | 4303 | CA | TRP | 649 | 59.554 | 33.224 | 82.738 | 1.00 | 40.96 | 0 |

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|---|---|---|---|---|---|---|---|---|---|
| ATOM | 4304 | CB | TRP | 649 | 60.719 | 34.161 | 82.465 | 1.00 | 11.77 | 0 |
| ATOM | 4305 | CG | TRP | 649 | 61.206 | 34.051 | 81.081 | 1.00 | 14.98 | 0 |
| ATOM | 4306 | CD2 | TRP | 649 | 62.393 | 33.394 | 80.653 | 1.00 | 14.05 | 0 |
| ATOM | 4307 | CE2 | TRP | 649 | 62.460 | 33.527 | 79.246 | 1.00 | 12.39 | 0 |
| ATOM | 4308 | CE3 | TRP | 649 | 63.412 | 32.703 | 81.320 | 1.00 | 25.06 | 0 |
| ATOM | 4309 | CD1 | TRP | 649 | 60.607 | 34.546 | 79.951 | 1.00 | 17.81 | 0 |
| ATOM | 4310 | NE1 | TRP | 649 | 61.356 | 34.232 | 78.846 | 1.00 | 15.30 | 0 |
| ATOM | 4312 | CZ2 | TRP | 649 | 63.510 | 32.995 | 78.495 | 1.00 | 13.58 | 0 |
| ATOM | 4313 | CZ3 | TRP | 649 | 64.456 | 32.174 | 80.576 | 1.00 | 15.93 | 0 |
| ATOM | 4314 | CH2 | TRP | 649 | 64.497 | 32.323 | 79.175 | 1.00 | 16.10 | 0 |
| ATOM | 4315 | C | TRP | 649 | 59.900 | 31.802 | 82.292 | 1.00 | 40.42 | 0 |
| ATOM | 4316 | O | TRP | 649 | 59.392 | 31.315 | 81.285 | 1.00 | 12.84 | 0 |
| ATOM | 4317 | N | LYS | 650 | 60.748 | 31.138 | 83.069 | 1.00 | 2.00 | 0 |
| ATOM | 4319 | CA | LYS | 650 | 61.179 | 29.776 | 82.796 | 1.00 | 2.00 | 0 |
| ATOM | 4320 | CB | LYS | 650 | 62.257 | 29.371 | 83.795 | 1.00 | 19.18 | 0 |
| ATOM | 4321 | CG | LYS | 650 | 63.420 | 30.343 | 83.820 | 1.00 | 4.52 | 0 |
| ATOM | 4322 | CD | LYS | 650 | 64.541 | 29.898 | 84.718 | 1.00 | 3.83 | 0 |
| ATOM | 4323 | CE | LYS | 650 | 65.148 | 28.593 | 84.221 | 1.00 | 11.09 | 0 |
| ATOM | 4324 | NZ | LYS | 650 | 66.096 | 27.974 | 85.202 | 1.00 | 11.03 | 0 |
| ATOM | 4328 | C | LYS | 650 | 59.976 | 28.851 | 82.892 | 1.00 | 2.00 | 0 |
| ATOM | 4329 | O | LYS | 650 | 59.926 | 27.805 | 82.239 | 1.00 | 5.16 | 0 |
| ATOM | 4330 | N | THR | 651 | 58.997 | 29.234 | 83.702 | 1.00 | 10.53 | 0 |
| ATOM | 4332 | CA | THR | 651 | 57.792 | 28.422 | 83.838 | 1.00 | 14.10 | 0 |
| ATOM | 4333 | CB | THR | 651 | 56.915 | 28.882 | 85.038 | 1.00 | 23.55 | 0 |
| ATOM | 4334 | OG1 | THR | 651 | 57.613 | 28.622 | 86.268 | 1.00 | 23.26 | 0 |
| ATOM | 4336 | CG2 | THR | 651 | 55.582 | 28.150 | 85.047 | 1.00 | 24.53 | 0 |
| ATOM | 4337 | C | THR | 651 | 57.012 | 28.543 | 82.539 | 1.00 | 14.03 | 0 |
| ATOM | 4338 | O | THR | 651 | 56.599 | 27.534 | 81.951 | 1.00 | 23.01 | 0 |
| ATOM | 4339 | N | PHE | 652 | 56.837 | 29.779 | 82.082 | 1.00 | 2.00 | 0 |
| ATOM | 4341 | CA | PHE | 652 | 56.127 | 30.032 | 80.840 | 1.00 | 2.00 | 0 |
| ATOM | 4342 | CB | PHE | 652 | 56.225 | 31.511 | 80.440 | 1.00 | 2.00 | 0 |
| ATOM | 4343 | CG | PHE | 652 | 55.027 | 32.320 | 80.821 | 1.00 | 2.00 | 0 |
| ATOM | 4344 | CD1 | PHE | 652 | 55.164 | 33.486 | 81.536 | 1.00 | 2.00 | 0 |
| ATOM | 4345 | CD2 | PHE | 652 | 53.753 | 31.919 | 80.459 | 1.00 | 2.00 | 0 |
| ATOM | 4346 | CE1 | PHE | 652 | 54.039 | 34.245 | 81.884 | 1.00 | 2.00 | 0 |
| ATOM | 4347 | CE2 | PHE | 652 | 52.630 | 32.678 | 80.808 | 1.00 | 2.00 | 0 |
| ATOM | 4348 | CZ | PHE | 652 | 52.775 | 33.832 | 81.515 | 1.00 | 2.00 | 0 |
| ATOM | 4349 | C | PHE | 652 | 56.717 | 29.160 | 79.743 | 1.00 | 2.00 | 0 |
| ATOM | 4350 | O | PHE | 652 | 55.981 | 28.456 | 79.067 | 1.00 | 2.00 | 0 |
| ATOM | 4351 | N | THR | 653 | 58.039 | 29.143 | 79.608 | 1.00 | 2.00 | 0 |
| ATOM | 4353 | CA | THR | 653 | 58.631 | 28.344 | 78.552 | 1.00 | 2.00 | 0 |
| ATOM | 4354 | CB | THR | 653 | 60.126 | 28.538 | 78.429 | 1.00 | 2.14 | 0 |
| ATOM | 4355 | OG1 | THR | 653 | 60.804 | 27.592 | 79.255 | 1.00 | 2.14 | 0 |
| ATOM | 4357 | CG2 | THR | 653 | 60.499 | 29.945 | 78.787 | 1.00 | 2.14 | 0 |
| ATOM | 4358 | C | THR | 653 | 58.371 | 26.846 | 78.588 | 1.00 | 2.00 | 0 |
| ATOM | 4359 | O | THR | 653 | 58.452 | 26.196 | 77.555 | 1.00 | 4.20 | 0 |
| ATOM | 4360 | N | ASP | 654 | 58.064 | 26.271 | 79.743 | 1.00 | 2.00 | 0 |
| ATOM | 4362 | CA | ASP | 654 | 57.803 | 24.839 | 79.749 | 1.00 | 2.00 | 0 |
| ATOM | 4363 | CB | ASP | 654 | 58.083 | 24.225 | 81.119 | 1.00 | 25.83 | 0 |
| ATOM | 4364 | CG | ASP | 654 | 58.607 | 22.794 | 81.018 | 1.00 | 26.00 | 0 |
| ATOM | 4365 | OD1 | ASP | 654 | 59.163 | 22.420 | 79.960 | 1.00 | 29.22 | 0 |
| ATOM | 4366 | OD2 | ASP | 654 | 58.472 | 22.043 | 82.006 | 1.00 | 28.12 | 0 |
| ATOM | 4367 | C | ASP | 654 | 56.367 | 24.603 | 79.332 | 1.00 | 2.00 | 0 |
| ATOM | 4368 | O | ASP | 654 | 56.014 | 23.518 | 78.874 | 1.00 | 18.75 | 0 |
| ATOM | 4369 | N | CYS | 655 | 55.537 | 25.625 | 79.503 | 1.00 | 27.58 | 0 |
| ATOM | 4371 | CA | CYS | 655 | 54.146 | 25.546 | 79.095 | 1.00 | 27.58 | 0 |
| ATOM | 4372 | CB | CYS | 655 | 53.333 | 26.675 | 79.722 | 1.00 | 8.45 | 0 |
| ATOM | 4373 | SG | CYS | 655 | 51.756 | 26.978 | 78.901 | 1.00 | 8.45 | 0 |
| ATOM | 4374 | C | CYS | 655 | 54.162 | 25.683 | 77.575 | 1.00 | 27.58 | 0 |
| ATOM | 4375 | O | CYS | 655 | 53.565 | 24.863 | 76.865 | 1.00 | 8.45 | 0 |
| ATOM | 4376 | N | PHE | 656 | 54.871 | 26.709 | 77.088 | 1.00 | 7.64 | 0 |
| ATOM | 4378 | CA | PHE | 656 | 55.018 | 26.966 | 75.653 | 1.00 | 7.64 | 0 |
| ATOM | 4379 | CB | PHE | 656 | 55.967 | 28.145 | 75.402 | 1.00 | 12.44 | 0 |
| ATOM | 4380 | CG | PHE | 656 | 55.384 | 29.483 | 75.747 | 1.00 | 12.44 | 0 |
| ATOM | 4381 | CD1 | PHE | 656 | 54.073 | 29.591 | 76.242 | 1.00 | 12.44 | 0 |
| ATOM | 4382 | CD2 | PHE | 656 | 56.144 | 30.641 | 75.594 | 1.00 | 12.44 | 0 |
| ATOM | 4383 | CE1 | PHE | 656 | 53.525 | 30.840 | 76.585 | 1.00 | 12.44 | 0 |
| ATOM | 4384 | CE2 | PHE | 656 | 55.614 | 31.891 | 75.929 | 1.00 | 12.44 | 0 |

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|---|---|---|---|---|---|---|---|---|---|---|
| ATOM | 4385 | CZ | PHE | 656 | 54.296 | 31.990 | 76.430 | 1.00 | 12.44 | 0 |
| ATOM | 4386 | C | PHE | 656 | 55.564 | 25.705 | 74.961 | 1.00 | 7.64 | 0 |
| ATOM | 4387 | O | PHE | 656 | 55.033 | 25.274 | 73.940 | 1.00 | 12.44 | 0 |
| ATOM | 4388 | N | ASN | 657 | 56.595 | 25.099 | 75.543 | 1.00 | 2.00 | 0 |
| ATOM | 4390 | CA | ASN | 657 | 57.198 | 23.896 | 75.006 | 1.00 | 2.00 | 0 |
| ATOM | 4391 | CB | ASN | 657 | 58.353 | 23.425 | 75.892 | 1.00 | 12.64 | 0 |
| ATOM | 4392 | CG | ASN | 657 | 59.614 | 24.233 | 75.690 | 1.00 | 12.64 | 0 |
| ATOM | 4393 | OD1 | ASN | 657 | 59.564 | 25.404 | 75.350 | 1.00 | 12.64 | 0 |
| ATOM | 4394 | ND2 | ASN | 657 | 60.757 | 23.607 | 75.896 | 1.00 | 12.64 | 0 |
| ATOM | 4397 | C | ASN | 657 | 56.202 | 22.772 | 74.881 | 1.00 | 2.00 | 0 |
| ATOM | 4398 | O | ASN | 657 | 56.585 | 21.668 | 74.532 | 1.00 | 12.64 | 0 |
| ATOM | 4399 | N | CYS | 658 | 54.934 | 23.017 | 75.196 | 1.00 | 2.00 | 0 |
| ATOM | 4401 | CA | CYS | 658 | 53.930 | 21.964 | 75.080 | 1.00 | 2.00 | 0 |
| ATOM | 4402 | CB | CYS | 658 | 53.543 | 21.468 | 76.475 | 1.00 | 10.87 | 0 |
| ATOM | 4403 | SG | CYS | 658 | 55.004 | 20.919 | 77.397 | 1.00 | 10.87 | 0 |
| ATOM | 4404 | C | CYS | 658 | 52.708 | 22.390 | 74.258 | 1.00 | 2.00 | 0 |
| ATOM | 4405 | O | CYS | 658 | 51.726 | 21.659 | 74.162 | 1.00 | 10.87 | 0 |
| ATOM | 4406 | N | LEU | 659 | 52.799 | 23.560 | 73.634 | 1.00 | 11.17 | 0 |
| ATOM | 4408 | CA | LEU | 659 | 51.739 | 24.085 | 72.781 | 1.00 | 11.17 | 0 |
| ATOM | 4409 | CB | LEU | 659 | 51.998 | 25.569 | 72.470 | 1.00 | 2.00 | 0 |
| ATOM | 4410 | CG | LEU | 659 | 51.757 | 26.629 | 73.542 | 1.00 | 2.00 | 0 |
| ATOM | 4411 | CD1 | LEU | 659 | 52.286 | 27.965 | 73.123 | 1.00 | 2.00 | 0 |
| ATOM | 4412 | CD2 | LEU | 659 | 50.307 | 26.759 | 73.767 | 1.00 | 2.00 | 0 |
| ATOM | 4413 | C | LEU | 659 | 51.651 | 23.298 | 71.450 | 1.00 | 11.17 | 0 |
| ATOM | 4414 | O | LEU | 659 | 52.681 | 22.845 | 70.900 | 1.00 | 2.00 | 0 |
| ATOM | 4415 | N | PRO | 660 | 50.415 | 23.109 | 70.931 | 1.00 | 14.96 | 0 |
| ATOM | 4416 | CD | PRO | 660 | 49.134 | 23.535 | 71.523 | 1.00 | 2.00 | 0 |
| ATOM | 4417 | CA | PRO | 660 | 50.166 | 22.398 | 69.680 | 1.00 | 14.96 | 0 |
| ATOM | 4418 | CB | PRO | 660 | 48.640 | 22.381 | 69.590 | 1.00 | 2.00 | 0 |
| ATOM | 4419 | CG | PRO | 660 | 48.194 | 22.472 | 71.028 | 1.00 | 2.00 | 0 |
| ATOM | 4420 | C | PRO | 660 | 50.796 | 23.248 | 68.579 | 1.00 | 14.96 | 0 |
| ATOM | 4421 | O | PRO | 660 | 50.888 | 24.474 | 68.709 | 1.00 | 2.00 | 0 |
| ATOM | 4422 | N | ILE | 661 | 51.195 | 22.603 | 67.488 | 1.00 | 28.66 | 0 |
| ATOM | 4424 | CA | ILE | 661 | 51.880 | 23.279 | 66.397 | 1.00 | 30.55 | 0 |
| ATOM | 4425 | CB | ILE | 661 | 53.126 | 22.480 | 66.036 | 1.00 | 19.83 | 0 |
| ATOM | 4426 | CG2 | ILE | 661 | 54.064 | 22.432 | 67.228 | 1.00 | 22.82 | 0 |
| ATOM | 4427 | CG1 | ILE | 661 | 52.728 | 21.050 | 65.669 | 1.00 | 24.89 | 0 |
| ATOM | 4428 | CD1 | ILE | 661 | 53.896 | 20.161 | 65.299 | 1.00 | 29.65 | 0 |
| ATOM | 4429 | C | ILE | 661 | 51.074 | 23.577 | 65.132 | 1.00 | 29.24 | 0 |
| ATOM | 4430 | O | ILE | 661 | 51.428 | 24.493 | 64.372 | 1.00 | 20.63 | 0 |
| ATOM | 4431 | N | ALA | 662 | 50.004 | 22.810 | 64.915 | 1.00 | 22.79 | 0 |
| ATOM | 4433 | CA | ALA | 662 | 49.112 | 22.970 | 63.751 | 1.00 | 22.79 | 0 |
| ATOM | 4434 | CB | ALA | 662 | 49.652 | 22.187 | 62.529 | 1.00 | 2.00 | 0 |
| ATOM | 4435 | C | ALA | 662 | 47.683 | 22.507 | 64.086 | 1.00 | 22.79 | 0 |
| ATOM | 4436 | O | ALA | 662 | 47.439 | 21.887 | 65.139 | 1.00 | 2.00 | 0 |
| ATOM | 4437 | N | ALA | 663 | 46.739 | 22.816 | 63.205 | 1.00 | 2.00 | 0 |
| ATOM | 4439 | CA | ALA | 663 | 45.347 | 22.438 | 63.410 | 1.00 | 2.00 | 0 |
| ATOM | 4440 | CB | ALA | 663 | 44.599 | 23.535 | 64.124 | 1.00 | 18.31 | 0 |
| ATOM | 4441 | C | ALA | 663 | 44.748 | 22.223 | 62.053 | 1.00 | 2.00 | 0 |
| ATOM | 4442 | O | ALA | 663 | 45.323 | 22.623 | 61.041 | 1.00 | 22.14 | 0 |
| ATOM | 4443 | N | ILE | 664 | 43.600 | 21.565 | 62.028 | 1.00 | 16.69 | 0 |
| ATOM | 4445 | CA | ILE | 664 | 42.892 | 21.300 | 60.788 | 1.00 | 16.69 | 0 |
| ATOM | 4446 | CB | ILE | 664 | 43.240 | 19.885 | 60.208 | 1.00 | 9.81 | 0 |
| ATOM | 4447 | CG2 | ILE | 664 | 42.396 | 19.597 | 58.976 | 1.00 | 9.81 | 0 |
| ATOM | 4448 | CG1 | ILE | 664 | 44.724 | 19.810 | 59.819 | 1.00 | 9.81 | 0 |
| ATOM | 4449 | CD1 | ILE | 664 | 45.161 | 18.450 | 59.316 | 1.00 | 9.81 | 0 |
| ATOM | 4450 | C | ILE | 664 | 41.408 | 21.397 | 61.118 | 1.00 | 16.69 | 0 |
| ATOM | 4451 | O | ILE | 664 | 40.880 | 20.603 | 61.899 | 1.00 | 9.81 | 0 |
| ATOM | 4452 | N | VAL | 665 | 40.754 | 22.408 | 60.561 | 1.00 | 14.09 | 0 |
| ATOM | 4454 | CA | VAL | 665 | 39.332 | 22.608 | 60.777 | 1.00 | 14.09 | 0 |
| ATOM | 4455 | CB | VAL | 665 | 38.954 | 24.091 | 60.742 | 1.00 | 2.00 | 0 |
| ATOM | 4456 | CG1 | VAL | 665 | 37.450 | 24.239 | 60.710 | 1.00 | 2.00 | 0 |
| ATOM | 4457 | CG2 | VAL | 665 | 39.500 | 24.788 | 61.950 | 1.00 | 2.00 | 0 |
| ATOM | 4458 | C | VAL | 665 | 38.509 | 21.873 | 59.729 | 1.00 | 14.09 | 0 |
| ATOM | 4459 | O | VAL | 665 | 38.768 | 21.972 | 58.524 | 1.00 | 2.00 | 0 |
| ATOM | 4460 | N | ASP | 666 | 37.517 | 21.137 | 60.219 | 1.00 | 2.00 | 0 |
| ATOM | 4462 | CA | ASP | 666 | 36.595 | 20.345 | 59.407 | 1.00 | 2.00 | 0 |
| ATOM | 4463 | CB | ASP | 666 | 35.443 | 21.235 | 58.933 | 1.00 | 65.64 | 0 |

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|---|---|---|---|---|---|---|---|---|---|---|
| ATOM | 4464 | CG | ASP | 666 | 34.545 | 21.675 | 60.081 | 1.00 | 73.26 | 0 |
| ATOM | 4465 | OD1 | ASP | 666 | 33.763 | 20.838 | 60.578 | 1.00 | 71.65 | 0 |
| ATOM | 4466 | OD2 | ASP | 666 | 34.623 | 22.851 | 60.493 | 1.00 | 75.52 | 0 |
| ATOM | 4467 | C | ASP | 666 | 37.234 | 19.577 | 58.235 | 1.00 | 2.00 | 0 |
| ATOM | 4468 | O | ASP | 666 | 36.648 | 19.467 | 57.158 | 1.00 | 57.66 | 0 |
| ATOM | 4469 | N | GLU | 667 | 38.439 | 19.048 | 58.472 | 1.00 | 17.20 | 0 |
| ATOM | 4471 | CA | GLU | 667 | 39.203 | 18.270 | 57.489 | 1.00 | 17.69 | 0 |
| ATOM | 4472 | CB | GLU | 667 | 38.455 | 16.981 | 57.138 | 1.00 | 42.87 | 0 |
| ATOM | 4473 | CG | GLU | 667 | 38.170 | 16.101 | 58.345 | 1.00 | 52.20 | 0 |
| ATOM | 4474 | CD | GLU | 667 | 37.457 | 14.806 | 57.988 | 1.00 | 53.85 | 0 |
| ATOM | 4475 | OE1 | GLU | 667 | 36.222 | 14.717 | 58.211 | 1.00 | 51.15 | 0 |
| ATOM | 4476 | OE2 | GLU | 667 | 38.139 | 13.877 | 57.494 | 1.00 | 55.67 | 0 |
| ATOM | 4477 | C | GLU | 667 | 39.584 | 19.015 | 56.207 | 1.00 | 17.24 | 0 |
| ATOM | 4478 | O | GLU | 667 | 40.146 | 18.421 | 55.286 | 1.00 | 34.30 | 0 |
| ATOM | 4479 | N | LYS | 668 | 39.314 | 20.319 | 56.172 | 1.00 | 26.53 | 0 |
| ATOM | 4481 | CA | LYS | 668 | 39.615 | 21.133 | 55.002 | 1.00 | 20.22 | 0 |
| ATOM | 4482 | CB | LYS | 668 | 38.318 | 21.709 | 54.410 | 1.00 | 13.48 | 0 |
| ATOM | 4483 | CG | LYS | 668 | 37.383 | 20.628 | 53.859 | 1.00 | 13.48 | 0 |
| ATOM | 4484 | CD | LYS | 668 | 38.119 | 19.779 | 52.819 | 1.00 | 13.48 | 0 |
| ATOM | 4485 | CE | LYS | 668 | 37.341 | 18.551 | 52.398 | 1.00 | 16.60 | 0 |
| ATOM | 4486 | NZ | LYS | 668 | 38.247 | 17.564 | 51.739 | 1.00 | 18.66 | 0 |
| ATOM | 4490 | C | LYS | 668 | 40.636 | 22.244 | 55.240 | 1.00 | 19.61 | 0 |
| ATOM | 4491 | O | LYS | 668 | 41.676 | 22.264 | 54.584 | 1.00 | 13.48 | 0 |
| ATOM | 4492 | N | ILE | 669 | 40.356 | 23.166 | 56.158 | 1.00 | 2.00 | 0 |
| ATOM | 4494 | CA | ILE | 669 | 41.295 | 24.263 | 56.424 | 1.00 | 2.00 | 0 |
| ATOM | 4495 | CB | ILE | 669 | 40.617 | 25.456 | 57.183 | 1.00 | 2.00 | 0 |
| ATOM | 4496 | CG2 | ILE | 669 | 41.521 | 26.680 | 57.166 | 1.00 | 2.00 | 0 |
| ATOM | 4497 | CG1 | ILE | 669 | 39.298 | 25.839 | 56.518 | 1.00 | 2.00 | 0 |
| ATOM | 4498 | CD1 | ILE | 669 | 38.581 | 26.960 | 57.189 | 1.00 | 2.00 | 0 |
| ATOM | 4499 | C | ILE | 669 | 42.439 | 23.721 | 57.279 | 1.00 | 2.00 | 0 |
| ATOM | 4500 | O | ILE | 669 | 42.201 | 23.034 | 58.269 | 1.00 | 2.00 | 0 |
| ATOM | 4501 | N | PHE | 670 | 43.673 | 24.010 | 56.892 | 1.00 | 2.00 | 0 |
| ATOM | 4503 | CA | PHE | 670 | 44.841 | 23.551 | 57.641 | 1.00 | 2.00 | 0 |
| ATOM | 4504 | CB | PHE | 670 | 45.804 | 22.801 | 56.718 | 1.00 | 2.00 | 0 |
| ATOM | 4505 | CG | PHE | 670 | 47.182 | 22.614 | 57.291 | 1.00 | 2.00 | 0 |
| ATOM | 4506 | CD1 | PHE | 670 | 47.503 | 21.473 | 58.007 | 1.00 | 2.00 | 0 |
| ATOM | 4507 | CD2 | PHE | 670 | 48.163 | 23.569 | 57.093 | 1.00 | 2.00 | 0 |
| ATOM | 4508 | CE1 | PHE | 670 | 48.769 | 21.288 | 58.506 | 1.00 | 2.00 | 0 |
| ATOM | 4509 | CE2 | PHE | 670 | 49.436 | 23.384 | 57.596 | 1.00 | 2.00 | 0 |
| ATOM | 4510 | CZ | PHE | 670 | 49.737 | 22.241 | 58.302 | 1.00 | 2.00 | 0 |
| ATOM | 4511 | C | PHE | 670 | 45.528 | 24.780 | 58.190 | 1.00 | 2.00 | 0 |
| ATOM | 4512 | O | PHE | 670 | 45.901 | 25.652 | 57.421 | 1.00 | 2.00 | 0 |
| ATOM | 4513 | N | CYS | 671 | 45.725 | 24.839 | 59.501 | 1.00 | 2.00 | 0 |
| ATOM | 4515 | CA | CYS | 671 | 46.353 | 25.992 | 60.120 | 1.00 | 2.00 | 0 |
| ATOM | 4516 | CB | CYS | 671 | 45.395 | 26.596 | 61.136 | 1.00 | 14.45 | 0 |
| ATOM | 4517 | SG | CYS | 671 | 43.708 | 26.779 | 60.568 | 1.00 | 25.33 | 0 |
| ATOM | 4518 | C | CYS | 671 | 47.685 | 25.701 | 60.816 | 1.00 | 2.00 | 0 |
| ATOM | 4519 | O | CYS | 671 | 47.921 | 24.589 | 61.310 | 1.00 | 8.01 | 0 |
| ATOM | 4520 | N | CYS | 672 | 48.546 | 26.714 | 60.845 | 1.00 | 2.00 | 0 |
| ATOM | 4522 | CA | CYS | 672 | 49.845 | 26.666 | 61.515 | 1.00 | 2.00 | 0 |
| ATOM | 4523 | CB | CYS | 672 | 50.826 | 25.741 | 60.792 | 1.00 | 9.00 | 0 |
| ATOM | 4524 | SG | CYS | 672 | 51.494 | 26.372 | 59.265 | 1.00 | 11.24 | 0 |
| ATOM | 4525 | C | CYS | 672 | 50.336 | 28.122 | 61.525 | 1.00 | 2.00 | 0 |
| ATOM | 4526 | O | CYS | 672 | 49.751 | 28.963 | 60.850 | 1.00 | 9.00 | 0 |
| ATOM | 4527 | N | HIS | 673 | 51.369 | 28.440 | 62.300 | 1.00 | 17.94 | 0 |
| ATOM | 4529 | CA | HIS | 673 | 51.855 | 29.817 | 62.360 | 1.00 | 17.94 | 0 |
| ATOM | 4530 | C | HIS | 673 | 52.456 | 30.359 | 61.065 | 1.00 | 17.94 | 0 |
| ATOM | 4531 | O | HIS | 673 | 51.960 | 31.349 | 60.514 | 1.00 | 2.00 | 0 |
| ATOM | 4532 | CB | HIS | 673 | 52.894 | 29.965 | 63.459 | 1.00 | 2.00 | 0 |
| ATOM | 4533 | CG | HIS | 673 | 53.283 | 31.383 | 63.724 | 1.00 | 2.00 | 0 |
| ATOM | 4534 | ND1 | HIS | 673 | 52.388 | 32.377 | 64.033 | 1.00 | 2.00 | 0 |
| ATOM | 4536 | CD2 | HIS | 673 | 54.503 | 31.975 | 63.718 | 1.00 | 2.00 | 0 |
| ATOM | 4537 | NE2 | HIS | 673 | 54.371 | 33.330 | 64.019 | 1.00 | 2.00 | 0 |
| ATOM | 4538 | CE1 | HIS | 673 | 53.072 | 33.512 | 64.199 | 1.00 | 2.00 | 0 |
| ATOM | 4539 | N | GLY | 674 | 53.545 | 29.721 | 60.626 | 1.00 | 2.00 | 0 |
| ATOM | 4541 | CA | GLY | 674 | 54.260 | 30.101 | 59.417 | 1.00 | 2.00 | 0 |
| ATOM | 4542 | C | GLY | 674 | 53.773 | 29.407 | 58.163 | 1.00 | 2.00 | 0 |
| ATOM | 4543 | O | GLY | 674 | 53.410 | 30.063 | 57.203 | 1.00 | 11.62 | 0 |

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|---|---|---|---|---|---|---|---|---|---|---|
| ATOM | 4544 | N | GLY | 675 | 53.759 | 28.087 | 58.136 | 1.00 | 6.25 | 0 |
| ATOM | 4546 | CA | GLY | 675 | 53.286 | 27.440 | 56.931 | 1.00 | 6.25 | 0 |
| ATOM | 4547 | C | GLY | 675 | 53.823 | 26.061 | 56.604 | 1.00 | 6.25 | 0 |
| ATOM | 4548 | O | GLY | 675 | 53.867 | 25.173 | 57.452 | 1.00 | 28.15 | 0 |
| ATOM | 4549 | N | LEU | 676 | 54.241 | 25.883 | 55.356 | 1.00 | 2.00 | 0 |
| ATOM | 4551 | CA | LEU | 676 | 54.723 | 24.591 | 54.886 | 1.00 | 2.00 | 0 |
| ATOM | 4552 | CB | LEU | 676 | 54.336 | 24.409 | 53.418 | 1.00 | 2.00 | 0 |
| ATOM | 4553 | CG | LEU | 676 | 52.827 | 24.625 | 53.244 | 1.00 | 2.00 | 0 |
| ATOM | 4554 | CD1 | LEU | 676 | 52.412 | 24.556 | 51.777 | 1.00 | 2.00 | 0 |
| ATOM | 4555 | CD2 | LEU | 676 | 52.100 | 23.575 | 54.075 | 1.00 | 2.00 | 0 |
| ATOM | 4556 | C | LEU | 676 | 56.207 | 24.333 | 55.095 | 1.00 | 2.00 | 0 |
| ATOM | 4557 | O | LEU | 676 | 56.981 | 25.248 | 55.381 | 1.00 | 2.00 | 0 |
| ATOM | 4558 | N | SER | 677 | 56.582 | 23.069 | 54.945 | 1.00 | 12.63 | 0 |
| ATOM | 4560 | CA | SER | 677 | 57.946 | 22.617 | 55.141 | 1.00 | 12.63 | 0 |
| ATOM | 4561 | CB | SER | 677 | 58.083 | 21.985 | 56.539 | 1.00 | 2.43 | 0 |
| ATOM | 4562 | OG | SER | 677 | 59.248 | 21.192 | 56.649 | 1.00 | 2.03 | 0 |
| ATOM | 4564 | C | SER | 677 | 58.247 | 21.556 | 54.095 | 1.00 | 12.63 | 0 |
| ATOM | 4565 | O | SER | 677 | 57.405 | 20.684 | 53.838 | 1.00 | 10.72 | 0 |
| ATOM | 4566 | N | PRO | 678 | 59.449 | 21.605 | 53.484 | 1.00 | 2.00 | 0 |
| ATOM | 4567 | CD | PRO | 678 | 60.474 | 22.638 | 53.681 | 1.00 | 15.59 | 0 |
| ATOM | 4568 | CA | PRO | 678 | 59.887 | 20.647 | 52.469 | 1.00 | 2.00 | 0 |
| ATOM | 4569 | CB | PRO | 678 | 61.329 | 21.076 | 52.184 | 1.00 | 15.59 | 0 |
| ATOM | 4570 | CG | PRO | 678 | 61.299 | 22.517 | 52.416 | 1.00 | 15.59 | 0 |
| ATOM | 4571 | C | PRO | 678 | 59.859 | 19.234 | 53.032 | 1.00 | 2.00 | 0 |
| ATOM | 4572 | O | PRO | 678 | 59.990 | 18.269 | 52.293 | 1.00 | 15.59 | 0 |
| ATOM | 4573 | N | ASP | 679 | 59.685 | 19.112 | 54.342 | 1.00 | 2.00 | 0 |
| ATOM | 4575 | CA | ASP | 679 | 59.687 | 17.813 | 54.992 | 1.00 | 2.00 | 0 |
| ATOM | 4576 | CB | ASP | 679 | 60.510 | 17.926 | 56.271 | 1.00 | 26.28 | 0 |
| ATOM | 4577 | CG | ASP | 679 | 61.766 | 18.758 | 56.073 | 1.00 | 24.05 | 0 |
| ATOM | 4578 | OD1 | ASP | 679 | 62.687 | 18.269 | 55.383 | 1.00 | 32.92 | 0 |
| ATOM | 4579 | OD2 | ASP | 679 | 61.826 | 19.902 | 56.586 | 1.00 | 28.53 | 0 |
| ATOM | 4580 | C | ASP | 679 | 58.303 | 17.278 | 55.314 | 1.00 | 2.00 | 0 |
| ATOM | 4581 | O | ASP | 679 | 58.129 | 16.094 | 55.576 | 1.00 | 24.04 | 0 |
| ATOM | 4582 | N | LEU | 680 | 57.315 | 18.149 | 55.279 | 1.00 | 2.00 | 0 |
| ATOM | 4584 | CA | LEU | 680 | 55.970 | 17.747 | 55.622 | 1.00 | 2.00 | 0 |
| ATOM | 4585 | CB | LEU | 680 | 55.147 | 19.000 | 55.916 | 1.00 | 4.45 | 0 |
| ATOM | 4586 | CG | LEU | 680 | 53.683 | 18.788 | 56.262 | 1.00 | 2.86 | 0 |
| ATOM | 4587 | CD1 | LEU | 680 | 53.540 | 17.791 | 57.398 | 1.00 | 2.86 | 0 |
| ATOM | 4588 | CD2 | LEU | 680 | 53.085 | 20.134 | 56.582 | 1.00 | 2.86 | 0 |
| ATOM | 4589 | C | LEU | 680 | 55.262 | 16.862 | 54.588 | 1.00 | 2.00 | 0 |
| ATOM | 4590 | O | LEU | 680 | 54.421 | 17.331 | 53.814 | 1.00 | 15.95 | 0 |
| ATOM | 4591 | N | GLN | 681 | 55.588 | 15.578 | 54.561 | 1.00 | 2.00 | 0 |
| ATOM | 4593 | CA | GLN | 681 | 54.922 | 14.686 | 53.611 | 1.00 | 2.00 | 0 |
| ATOM | 4594 | CB | GLN | 681 | 55.719 | 13.410 | 53.385 | 1.00 | 36.99 | 0 |
| ATOM | 4595 | CG | GLN | 681 | 57.097 | 13.620 | 52.863 | 1.00 | 36.99 | 0 |
| ATOM | 4596 | CD | GLN | 681 | 57.716 | 12.321 | 52.468 | 1.00 | 36.99 | 0 |
| ATOM | 4597 | OE1 | GLN | 681 | 57.589 | 11.894 | 51.326 | 1.00 | 36.99 | 0 |
| ATOM | 4598 | NE2 | GLN | 681 | 58.377 | 11.663 | 53.409 | 1.00 | 36.99 | 0 |
| ATOM | 4601 | C | GLN | 681 | 53.551 | 14.319 | 54.159 | 1.00 | 2.00 | 0 |
| ATOM | 4602 | O | GLN | 681 | 52.547 | 14.392 | 53.445 | 1.00 | 11.55 | 0 |
| ATOM | 4603 | N | SER | 682 | 53.505 | 13.923 | 55.423 | 1.00 | 39.00 | 0 |
| ATOM | 4605 | CA | SER | 682 | 52.238 | 13.566 | 56.027 | 1.00 | 42.03 | 0 |
| ATOM | 4606 | CB | SER | 682 | 52.131 | 12.048 | 56.224 | 1.00 | 2.00 | 0 |
| ATOM | 4607 | OG | SER | 682 | 53.198 | 11.507 | 56.993 | 1.00 | 2.00 | 0 |
| ATOM | 4609 | C | SER | 682 | 52.003 | 14.284 | 57.343 | 1.00 | 38.75 | 0 |
| ATOM | 4610 | O | SER | 682 | 52.941 | 14.742 | 58.009 | 1.00 | 2.00 | 0 |
| ATOM | 4611 | N | MET | 683 | 50.730 | 14.397 | 57.698 | 1.00 | 15.16 | 0 |
| ATOM | 4613 | CA | MET | 683 | 50.338 | 15.029 | 58.938 | 1.00 | 15.16 | 0 |
| ATOM | 4614 | CB | MET | 683 | 48.820 | 15.069 | 59.044 | 1.00 | 11.68 | 0 |
| ATOM | 4615 | CG | MET | 683 | 48.099 | 15.565 | 57.799 | 1.00 | 12.75 | 0 |
| ATOM | 4616 | SD | MET | 683 | 48.197 | 17.328 | 57.477 | 1.00 | 11.68 | 0 |
| ATOM | 4617 | CE | MET | 683 | 49.486 | 17.429 | 56.200 | 1.00 | 12.61 | 0 |
| ATOM | 4618 | C | MET | 683 | 50.906 | 14.131 | 60.024 | 1.00 | 15.16 | 0 |
| ATOM | 4619 | O | MET | 683 | 51.215 | 14.585 | 61.116 | 1.00 | 15.01 | 0 |
| ATOM | 4620 | N | GLU | 684 | 51.050 | 12.848 | 59.705 | 1.00 | 40.22 | 0 |
| ATOM | 4622 | CA | GLU | 684 | 51.597 | 11.881 | 60.644 | 1.00 | 41.85 | 0 |
| ATOM | 4623 | CB | GLU | 684 | 52.007 | 10.594 | 59.937 | 1.00 | 63.04 | 0 |
| ATOM | 4624 | CG | GLU | 684 | 52.850 | 9.689 | 60.823 | 1.00 | 72.94 | 0 |

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|---|---|---|---|---|---|---|---|---|---|---|
| ATOM | 4625 | CD | GLU | 684 | 53.111 | 8.343 | 60.206 | 1.00 | 77.43 | 0 |
| ATOM | 4626 | OE1 | GLU | 684 | 52.139 | 7.716 | 59.730 | 1.00 | 77.96 | 0 |
| ATOM | 4627 | OE2 | GLU | 684 | 54.285 | 7.909 | 60.201 | 1.00 | 79.67 | 0 |
| ATOM | 4628 | C | GLU | 684 | 52.819 | 12.471 | 61.297 | 1.00 | 40.42 | 0 |
| ATOM | 4629 | O | GLU | 684 | 52.932 | 12.495 | 62.517 | 1.00 | 62.00 | 0 |
| ATOM | 4630 | N | GLN | 685 | 53.727 | 12.959 | 60.466 | 1.00 | 2.00 | 0 |
| ATOM | 4632 | CA | GLN | 685 | 54.945 | 13.559 | 60.952 | 1.00 | 2.00 | 0 |
| ATOM | 4633 | CB | GLN | 685 | 55.703 | 14.200 | 59.797 | 1.00 | 52.45 | 0 |
| ATOM | 4634 | CG | GLN | 685 | 56.162 | 13.188 | 58.775 | 1.00 | 57.01 | 0 |
| ATOM | 4635 | CD | GLN | 685 | 56.779 | 13.832 | 57.574 | 1.00 | 58.68 | 0 |
| ATOM | 4636 | OE1 | GLN | 685 | 56.258 | 13.728 | 56.471 | 1.00 | 68.68 | 0 |
| ATOM | 4637 | NE2 | GLN | 685 | 57.895 | 14.510 | 57.778 | 1.00 | 65.77 | 0 |
| ATOM | 4640 | C | GLN | 685 | 54.627 | 14.585 | 62.029 | 1.00 | 2.00 | 0 |
| ATOM | 4641 | O | GLN | 685 | 55.312 | 14.631 | 63.056 | 1.00 | 54.77 | 0 |
| ATOM | 4642 | N | ILE | 686 | 53.579 | 15.387 | 61.816 | 1.00 | 16.80 | 0 |
| ATOM | 4644 | CA | ILE | 686 | 53.179 | 16.391 | 62.807 | 1.00 | 14.42 | 0 |
| ATOM | 4645 | CB | ILE | 686 | 51.990 | 17.270 | 62.307 | 1.00 | 2.00 | 0 |
| ATOM | 4646 | CG2 | ILE | 686 | 51.754 | 18.441 | 63.247 | 1.00 | 2.00 | 0 |
| ATOM | 4647 | CG1 | ILE | 686 | 52.304 | 17.869 | 60.944 | 1.00 | 2.00 | 0 |
| ATOM | 4648 | CD1 | ILE | 686 | 51.139 | 18.668 | 60.369 | 1.00 | 2.00 | 0 |
| ATOM | 4649 | C | ILE | 686 | 52.761 | 15.633 | 64.079 | 1.00 | 13.83 | 0 |
| ATOM | 4650 | O | ILE | 686 | 53.289 | 15.884 | 65.165 | 1.00 | 2.00 | 0 |
| ATOM | 4651 | N | ARG | 687 | 51.856 | 14.669 | 63.914 | 1.00 | 3.14 | 0 |
| ATOM | 4653 | CA | ARG | 687 | 51.367 | 13.855 | 65.027 | 1.00 | 3.14 | 0 |
| ATOM | 4654 | CB | ARG | 687 | 50.307 | 12.835 | 64.564 | 1.00 | 23.50 | 0 |
| ATOM | 4655 | CG | ARG | 687 | 49.266 | 13.324 | 63.559 | 1.00 | 26.96 | 0 |
| ATOM | 4656 | CD | ARG | 687 | 48.288 | 12.211 | 63.083 | 1.00 | 35.95 | 0 |
| ATOM | 4657 | NE | ARG | 687 | 48.878 | 11.199 | 62.190 | 1.00 | 41.22 | 0 |
| ATOM | 4659 | CZ | ARG | 687 | 49.583 | 10.138 | 62.594 | 1.00 | 45.24 | 0 |
| ATOM | 4660 | NH1 | ARG | 687 | 50.062 | 9.283 | 61.702 | 1.00 | 43.65 | 0 |
| ATOM | 4663 | NH2 | ARG | 687 | 49.827 | 9.922 | 63.887 | 1.00 | 36.26 | 0 |
| ATOM | 4666 | C | ARG | 687 | 52.504 | 13.060 | 65.665 | 1.00 | 3.14 | 0 |
| ATOM | 4667 | O | ARG | 687 | 52.260 | 12.327 | 66.613 | 1.00 | 18.08 | 0 |
| ATOM | 4668 | N | ARG | 688 | 53.722 | 13.157 | 65.136 | 1.00 | 11.08 | 0 |
| ATOM | 4670 | CA | ARG | 688 | 54.841 | 12.402 | 65.694 | 1.00 | 10.97 | 0 |
| ATOM | 4671 | CB | ARG | 688 | 55.576 | 11.624 | 64.595 | 1.00 | 52.72 | 0 |
| ATOM | 4672 | CG | ARG | 688 | 54.794 | 10.485 | 63.995 | 1.00 | 52.20 | 0 |
| ATOM | 4673 | CD | ARG | 688 | 54.421 | 9.463 | 65.035 | 1.00 | 55.85 | 0 |
| ATOM | 4674 | NE | ARG | 688 | 53.634 | 8.372 | 64.468 | 1.00 | 50.50 | 0 |
| ATOM | 4676 | CZ | ARG | 688 | 54.145 | 7.254 | 63.956 | 1.00 | 54.57 | 0 |
| ATOM | 4677 | NH1 | ARG | 688 | 53.335 | 6.326 | 63.465 | 1.00 | 53.02 | 0 |
| ATOM | 4680 | NH2 | ARG | 688 | 55.457 | 7.056 | 63.931 | 1.00 | 50.07 | 0 |
| ATOM | 4683 | C | ARG | 688 | 55.853 | 13.257 | 66.457 | 1.00 | 9.37 | 0 |
| ATOM | 4684 | O | ARG | 688 | 56.771 | 12.719 | 67.084 | 1.00 | 54.51 | 0 |
| ATOM | 4685 | N | ILE | 689 | 55.698 | 14.576 | 66.398 | 1.00 | 38.26 | 0 |
| ATOM | 4687 | CA | ILE | 689 | 56.614 | 15.487 | 67.081 | 1.00 | 36.62 | 0 |
| ATOM | 4688 | CB | ILE | 689 | 56.319 | 16.952 | 66.673 | 1.00 | 2.00 | 0 |
| ATOM | 4689 | CG2 | ILE | 689 | 57.248 | 17.901 | 67.399 | 1.00 | 2.00 | 0 |
| ATOM | 4690 | CG1 | ILE | 689 | 56.493 | 17.119 | 65.160 | 1.00 | 2.00 | 0 |
| ATOM | 4691 | CD1 | ILE | 689 | 56.670 | 18.556 | 64.711 | 1.00 | 2.00 | 0 |
| ATOM | 4692 | C | ILE | 689 | 56.552 | 15.347 | 68.620 | 1.00 | 42.28 | 0 |
| ATOM | 4693 | O | ILE | 689 | 55.468 | 15.462 | 69.226 | 1.00 | 2.00 | 0 |
| ATOM | 4694 | N | MET | 690 | 57.710 | 15.084 | 69.242 | 1.00 | 2.00 | 0 |
| ATOM | 4696 | CA | MET | 690 | 57.794 | 14.930 | 70.704 | 1.00 | 2.00 | 0 |
| ATOM | 4697 | CB | MET | 690 | 59.204 | 14.516 | 71.138 | 1.00 | 31.54 | 0 |
| ATOM | 4698 | CG | MET | 690 | 59.657 | 13.160 | 70.616 | 1.00 | 36.54 | 0 |
| ATOM | 4699 | SD | MET | 690 | 58.703 | 11.742 | 71.207 | 1.00 | 43.14 | 0 |
| ATOM | 4700 | CE | MET | 690 | 59.784 | 10.411 | 70.721 | 1.00 | 40.70 | 0 |
| ATOM | 4701 | C | MET | 690 | 57.491 | 16.313 | 71.227 | 1.00 | 2.00 | 0 |
| ATOM | 4702 | O | MET | 690 | 58.189 | 17.269 | 70.864 | 1.00 | 21.20 | 0 |
| ATOM | 4703 | N | ARG | 691 | 56.489 | 16.441 | 72.092 | 1.00 | 59.62 | 0 |
| ATOM | 4705 | CA | ARG | 691 | 56.135 | 17.780 | 72.507 | 1.00 | 65.12 | 0 |
| ATOM | 4706 | CB | ARG | 691 | 54.678 | 17.879 | 72.869 | 1.00 | 2.00 | 0 |
| ATOM | 4707 | CG | ARG | 691 | 54.077 | 19.116 | 72.206 | 1.00 | 2.00 | 0 |
| ATOM | 4708 | CD | ARG | 691 | 52.598 | 19.166 | 72.384 | 1.00 | 2.00 | 0 |
| ATOM | 4709 | NE | ARG | 691 | 52.082 | 17.820 | 72.551 | 1.00 | 2.00 | 0 |
| ATOM | 4711 | CZ | ARG | 691 | 50.832 | 17.540 | 72.862 | 1.00 | 2.00 | 0 |
| ATOM | 4712 | NH1 | ARG | 691 | 49.957 | 18.525 | 73.024 | 1.00 | 2.00 | 0 |

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|---|---|---|---|---|---|---|---|---|---|---|
| ATOM | 4715 | NH2 | ARG | 691 | 50.482 | 16.273 | 73.046 | 1.00 | 2.00 | 0 |
| ATOM | 4718 | C | ARG | 691 | 56.930 | 18.632 | 73.458 | 1.00 | 64.88 | 0 |
| ATOM | 4719 | O | ARG | 691 | 57.176 | 19.794 | 73.100 | 1.00 | 2.00 | 0 |
| ATOM | 4720 | N | PRO | 692 | 57.265 | 18.151 | 74.693 | 1.00 | 0.89 | 0 |
| ATOM | 4721 | CD | PRO | 692 | 56.930 | 16.947 | 75.482 | 1.00 | 19.88 | 0 |
| ATOM | 4722 | CA | PRO | 692 | 58.060 | 19.115 | 75.500 | 1.00 | 0.77 | 0 |
| ATOM | 4723 | CB | PRO | 692 | 58.305 | 18.357 | 76.811 | 1.00 | 21.87 | 0 |
| ATOM | 4724 | CG | PRO | 692 | 57.071 | 17.462 | 76.911 | 1.00 | 19.02 | 0 |
| ATOM | 4725 | C | PRO | 692 | 59.327 | 19.317 | 74.643 | 1.00 | 0.10 | 0 |
| ATOM | 4726 | O | PRO | 692 | 60.258 | 18.502 | 74.690 | 1.00 | 22.15 | 0 |
| ATOM | 4727 | N | THR | 693 | 59.310 | 20.362 | 73.811 | 1.00 | 2.00 | 0 |
| ATOM | 4729 | CA | THR | 693 | 60.395 | 20.605 | 72.896 | 1.00 | 2.00 | 0 |
| ATOM | 4730 | CB | THR | 693 | 60.153 | 19.842 | 71.569 | 1.00 | 39.91 | 0 |
| ATOM | 4731 | OG1 | THR | 693 | 61.310 | 19.947 | 70.728 | 1.00 | 47.46 | 0 |
| ATOM | 4733 | CG2 | THR | 693 | 58.944 | 20.419 | 70.830 | 1.00 | 46.31 | 0 |
| ATOM | 4734 | C | THR | 693 | 60.567 | 22.057 | 72.560 | 1.00 | 2.00 | 0 |
| ATOM | 4735 | O | THR | 693 | 59.640 | 22.848 | 72.678 | 1.00 | 41.07 | 0 |
| ATOM | 4736 | N | ASP | 694 | 61.782 | 22.399 | 72.154 | 1.00 | 4.51 | 0 |
| ATOM | 4738 | CA | ASP | 694 | 62.075 | 23.747 | 71.736 | 1.00 | 4.51 | 0 |
| ATOM | 4739 | CB | ASP | 694 | 63.429 | 24.203 | 72.283 | 1.00 | 83.74 | 0 |
| ATOM | 4740 | CG | ASP | 694 | 63.337 | 25.520 | 73.041 | 1.00 | 83.74 | 0 |
| ATOM | 4741 | OD1 | ASP | 694 | 63.231 | 25.484 | 74.285 | 1.00 | 83.74 | 0 |
| ATOM | 4742 | OD2 | ASP | 694 | 63.366 | 26.594 | 72.400 | 1.00 | 83.74 | 0 |
| ATOM | 4743 | C | ASP | 694 | 62.101 | 23.682 | 70.201 | 1.00 | 4.51 | 0 |
| ATOM | 4744 | O | ASP | 694 | 62.403 | 22.632 | 69.629 | 1.00 | 83.74 | 0 |
| ATOM | 4745 | N | VAL | 695 | 61.743 | 24.784 | 69.546 | 1.00 | 31.71 | 0 |
| ATOM | 4747 | CA | VAL | 695 | 61.760 | 24.864 | 68.087 | 1.00 | 37.86 | 0 |
| ATOM | 4748 | CB | VAL | 695 | 61.212 | 26.224 | 67.623 | 1.00 | 72.52 | 0 |
| ATOM | 4749 | CG1 | VAL | 695 | 61.120 | 26.268 | 66.113 | 1.00 | 68.63 | 0 |
| ATOM | 4750 | CG2 | VAL | 695 | 59.863 | 26.474 | 68.253 | 1.00 | 68.27 | 0 |
| ATOM | 4751 | C | VAL | 695 | 63.242 | 24.744 | 67.687 | 1.00 | 34.22 | 0 |
| ATOM | 4752 | O | VAL | 695 | 64.070 | 25.548 | 68.123 | 1.00 | 75.22 | 0 |
| ATOM | 4753 | N | PRO | 696 | 63.599 | 23.730 | 66.873 | 1.00 | 2.00 | 0 |
| ATOM | 4754 | CD | PRO | 696 | 62.777 | 22.616 | 66.373 | 1.00 | 5.25 | 0 |
| ATOM | 4755 | CA | PRO | 696 | 64.998 | 23.549 | 66.462 | 1.00 | 2.00 | 0 |
| ATOM | 4756 | CB | PRO | 696 | 64.997 | 22.163 | 65.803 | 1.00 | 5.25 | 0 |
| ATOM | 4757 | CG | PRO | 696 | 63.768 | 21.486 | 66.381 | 1.00 | 5.25 | 0 |
| ATOM | 4758 | C | PRO | 696 | 65.570 | 24.612 | 65.536 | 1.00 | 2.00 | 0 |
| ATOM | 4759 | O | PRO | 696 | 64.878 | 25.556 | 65.137 | 1.00 | 5.25 | 0 |
| ATOM | 4760 | N | ASP | 697 | 66.850 | 24.431 | 65.214 | 1.00 | 34.70 | 0 |
| ATOM | 4762 | CA | ASP | 697 | 67.598 | 25.311 | 64.321 | 1.00 | 35.10 | 0 |
| ATOM | 4763 | CB | ASP | 697 | 69.098 | 24.951 | 64.376 | 1.00 | 81.36 | 0 |
| ATOM | 4764 | CG | ASP | 697 | 69.630 | 24.774 | 65.825 | 1.00 | 81.80 | 0 |
| ATOM | 4765 | OD1 | ASP | 697 | 69.612 | 23.613 | 66.347 | 1.00 | 0.89 | 0 |
| ATOM | 4766 | OD2 | ASP | 697 | 70.075 | 25.792 | 66.436 | 1.00 | 0.05 | 0 |
| ATOM | 4767 | C | ASP | 697 | 67.037 | 25.099 | 62.894 | 1.00 | 36.63 | 0 |
| ATOM | 4768 | O | ASP | 697 | 67.014 | 26.022 | 62.069 | 1.00 | 0.75 | 0 |
| ATOM | 4769 | N | GLN | 698 | 66.576 | 23.877 | 62.620 | 1.00 | 8.48 | 0 |
| ATOM | 4771 | CA | GLN | 698 | 65.997 | 23.510 | 61.335 | 1.00 | 2.00 | 0 |
| ATOM | 4772 | CB | GLN | 698 | 67.089 | 23.346 | 60.285 | 1.00 | 43.65 | 0 |
| ATOM | 4773 | CG | GLN | 698 | 68.191 | 22.376 | 60.649 | 1.00 | 44.93 | 0 |
| ATOM | 4774 | CD | GLN | 698 | 69.158 | 22.169 | 59.501 | 1.00 | 43.25 | 0 |
| ATOM | 4775 | OE1 | GLN | 698 | 68.781 | 22.242 | 58.327 | 1.00 | 45.90 | 0 |
| ATOM | 4776 | NE2 | GLN | 698 | 70.411 | 21.911 | 59.830 | 1.00 | 44.14 | 0 |
| ATOM | 4779 | C | GLN | 698 | 65.211 | 22.216 | 61.482 | 1.00 | 2.32 | 0 |
| ATOM | 4780 | O | GLN | 698 | 65.396 | 21.486 | 62.452 | 1.00 | 42.62 | 0 |
| ATOM | 4781 | N | GLY | 699 | 64.324 | 21.939 | 60.530 | 1.00 | 2.00 | 0 |
| ATOM | 4783 | CA | GLY | 699 | 63.510 | 20.728 | 60.576 | 1.00 | 2.00 | 0 |
| ATOM | 4784 | C | GLY | 699 | 62.046 | 21.059 | 60.346 | 1.00 | 2.00 | 0 |
| ATOM | 4785 | O | GLY | 699 | 61.726 | 22.204 | 60.013 | 1.00 | 2.00 | 0 |
| ATOM | 4786 | N | LEU | 700 | 61.153 | 20.090 | 60.545 | 1.00 | 2.00 | 0 |
| ATOM | 4788 | CA | LEU | 700 | 59.700 | 20.297 | 60.352 | 1.00 | 2.00 | 0 |
| ATOM | 4789 | CB | LEU | 700 | 58.941 | 18.962 | 60.555 | 1.00 | 4.64 | 0 |
| ATOM | 4790 | CG | LEU | 700 | 57.436 | 18.836 | 60.273 | 1.00 | 8.84 | 0 |
| ATOM | 4791 | CD1 | LEU | 700 | 57.219 | 18.881 | 58.793 | 1.00 | 8.28 | 0 |
| ATOM | 4792 | CD2 | LEU | 700 | 56.879 | 17.536 | 60.803 | 1.00 | 5.23 | 0 |
| ATOM | 4793 | C | LEU | 700 | 59.086 | 21.400 | 61.247 | 1.00 | 2.00 | 0 |
| ATOM | 4794 | O | LEU | 700 | 58.365 | 22.261 | 60.763 | 1.00 | 8.77 | 0 |

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|---|---|---|---|---|---|---|---|---|---|---|
| ATOM | 4795 | N | LEU | 701 | 59.394 | 21.381 | 62.540 | 1.00 | 12.05 | 0 |
| ATOM | 4797 | CA | LEU | 701 | 58.860 | 22.362 | 63.477 | 1.00 | 11.21 | 0 |
| ATOM | 4798 | CB | LEU | 701 | 59.278 | 22.039 | 64.908 | 1.00 | 2.00 | 0 |
| ATOM | 4799 | CG | LEU | 701 | 58.156 | 21.874 | 65.942 | 1.00 | 2.00 | 0 |
| ATOM | 4800 | CD1 | LEU | 701 | 58.759 | 21.879 | 67.354 | 1.00 | 2.00 | 0 |
| ATOM | 4801 | CD2 | LEU | 701 | 57.124 | 22.994 | 65.800 | 1.00 | 2.00 | 0 |
| ATOM | 4802 | C | LEU | 701 | 59.339 | 23.747 | 63.153 | 1.00 | 6.49 | 0 |
| ATOM | 4803 | O | LEU | 701 | 58.562 | 24.691 | 63.157 | 1.00 | 2.00 | 0 |
| ATOM | 4804 | N | CYS | 702 | 60.626 | 23.881 | 62.890 | 1.00 | 2.00 | 0 |
| ATOM | 4806 | CA | CYS | 702 | 61.158 | 25.191 | 62.572 | 1.00 | 2.00 | 0 |
| ATOM | 4807 | CB | CYS | 702 | 62.646 | 25.117 | 62.269 | 1.00 | 10.82 | 0 |
| ATOM | 4808 | SG | CYS | 702 | 63.290 | 26.639 | 61.543 | 1.00 | 10.82 | 0 |
| ATOM | 4809 | C | CYS | 702 | 60.442 | 25.786 | 61.365 | 1.00 | 2.00 | 0 |
| ATOM | 4810 | O | CYS | 702 | 60.022 | 26.954 | 61.384 | 1.00 | 10.82 | 0 |
| ATOM | 4811 | N | ASP | 703 | 60.292 | 24.980 | 60.316 | 1.00 | 2.00 | 0 |
| ATOM | 4813 | CA | ASP | 703 | 59.641 | 25.442 | 59.104 | 1.00 | 2.00 | 0 |
| ATOM | 4814 | CB | ASP | 703 | 59.790 | 24.391 | 58.010 | 1.00 | 9.22 | 0 |
| ATOM | 4815 | CG | ASP | 703 | 61.251 | 24.076 | 57.698 | 1.00 | 9.98 | 0 |
| ATOM | 4816 | OD1 | ASP | 703 | 62.126 | 24.940 | 57.943 | 1.00 | 9.22 | 0 |
| ATOM | 4817 | OD2 | ASP | 703 | 61.537 | 22.956 | 57.213 | 1.00 | 9.22 | 0 |
| ATOM | 4818 | C | ASP | 703 | 58.187 | 25.760 | 59.377 | 1.00 | 2.00 | 0 |
| ATOM | 4819 | O | ASP | 703 | 57.694 | 26.823 | 59.023 | 1.00 | 11.43 | 0 |
| ATOM | 4820 | N | LEU | 704 | 57.519 | 24.861 | 60.072 | 1.00 | 2.00 | 0 |
| ATOM | 4822 | CA | LEU | 704 | 56.113 | 25.051 | 60.391 | 1.00 | 2.00 | 0 |
| ATOM | 4823 | CB | LEU | 704 | 55.630 | 23.942 | 61.338 | 1.00 | 22.47 | 0 |
| ATOM | 4824 | CG | LEU | 704 | 55.412 | 22.533 | 60.780 | 1.00 | 21.16 | 0 |
| ATOM | 4825 | CD1 | LEU | 704 | 55.366 | 21.528 | 61.911 | 1.00 | 24.29 | 0 |
| ATOM | 4826 | CD2 | LEU | 704 | 54.132 | 22.489 | 59.973 | 1.00 | 22.40 | 0 |
| ATOM | 4827 | C | LEU | 704 | 55.809 | 26.417 | 61.006 | 1.00 | 2.00 | 0 |
| ATOM | 4828 | O | LEU | 704 | 54.736 | 26.979 | 60.773 | 1.00 | 15.38 | 0 |
| ATOM | 4829 | N | LEU | 705 | 56.757 | 26.967 | 61.763 | 1.00 | 39.58 | 0 |
| ATOM | 4831 | CA | LEU | 705 | 56.538 | 28.248 | 62.439 | 1.00 | 39.58 | 0 |
| ATOM | 4832 | CB | LEU | 705 | 56.884 | 28.108 | 63.913 | 1.00 | 2.00 | 0 |
| ATOM | 4833 | CG | LEU | 705 | 56.841 | 26.725 | 64.552 | 1.00 | 2.00 | 0 |
| ATOM | 4834 | CD1 | LEU | 705 | 57.376 | 26.870 | 65.950 | 1.00 | 2.00 | 0 |
| ATOM | 4835 | CD2 | LEU | 705 | 55.446 | 26.156 | 64.566 | 1.00 | 2.00 | 0 |
| ATOM | 4836 | C | LEU | 705 | 57.279 | 29.466 | 61.900 | 1.00 | 39.58 | 0 |
| ATOM | 4837 | O | LEU | 705 | 56.924 | 30.598 | 62.240 | 1.00 | 2.00 | 0 |
| ATOM | 4838 | N | TRP | 706 | 58.307 | 29.237 | 61.086 | 1.00 | 2.00 | 0 |
| ATOM | 4840 | CA | TRP | 706 | 59.117 | 30.319 | 60.523 | 1.00 | 2.00 | 0 |
| ATOM | 4841 | CB | TRP | 706 | 60.594 | 30.025 | 60.777 | 1.00 | 23.95 | 0 |
| ATOM | 4842 | CG | TRP | 706 | 61.025 | 30.261 | 62.165 | 1.00 | 23.95 | 0 |
| ATOM | 4843 | CD2 | TRP | 706 | 61.380 | 31.520 | 62.742 | 1.00 | 23.95 | 0 |
| ATOM | 4844 | CE2 | TRP | 706 | 61.735 | 31.278 | 64.083 | 1.00 | 23.95 | 0 |
| ATOM | 4845 | CE3 | TRP | 706 | 61.434 | 32.832 | 62.254 | 1.00 | 23.95 | 0 |
| ATOM | 4846 | CD1 | TRP | 706 | 61.173 | 29.329 | 63.150 | 1.00 | 23.95 | 0 |
| ATOM | 4847 | NE1 | TRP | 706 | 61.599 | 29.932 | 64.307 | 1.00 | 23.95 | 0 |
| ATOM | 4849 | CZ2 | TRP | 706 | 62.141 | 32.303 | 64.946 | 1.00 | 23.95 | 0 |
| ATOM | 4850 | CZ3 | TRP | 706 | 61.835 | 33.850 | 63.108 | 1.00 | 23.95 | 0 |
| ATOM | 4851 | CH2 | TRP | 706 | 62.184 | 33.580 | 64.439 | 1.00 | 23.95 | 0 |
| ATOM | 4852 | C | TRP | 706 | 58.947 | 30.619 | 59.028 | 1.00 | 2.00 | 0 |
| ATOM | 4853 | O | TRP | 706 | 59.186 | 31.751 | 58.598 | 1.00 | 23.95 | 0 |
| ATOM | 4854 | N | SER | 707 | 58.564 | 29.604 | 58.249 | 1.00 | 17.80 | 0 |
| ATOM | 4856 | CA | SER | 707 | 58.423 | 29.730 | 56.796 | 1.00 | 12.52 | 0 |
| ATOM | 4857 | CB | SER | 707 | 58.034 | 28.383 | 56.160 | 1.00 | 9.59 | 0 |
| ATOM | 4858 | OG | SER | 707 | 56.693 | 28.010 | 56.444 | 1.00 | 8.78 | 0 |
| ATOM | 4860 | C | SER | 707 | 57.459 | 30.806 | 56.328 | 1.00 | 18.86 | 0 |
| ATOM | 4861 | O | SER | 707 | 56.521 | 31.179 | 57.035 | 1.00 | 6.18 | 0 |
| ATOM | 4862 | N | ASP | 708 | 57.700 | 31.303 | 55.124 | 1.00 | 7.67 | 0 |
| ATOM | 4864 | CA | ASP | 708 | 56.860 | 32.328 | 54.547 | 1.00 | 7.67 | 0 |
| ATOM | 4865 | CB | ASP | 708 | 57.546 | 33.676 | 54.656 | 1.00 | 8.53 | 0 |
| ATOM | 4866 | CG | ASP | 708 | 57.720 | 34.104 | 56.079 | 1.00 | 10.12 | 0 |
| ATOM | 4867 | OD1 | ASP | 708 | 58.844 | 34.049 | 56.597 | 1.00 | 10.18 | 0 |
| ATOM | 4868 | OD2 | ASP | 708 | 56.717 | 34.483 | 56.689 | 1.00 | 10.95 | 0 |
| ATOM | 4869 | C | ASP | 708 | 56.609 | 31.998 | 53.104 | 1.00 | 7.67 | 0 |
| ATOM | 4870 | O | ASP | 708 | 57.461 | 31.432 | 52.444 | 1.00 | 11.43 | 0 |
| ATOM | 4871 | N | PRO | 709 | 55.425 | 32.328 | 52.596 | 1.00 | 2.00 | 0 |
| ATOM | 4872 | CD | PRO | 709 | 54.346 | 33.006 | 53.302 | 1.00 | 2.00 | 0 |

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|---|---|---|---|---|---|---|---|---|---|---|
| ATOM | 4873 | CA | PRO | 709 | 55.029 | 32.078 | 51.214 | 1.00 | 2.00 | 0 |
| ATOM | 4874 | CB | PRO | 709 | 53.507 | 32.036 | 51.283 | 1.00 | 2.00 | 0 |
| ATOM | 4875 | CG | PRO | 709 | 53.169 | 32.316 | 52.728 | 1.00 | 2.00 | 0 |
| ATOM | 4876 | C | PRO | 709 | 55.475 | 33.269 | 50.406 | 1.00 | 2.00 | 0 |
| ATOM | 4877 | O | PRO | 709 | 55.071 | 34.393 | 50.712 | 1.00 | 2.00 | 0 |
| ATOM | 4878 | N | ASP | 710 | 56.306 | 33.046 | 49.393 | 1.00 | 2.57 | 0 |
| ATOM | 4880 | CA | ASP | 710 | 56.769 | 34.155 | 48.576 | 1.00 | 4.76 | 0 |
| ATOM | 4881 | CB | ASP | 710 | 58.297 | 34.215 | 48.537 | 1.00 | 18.70 | 0 |
| ATOM | 4882 | CG | ASP | 710 | 58.824 | 35.631 | 48.303 | 1.00 | 26.43 | 0 |
| ATOM | 4883 | OD1 | ASP | 710 | 58.070 | 36.497 | 47.793 | 1.00 | 26.58 | 0 |
| ATOM | 4884 | OD2 | ASP | 710 | 60.002 | 35.884 | 48.635 | 1.00 | 30.90 | 0 |
| ATOM | 4885 | C | ASP | 710 | 56.211 | 34.045 | 47.168 | 1.00 | 5.37 | 0 |
| ATOM | 4886 | O | ASP | 710 | 56.454 | 33.056 | 46.467 | 1.00 | 15.67 | 0 |
| ATOM | 4887 | N | LYS | 711 | 55.449 | 35.074 | 46.789 | 1.00 | 10.56 | 0 |
| ATOM | 4889 | CA | LYS | 711 | 54.802 | 35.217 | 45.480 | 1.00 | 16.19 | 0 |
| ATOM | 4890 | CB | LYS | 711 | 54.266 | 36.661 | 45.368 | 1.00 | 35.75 | 0 |
| ATOM | 4891 | CG | LYS | 711 | 53.743 | 37.109 | 44.007 | 1.00 | 43.76 | 0 |
| ATOM | 4892 | CD | LYS | 711 | 54.843 | 37.750 | 43.146 | 1.00 | 49.83 | 0 |
| ATOM | 4893 | CE | LYS | 711 | 55.459 | 38.976 | 43.819 | 1.00 | 54.70 | 0 |
| ATOM | 4894 | NZ | LYS | 711 | 56.632 | 39.514 | 43.064 | 1.00 | 58.93 | 0 |
| ATOM | 4898 | C | LYS | 711 | 55.753 | 34.877 | 44.331 | 1.00 | 16.03 | 0 |
| ATOM | 4899 | O | LYS | 711 | 55.459 | 34.001 | 43.518 | 1.00 | 37.96 | 0 |
| ATOM | 4900 | N | ASP | 712 | 56.894 | 35.560 | 44.282 | 1.00 | 2.00 | 0 |
| ATOM | 4902 | CA | ASP | 712 | 57.890 | 35.330 | 43.252 | 1.00 | 2.00 | 0 |
| ATOM | 4903 | CB | ASP | 712 | 58.655 | 36.629 | 42.927 | 1.00 | 75.12 | 0 |
| ATOM | 4904 | CG | ASP | 712 | 59.362 | 37.231 | 44.134 | 1.00 | 75.41 | 0 |
| ATOM | 4905 | OD1 | ASP | 712 | 58.723 | 38.013 | 44.866 | 1.00 | 77.74 | 0 |
| ATOM | 4906 | OD2 | ASP | 712 | 60.561 | 36.937 | 44.341 | 1.00 | 84.37 | 0 |
| ATOM | 4907 | C | ASP | 712 | 58.863 | 34.189 | 43.597 | 1.00 | 2.00 | 0 |
| ATOM | 4908 | O | ASP | 712 | 60.083 | 34.366 | 43.607 | 1.00 | 77.12 | 0 |
| ATOM | 4909 | N | VAL | 713 | 58.298 | 33.016 | 43.866 | 1.00 | 27.09 | 0 |
| ATOM | 4911 | CA | VAL | 713 | 59.057 | 31.811 | 44.188 | 1.00 | 17.74 | 0 |
| ATOM | 4912 | CB | VAL | 713 | 59.166 | 31.579 | 45.727 | 1.00 | 2.00 | 0 |
| ATOM | 4913 | CG1 | VAL | 713 | 59.124 | 30.098 | 46.069 | 1.00 | 2.00 | 0 |
| ATOM | 4914 | CG2 | VAL | 713 | 60.481 | 32.120 | 46.224 | 1.00 | 2.00 | 0 |
| ATOM | 4915 | C | VAL | 713 | 58.319 | 30.653 | 43.538 | 1.00 | 21.93 | 0 |
| ATOM | 4916 | O | VAL | 713 | 57.092 | 30.567 | 43.593 | 1.00 | 2.00 | 0 |
| ATOM | 4917 | N | LEU | 714 | 59.063 | 29.766 | 42.903 | 1.00 | 15.32 | 0 |
| ATOM | 4919 | CA | LEU | 714 | 58.434 | 28.642 | 42.249 | 1.00 | 10.30 | 0 |
| ATOM | 4920 | CB | LEU | 714 | 59.285 | 28.147 | 41.078 | 1.00 | 48.90 | 0 |
| ATOM | 4921 | CG | LEU | 714 | 58.662 | 27.005 | 40.272 | 1.00 | 42.23 | 0 |
| ATOM | 4922 | CD1 | LEU | 714 | 57.229 | 27.357 | 39.909 | 1.00 | 43.72 | 0 |
| ATOM | 4923 | CD2 | LEU | 714 | 59.478 | 26.753 | 39.025 | 1.00 | 42.86 | 0 |
| ATOM | 4924 | C | LEU | 714 | 58.224 | 27.530 | 43.235 | 1.00 | 13.23 | 0 |
| ATOM | 4925 | O | LEU | 714 | 57.096 | 27.099 | 43.445 | 1.00 | 44.72 | 0 |
| ATOM | 4926 | N | GLY | 715 | 59.322 | 27.075 | 43.834 | 1.00 | 76.36 | 0 |
| ATOM | 4928 | CA | GLY | 715 | 59.263 | 25.995 | 44.800 | 1.00 | 76.36 | 0 |
| ATOM | 4929 | C | GLY | 715 | 59.630 | 26.420 | 46.206 | 1.00 | 76.36 | 0 |
| ATOM | 4930 | O | GLY | 715 | 58.814 | 26.974 | 46.929 | 1.00 | 19.62 | 0 |
| ATOM | 4931 | N | TRP | 716 | 60.875 | 26.183 | 46.583 | 1.00 | 4.87 | 0 |
| ATOM | 4933 | CA | TRP | 716 | 61.365 | 26.503 | 47.918 | 1.00 | 4.87 | 0 |
| ATOM | 4934 | CB | TRP | 716 | 61.944 | 25.241 | 48.554 | 1.00 | 2.00 | 0 |
| ATOM | 4935 | CG | TRP | 716 | 60.884 | 24.317 | 48.932 | 1.00 | 2.00 | 0 |
| ATOM | 4936 | CD2 | TRP | 716 | 59.936 | 24.529 | 49.962 | 1.00 | 2.00 | 0 |
| ATOM | 4937 | CE2 | TRP | 716 | 59.050 | 23.439 | 49.943 | 1.00 | 2.00 | 0 |
| ATOM | 4938 | CE3 | TRP | 716 | 59.750 | 25.541 | 50.909 | 1.00 | 2.00 | 0 |
| ATOM | 4939 | CD1 | TRP | 716 | 60.562 | 23.134 | 48.343 | 1.00 | 2.00 | 0 |
| ATOM | 4940 | NE1 | TRP | 716 | 59.454 | 22.597 | 48.940 | 1.00 | 2.00 | 0 |
| ATOM | 4942 | CZ2 | TRP | 716 | 57.994 | 23.334 | 50.830 | 1.00 | 2.00 | 0 |
| ATOM | 4943 | CZ3 | TRP | 716 | 58.715 | 25.438 | 51.783 | 1.00 | 2.00 | 0 |
| ATOM | 4944 | CH2 | TRP | 716 | 57.843 | 24.343 | 51.743 | 1.00 | 2.00 | 0 |
| ATOM | 4945 | C | TRP | 716 | 62.406 | 27.594 | 47.954 | 1.00 | 4.87 | 0 |
| ATOM | 4946 | O | TRP | 716 | 63.596 | 27.315 | 47.871 | 1.00 | 2.00 | 0 |
| ATOM | 4947 | N | GLY | 717 | 61.968 | 28.837 | 48.067 | 1.00 | 2.00 | 0 |
| ATOM | 4949 | CA | GLY | 717 | 62.911 | 29.937 | 48.124 | 1.00 | 2.00 | 0 |
| ATOM | 4950 | C | GLY | 717 | 63.725 | 30.031 | 49.414 | 1.00 | 2.00 | 0 |
| ATOM | 4951 | O | GLY | 717 | 63.443 | 29.343 | 50.404 | 1.00 | 2.00 | 0 |
| ATOM | 4952 | N | GLU | 718 | 64.752 | 30.880 | 49.387 | 1.00 | 4.99 | 0 |

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|---|---|---|---|---|---|---|---|---|---|---|
| ATOM | 4954 | CA | GLU | 718 | 65.606 | 31.113 | 50.538 | 1.00 | 8.49 | 0 |
| ATOM | 4955 | CB | GLU | 718 | 66.980 | 31.619 | 50.092 | 1.00 | 86.14 | 0 |
| ATOM | 4956 | CG | GLU | 718 | 68.026 | 31.716 | 51.211 | 1.00 | 89.35 | 0 |
| ATOM | 4957 | CD | GLU | 718 | 68.627 | 30.371 | 51.633 | 1.00 | 87.67 | 0 |
| ATOM | 4958 | OE1 | GLU | 718 | 69.392 | 30.358 | 52.624 | 1.00 | 95.59 | 0 |
| ATOM | 4959 | OE2 | GLU | 718 | 68.353 | 29.336 | 50.986 | 1.00 | 88.92 | 0 |
| ATOM | 4960 | C | GLU | 718 | 64.883 | 32.182 | 51.340 | 1.00 | 9.60 | 0 |
| ATOM | 4961 | O | GLU | 718 | 64.597 | 33.269 | 50.828 | 1.00 | 90.23 | 0 |
| ATOM | 4962 | N | ASN | 719 | 64.560 | 31.863 | 52.590 | 1.00 | 32.81 | 0 |
| ATOM | 4964 | CA | ASN | 719 | 63.848 | 32.804 | 53.444 | 1.00 | 33.93 | 0 |
| ATOM | 4965 | CB | ASN | 719 | 63.159 | 32.083 | 54.591 | 1.00 | 14.30 | 0 |
| ATOM | 4966 | CG | ASN | 719 | 62.159 | 32.965 | 55.296 | 1.00 | 14.30 | 0 |
| ATOM | 4967 | OD1 | ASN | 719 | 62.533 | 33.912 | 55.983 | 1.00 | 14.30 | 0 |
| ATOM | 4968 | ND2 | ASN | 719 | 60.879 | 32.676 | 55.110 | 1.00 | 14.30 | 0 |
| ATOM | 4971 | C | ASN | 719 | 64.781 | 33.855 | 54.007 | 1.00 | 33.45 | 0 |
| ATOM | 4972 | O | ASN | 719 | 65.825 | 33.529 | 54.566 | 1.00 | 14.30 | 0 |
| ATOM | 4973 | N | ASP | 720 | 64.388 | 35.117 | 53.878 | 1.00 | 42.61 | 0 |
| ATOM | 4975 | CA | ASP | 720 | 65.212 | 36.222 | 54.351 | 1.00 | 47.00 | 0 |
| ATOM | 4976 | CB | ASP | 720 | 64.744 | 37.535 | 53.706 | 1.00 | 77.30 | 0 |
| ATOM | 4977 | CG | ASP | 720 | 65.025 | 37.574 | 52.200 | 1.00 | 92.85 | 0 |
| ATOM | 4978 | OD1 | ASP | 720 | 66.104 | 38.071 | 51.801 | 1.00 | 92.39 | 0 |
| ATOM | 4979 | OD2 | ASP | 720 | 64.172 | 37.094 | 51.416 | 1.00 | 90.51 | 0 |
| ATOM | 4980 | C | ASP | 720 | 65.328 | 36.352 | 55.869 | 1.00 | 39.89 | 0 |
| ATOM | 4981 | O | ASP | 720 | 66.255 | 36.986 | 56.370 | 1.00 | 74.64 | 0 |
| ATOM | 4982 | N | ARG | 721 | 64.411 | 35.728 | 56.602 | 1.00 | 13.83 | 0 |
| ATOM | 4984 | CA | ARG | 721 | 64.446 | 35.759 | 58.060 | 1.00 | 12.18 | 0 |
| ATOM | 4985 | CB | ARG | 721 | 63.262 | 35.007 | 58.649 | 1.00 | 15.37 | 0 |
| ATOM | 4986 | CG | ARG | 721 | 61.946 | 35.693 | 58.572 | 1.00 | 7.28 | 0 |
| ATOM | 4987 | CD | ARG | 721 | 60.950 | 34.836 | 59.300 | 1.00 | 7.28 | 0 |
| ATOM | 4988 | NE | ARG | 721 | 59.593 | 35.306 | 59.103 | 1.00 | 8.88 | 0 |
| ATOM | 4990 | CZ | ARG | 721 | 59.051 | 36.315 | 59.766 | 1.00 | 9.83 | 0 |
| ATOM | 4991 | NH1 | ARG | 721 | 59.751 | 36.965 | 60.690 | 1.00 | 8.95 | 0 |
| ATOM | 4994 | NH2 | ARG | 721 | 57.809 | 36.682 | 59.485 | 1.00 | 8.62 | 0 |
| ATOM | 4997 | C | ARG | 721 | 65.710 | 35.093 | 58.592 | 1.00 | 8.44 | 0 |
| ATOM | 4998 | O | ARG | 721 | 65.982 | 35.142 | 59.798 | 1.00 | 10.25 | 0 |
| ATOM | 4999 | N | GLY | 722 | 66.449 | 34.437 | 57.697 | 1.00 | 4.85 | 0 |
| ATOM | 5001 | CA | GLY | 722 | 67.668 | 33.752 | 58.083 | 1.00 | 4.85 | 0 |
| ATOM | 5002 | C | GLY | 722 | 67.392 | 32.344 | 58.592 | 1.00 | 4.85 | 0 |
| ATOM | 5003 | O | GLY | 722 | 68.305 | 31.655 | 59.052 | 1.00 | 76.68 | 0 |
| ATOM | 5004 | N | VAL | 723 | 66.134 | 31.918 | 58.508 | 1.00 | 10.85 | 0 |
| ATOM | 5006 | CA | VAL | 723 | 65.717 | 30.591 | 58.958 | 1.00 | 10.85 | 0 |
| ATOM | 5007 | CB | VAL | 723 | 65.259 | 30.574 | 60.471 | 1.00 | 2.00 | 0 |
| ATOM | 5008 | CG1 | VAL | 723 | 66.449 | 30.400 | 61.386 | 1.00 | 2.00 | 0 |
| ATOM | 5009 | CG2 | VAL | 723 | 64.504 | 31.858 | 60.825 | 1.00 | 2.00 | 0 |
| ATOM | 5010 | C | VAL | 723 | 64.546 | 30.100 | 58.105 | 1.00 | 10.85 | 0 |
| ATOM | 5011 | O | VAL | 723 | 63.667 | 30.883 | 57.714 | 1.00 | 2.00 | 0 |
| ATOM | 5012 | N | SER | 724 | 64.541 | 28.802 | 57.824 | 1.00 | 42.15 | 0 |
| ATOM | 5014 | CA | SER | 724 | 63.479 | 28.193 | 57.040 | 1.00 | 42.15 | 0 |
| ATOM | 5015 | CB | SER | 724 | 62.127 | 28.609 | 57.623 | 1.00 | 2.00 | 0 |
| ATOM | 5016 | OG | SER | 724 | 61.077 | 27.808 | 57.106 | 1.00 | 2.00 | 0 |
| ATOM | 5018 | C | SER | 724 | 63.583 | 28.588 | 55.561 | 1.00 | 42.15 | 0 |
| ATOM | 5019 | O | SER | 724 | 64.680 | 28.820 | 55.049 | 1.00 | 2.00 | 0 |
| ATOM | 5020 | N | PHE | 725 | 62.454 | 28.643 | 54.863 | 1.00 | 2.00 | 0 |
| ATOM | 5022 | CA | PHE | 725 | 62.464 | 29.007 | 53.457 | 1.00 | 2.00 | 0 |
| ATOM | 5023 | CB | PHE | 725 | 62.461 | 27.779 | 52.541 | 1.00 | 2.00 | 0 |
| ATOM | 5024 | CG | PHE | 725 | 62.891 | 26.551 | 53.205 | 1.00 | 2.00 | 0 |
| ATOM | 5025 | CD1 | PHE | 725 | 62.047 | 25.916 | 54.089 | 1.00 | 2.00 | 0 |
| ATOM | 5026 | CD2 | PHE | 725 | 64.151 | 26.044 | 52.984 | 1.00 | 2.00 | 0 |
| ATOM | 5027 | CE1 | PHE | 725 | 62.458 | 24.791 | 54.750 | 1.00 | 2.00 | 0 |
| ATOM | 5028 | CE2 | PHE | 725 | 64.578 | 24.906 | 53.646 | 1.00 | 2.00 | 0 |
| ATOM | 5029 | CZ | PHE | 725 | 63.733 | 24.280 | 54.530 | 1.00 | 2.00 | 0 |
| ATOM | 5030 | C | PHE | 725 | 61.222 | 29.787 | 53.146 | 1.00 | 2.00 | 0 |
| ATOM | 5031 | O | PHE | 725 | 60.382 | 30.040 | 54.009 | 1.00 | 2.00 | 0 |
| ATOM | 5032 | N | THR | 726 | 61.132 | 30.162 | 51.886 | 1.00 | 34.54 | 0 |
| ATOM | 5034 | CA | THR | 726 | 60.009 | 30.877 | 51.357 | 1.00 | 30.82 | 0 |
| ATOM | 5035 | CB | THR | 726 | 60.468 | 32.154 | 50.661 | 1.00 | 2.00 | 0 |
| ATOM | 5036 | OG1 | THR | 726 | 61.880 | 32.098 | 50.406 | 1.00 | 2.00 | 0 |
| ATOM | 5038 | CG2 | THR | 726 | 60.222 | 33.327 | 51.561 | 1.00 | 2.00 | 0 |

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|---|---|---|---|---|---|---|---|---|---|---|
| ATOM | 5039 | C | THR | 726 | 59.450 | 29.866 | 50.382 | 1.00 | 34.20 | 0 |
| ATOM | 5040 | O | THR | 726 | 60.201 | 29.208 | 49.684 | 1.00 | 2.00 | 0 |
| ATOM | 5041 | N | PHE | 727 | 58.144 | 29.685 | 50.375 | 1.00 | 2.00 | 0 |
| ATOM | 5043 | CA | PHE | 727 | 57.555 | 28.712 | 49.483 | 1.00 | 2.00 | 0 |
| ATOM | 5044 | CB | PHE | 727 | 56.852 | 27.612 | 50.275 | 1.00 | 9.97 | 0 |
| ATOM | 5045 | CG | PHE | 727 | 55.698 | 28.096 | 51.105 | 1.00 | 15.33 | 0 |
| ATOM | 5046 | CD1 | PHE | 727 | 54.394 | 27.922 | 50.666 | 1.00 | 9.89 | 0 |
| ATOM | 5047 | CD2 | PHE | 727 | 55.916 | 28.726 | 52.323 | 1.00 | 15.65 | 0 |
| ATOM | 5048 | CE1 | PHE | 727 | 53.338 | 28.360 | 51.418 | 1.00 | 11.89 | 0 |
| ATOM | 5049 | CE2 | PHE | 727 | 54.852 | 29.171 | 53.087 | 1.00 | 6.87 | 0 |
| ATOM | 5050 | CZ | PHE | 727 | 53.563 | 28.986 | 52.631 | 1.00 | 11.72 | 0 |
| ATOM | 5051 | C | PHE | 727 | 56.580 | 29.398 | 48.553 | 1.00 | 2.00 | 0 |
| ATOM | 5052 | O | PHE | 727 | 55.848 | 30.312 | 48.982 | 1.00 | 18.77 | 0 |
| ATOM | 5053 | N | GLY | 728 | 56.576 | 28.956 | 47.289 | 1.00 | 13.14 | 0 |
| ATOM | 5055 | CA | GLY | 728 | 55.709 | 29.542 | 46.277 | 1.00 | 12.12 | 0 |
| ATOM | 5056 | C | GLY | 728 | 54.348 | 28.894 | 46.174 | 1.00 | 13.69 | 0 |
| ATOM | 5057 | O | GLY | 728 | 54.062 | 27.913 | 46.862 | 1.00 | 2.00 | 0 |
| ATOM | 5058 | N | ALA | 729 | 53.513 | 29.436 | 45.292 | 1.00 | 33.39 | 0 |
| ATOM | 5060 | CA | ALA | 729 | 52.161 | 28.916 | 45.080 | 1.00 | 33.11 | 0 |
| ATOM | 5061 | CB | ALA | 729 | 51.375 | 29.862 | 44.200 | 1.00 | 16.31 | 0 |
| ATOM | 5062 | C | ALA | 729 | 52.139 | 27.507 | 44.485 | 1.00 | 31.34 | 0 |
| ATOM | 5063 | O | ALA | 729 | 51.143 | 26.796 | 44.600 | 1.00 | 16.31 | 0 |
| ATOM | 5064 | N | GLU | 730 | 53.221 | 27.105 | 43.831 | 1.00 | 22.53 | 0 |
| ATOM | 5066 | CA | GLU | 730 | 53.284 | 25.761 | 43.281 | 1.00 | 26.87 | 0 |
| ATOM | 5067 | CB | GLU | 730 | 54.622 | 25.551 | 42.570 | 1.00 | 59.75 | 0 |
| ATOM | 5068 | CG | GLU | 730 | 54.893 | 24.117 | 42.142 | 1.00 | 62.63 | 0 |
| ATOM | 5069 | CD | GLU | 730 | 56.138 | 23.984 | 41.283 | 1.00 | 68.00 | 0 |
| ATOM | 5070 | OE1 | GLU | 730 | 57.213 | 23.624 | 41.822 | 1.00 | 74.97 | 0 |
| ATOM | 5071 | OE2 | GLU | 730 | 56.034 | 24.238 | 40.063 | 1.00 | 67.31 | 0 |
| ATOM | 5072 | C | GLU | 730 | 53.140 | 24.781 | 44.446 | 1.00 | 24.85 | 0 |
| ATOM | 5073 | O | GLU | 730 | 52.285 | 23.899 | 44.425 | 1.00 | 58.27 | 0 |
| ATOM | 5074 | N | VAL | 731 | 53.958 | 24.989 | 45.477 | 1.00 | 24.13 | 0 |
| ATOM | 5076 | CA | VAL | 731 | 53.985 | 24.157 | 46.679 | 1.00 | 19.42 | 0 |
| ATOM | 5077 | CB | VAL | 731 | 55.079 | 24.628 | 47.645 | 1.00 | 19.11 | 0 |
| ATOM | 5078 | CG1 | VAL | 731 | 55.159 | 23.699 | 48.824 | 1.00 | 19.11 | 0 |
| ATOM | 5079 | CG2 | VAL | 731 | 56.412 | 24.691 | 46.942 | 1.00 | 19.11 | 0 |
| ATOM | 5080 | C | VAL | 731 | 52.659 | 24.165 | 47.423 | 1.00 | 16.89 | 0 |
| ATOM | 5081 | O | VAL | 731 | 52.210 | 23.128 | 47.900 | 1.00 | 19.11 | 0 |
| ATOM | 5082 | N | VAL | 732 | 52.035 | 25.332 | 47.525 | 1.00 | 15.54 | 0 |
| ATOM | 5084 | CA | VAL | 732 | 50.750 | 25.449 | 48.209 | 1.00 | 15.54 | 0 |
| ATOM | 5085 | CB | VAL | 732 | 50.254 | 26.898 | 48.240 | 1.00 | 20.17 | 0 |
| ATOM | 5086 | CG1 | VAL | 732 | 48.907 | 26.985 | 48.962 | 1.00 | 20.17 | 0 |
| ATOM | 5087 | CG2 | VAL | 732 | 51.272 | 27.764 | 48.902 | 1.00 | 20.17 | 0 |
| ATOM | 5088 | C | VAL | 732 | 49.653 | 24.609 | 47.554 | 1.00 | 15.54 | 0 |
| ATOM | 5089 | O | VAL | 732 | 49.011 | 23.791 | 48.222 | 1.00 | 20.17 | 0 |
| ATOM | 5090 | N | ALA | 733 | 49.437 | 24.822 | 46.253 | 1.00 | 16.29 | 0 |
| ATOM | 5092 | CA | ALA | 733 | 48.408 | 24.109 | 45.501 | 1.00 | 16.29 | 0 |
| ATOM | 5093 | CB | ALA | 733 | 48.260 | 24.717 | 44.131 | 1.00 | 17.33 | 0 |
| ATOM | 5094 | C | ALA | 733 | 48.703 | 22.618 | 45.390 | 1.00 | 16.29 | 0 |
| ATOM | 5095 | O | ALA | 733 | 47.776 | 21.795 | 45.349 | 1.00 | 17.78 | 0 |
| ATOM | 5096 | N | LYS | 734 | 49.996 | 22.287 | 45.348 | 1.00 | 2.00 | 0 |
| ATOM | 5098 | CA | LYS | 734 | 50.499 | 20.905 | 45.259 | 1.00 | 2.00 | 0 |
| ATOM | 5099 | CB | LYS | 734 | 52.012 | 20.936 | 45.015 | 1.00 | 23.03 | 0 |
| ATOM | 5100 | CG | LYS | 734 | 52.507 | 20.244 | 43.759 | 1.00 | 25.55 | 0 |
| ATOM | 5101 | CD | LYS | 734 | 52.696 | 21.212 | 42.594 | 1.00 | 35.13 | 0 |
| ATOM | 5102 | CE | LYS | 734 | 53.613 | 20.608 | 41.521 | 1.00 | 40.96 | 0 |
| ATOM | 5103 | NZ | LYS | 734 | 55.006 | 20.311 | 42.001 | 1.00 | 46.09 | 0 |
| ATOM | 5107 | C | LYS | 734 | 50.222 | 20.146 | 46.578 | 1.00 | 2.00 | 0 |
| ATOM | 5108 | O | LYS | 734 | 49.995 | 18.926 | 46.591 | 1.00 | 16.68 | 0 |
| ATOM | 5109 | N | PHE | 735 | 50.263 | 20.915 | 47.670 | 1.00 | 36.96 | 0 |
| ATOM | 5111 | CA | PHE | 735 | 50.036 | 20.478 | 49.047 | 1.00 | 33.73 | 0 |
| ATOM | 5112 | CB | PHE | 735 | 50.606 | 21.554 | 49.991 | 1.00 | 8.60 | 0 |
| ATOM | 5113 | CG | PHE | 735 | 50.320 | 21.323 | 51.465 | 1.00 | 8.60 | 0 |
| ATOM | 5114 | CD1 | PHE | 735 | 50.955 | 20.298 | 52.169 | 1.00 | 8.60 | 0 |
| ATOM | 5115 | CD2 | PHE | 735 | 49.412 | 22.135 | 52.142 | 1.00 | 8.60 | 0 |
| ATOM | 5116 | CE1 | PHE | 735 | 50.690 | 20.086 | 53.512 | 1.00 | 8.60 | 0 |
| ATOM | 5117 | CE2 | PHE | 735 | 49.143 | 21.929 | 53.483 | 1.00 | 8.60 | 0 |
| ATOM | 5118 | CZ | PHE | 735 | 49.784 | 20.900 | 54.168 | 1.00 | 8.60 | 0 |

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|---|---|---|---|---|---|---|---|---|---|---|
| ATOM | 5119 | C | PHE | 735 | 48.546 | 20.256 | 49.334 | 1.00 | 34.15 | 0 |
| ATOM | 5120 | O | PHE | 735 | 48.151 | 19.181 | 49.801 | 1.00 | 8.60 | 0 |
| ATOM | 5121 | N | LEU | 736 | 47.731 | 21.281 | 49.075 | 1.00 | 2.00 | 0 |
| ATOM | 5123 | CA | LEU | 736 | 46.289 | 21.208 | 49.299 | 1.00 | 2.00 | 0 |
| ATOM | 5124 | CB | LEU | 736 | 45.599 | 22.451 | 48.770 | 1.00 | 2.00 | 0 |
| ATOM | 5125 | CG | LEU | 736 | 45.937 | 23.760 | 49.456 | 1.00 | 2.00 | 0 |
| ATOM | 5126 | CD1 | LEU | 736 | 45.314 | 24.887 | 48.689 | 1.00 | 2.00 | 0 |
| ATOM | 5127 | CD2 | LEU | 736 | 45.415 | 23.743 | 50.896 | 1.00 | 2.00 | 0 |
| ATOM | 5128 | C | LEU | 736 | 45.741 | 20.014 | 48.567 | 1.00 | 2.00 | 0 |
| ATOM | 5129 | O | LEU | 736 | 44.986 | 19.215 | 49.121 | 1.00 | 2.00 | 0 |
| ATOM | 5130 | N | HIS | 737 | 46.147 | 19.906 | 47.308 | 1.00 | 25.73 | 0 |
| ATOM | 5132 | CA | HIS | 737 | 45.747 | 18.818 | 46.427 | 1.00 | 25.73 | 0 |
| ATOM | 5133 | CB | HIS | 737 | 46.423 | 19.037 | 45.057 | 1.00 | 69.97 | 0 |
| ATOM | 5134 | CG | HIS | 737 | 46.638 | 17.784 | 44.263 | 1.00 | 68.65 | 0 |
| ATOM | 5135 | CD2 | HIS | 737 | 47.779 | 17.169 | 43.868 | 1.00 | 71.13 | 0 |
| ATOM | 5136 | ND1 | HIS | 737 | 45.601 | 17.012 | 43.783 | 1.00 | 76.45 | 0 |
| ATOM | 5138 | CE1 | HIS | 737 | 46.093 | 15.974 | 43.129 | 1.00 | 76.42 | 0 |
| ATOM | 5139 | NE2 | HIS | 737 | 47.412 | 16.046 | 43.166 | 1.00 | 74.54 | 0 |
| ATOM | 5141 | C | HIS | 737 | 46.088 | 17.440 | 47.037 | 1.00 | 25.73 | 0 |
| ATOM | 5142 | O | HIS | 737 | 45.223 | 16.570 | 47.166 | 1.00 | 61.28 | 0 |
| ATOM | 5143 | N | LYS | 738 | 47.347 | 17.266 | 47.422 | 1.00 | 11.82 | 0 |
| ATOM | 5145 | CA | LYS | 738 | 47.836 | 16.028 | 48.010 | 1.00 | 10.83 | 0 |
| ATOM | 5146 | CB | LYS | 738 | 49.343 | 16.163 | 48.256 | 1.00 | 10.15 | 0 |
| ATOM | 5147 | CG | LYS | 738 | 49.999 | 15.111 | 49.119 | 1.00 | 13.96 | 0 |
| ATOM | 5148 | CD | LYS | 738 | 51.516 | 15.253 | 49.005 | 1.00 | 16.98 | 0 |
| ATOM | 5149 | CE | LYS | 738 | 52.278 | 14.809 | 50.274 | 1.00 | 14.10 | 0 |
| ATOM | 5150 | NZ | LYS | 738 | 52.154 | 13.362 | 50.650 | 1.00 | 13.23 | 0 |
| ATOM | 5154 | C | LYS | 738 | 47.121 | 15.655 | 49.301 | 1.00 | 17.32 | 0 |
| ATOM | 5155 | O | LYS | 738 | 47.038 | 14.473 | 49.640 | 1.00 | 16.32 | 0 |
| ATOM | 5156 | N | HIS | 739 | 46.598 | 16.642 | 50.028 | 1.00 | 2.00 | 0 |
| ATOM | 5158 | CA | HIS | 739 | 45.935 | 16.319 | 51.284 | 1.00 | 2.00 | 0 |
| ATOM | 5159 | CB | HIS | 739 | 46.689 | 16.965 | 52.460 | 1.00 | 9.90 | 0 |
| ATOM | 5160 | CG | HIS | 739 | 48.099 | 16.482 | 52.597 | 1.00 | 8.91 | 0 |
| ATOM | 5161 | CD2 | HIS | 739 | 48.603 | 15.318 | 53.077 | 1.00 | 3.85 | 0 |
| ATOM | 5162 | ND1 | HIS | 739 | 49.182 | 17.212 | 52.148 | 1.00 | 7.65 | 0 |
| ATOM | 5164 | CE1 | HIS | 739 | 50.291 | 16.517 | 52.340 | 1.00 | 6.50 | 0 |
| ATOM | 5165 | NE2 | HIS | 739 | 49.966 | 15.364 | 52.901 | 1.00 | 3.85 | 0 |
| ATOM | 5167 | C | HIS | 739 | 44.442 | 16.598 | 51.378 | 1.00 | 2.00 | 0 |
| ATOM | 5168 | O | HIS | 739 | 43.913 | 16.722 | 52.477 | 1.00 | 18.58 | 0 |
| ATOM | 5169 | N | ASP | 740 | 43.763 | 16.678 | 50.236 | 1.00 | 2.00 | 0 |
| ATOM | 5171 | CA | ASP | 740 | 42.314 | 16.912 | 50.191 | 1.00 | 2.00 | 0 |
| ATOM | 5172 | CB | ASP | 740 | 41.567 | 15.695 | 50.758 | 1.00 | 37.08 | 0 |
| ATOM | 5173 | CG | ASP | 740 | 42.092 | 14.367 | 50.206 | 1.00 | 45.58 | 0 |
| ATOM | 5174 | OD1 | ASP | 740 | 42.974 | 13.754 | 50.856 | 1.00 | 45.42 | 0 |
| ATOM | 5175 | OD2 | ASP | 740 | 41.622 | 13.932 | 49.129 | 1.00 | 41.93 | 0 |
| ATOM | 5176 | C | ASP | 740 | 41.900 | 18.170 | 50.955 | 1.00 | 2.00 | 0 |
| ATOM | 5177 | O | ASP | 740 | 40.773 | 18.286 | 51.432 | 1.00 | 36.93 | 0 |
| ATOM | 5178 | N | LEU | 741 | 42.824 | 19.113 | 51.045 | 1.00 | 2.00 | 0 |
| ATOM | 5180 | CA | LEU | 741 | 42.610 | 20.357 | 51.764 | 1.00 | 2.00 | 0 |
| ATOM | 5181 | CB | LEU | 741 | 43.920 | 20.818 | 52.415 | 1.00 | 2.00 | 0 |
| ATOM | 5182 | CG | LEU | 741 | 44.572 | 19.861 | 53.388 | 1.00 | 2.00 | 0 |
| ATOM | 5183 | CD1 | LEU | 741 | 45.906 | 20.394 | 53.859 | 1.00 | 2.00 | 0 |
| ATOM | 5184 | CD2 | LEU | 741 | 43.620 | 19.673 | 54.519 | 1.00 | 2.00 | 0 |
| ATOM | 5185 | C | LEU | 741 | 42.122 | 21.433 | 50.818 | 1.00 | 2.00 | 0 |
| ATOM | 5186 | O | LEU | 741 | 42.261 | 21.301 | 49.611 | 1.00 | 2.00 | 0 |
| ATOM | 5187 | N | ASP | 742 | 41.588 | 22.510 | 51.385 | 1.00 | 2.00 | 0 |
| ATOM | 5189 | CA | ASP | 742 | 41.080 | 23.620 | 50.607 | 1.00 | 2.00 | 0 |
| ATOM | 5190 | CB | ASP | 742 | 39.605 | 23.858 | 50.909 | 1.00 | 21.53 | 0 |
| ATOM | 5191 | CG | ASP | 742 | 38.717 | 22.741 | 50.433 | 1.00 | 26.90 | 0 |
| ATOM | 5192 | OD1 | ASP | 742 | 39.159 | 21.898 | 49.622 | 1.00 | 27.19 | 0 |
| ATOM | 5193 | OD2 | ASP | 742 | 37.555 | 22.714 | 50.876 | 1.00 | 25.85 | 0 |
| ATOM | 5194 | C | ASP | 742 | 41.810 | 24.913 | 50.887 | 1.00 | 2.00 | 0 |
| ATOM | 5195 | O | ASP | 742 | 42.064 | 25.698 | 49.970 | 1.00 | 14.77 | 0 |
| ATOM | 5196 | N | LEU | 743 | 42.141 | 25.152 | 52.149 | 1.00 | 5.78 | 0 |
| ATOM | 5198 | CA | LEU | 743 | 42.785 | 26.407 | 52.509 | 1.00 | 5.78 | 0 |
| ATOM | 5199 | CB | LEU | 743 | 41.744 | 27.312 | 53.185 | 1.00 | 2.00 | 0 |
| ATOM | 5200 | CG | LEU | 743 | 41.689 | 28.847 | 53.088 | 1.00 | 2.00 | 0 |
| ATOM | 5201 | CD1 | LEU | 743 | 40.947 | 29.364 | 54.297 | 1.00 | 2.00 | 0 |

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|---|---|---|---|---|---|---|---|---|---|---|
| ATOM | 5202 | CD2 | LEU | 743 | 43.051 | 29.469 | 53.053 | 1.00 | 2.00 | 0 |
| ATOM | 5203 | C | LEU | 743 | 43.919 | 26.152 | 53.483 | 1.00 | 5.78 | 0 |
| ATOM | 5204 | O | LEU | 743 | 43.973 | 25.091 | 54.088 | 1.00 | 2.00 | 0 |
| ATOM | 5205 | N | ILE | 744 | 44.837 | 27.104 | 53.599 | 1.00 | 2.00 | 0 |
| ATOM | 5207 | CA | ILE | 744 | 45.916 | 27.031 | 54.574 | 1.00 | 2.00 | 0 |
| ATOM | 5208 | CB | ILE | 744 | 47.338 | 27.043 | 53.968 | 1.00 | 2.00 | 0 |
| ATOM | 5209 | CG2 | ILE | 744 | 48.360 | 27.214 | 55.089 | 1.00 | 2.00 | 0 |
| ATOM | 5210 | CG1 | ILE | 744 | 47.637 | 25.754 | 53.204 | 1.00 | 2.00 | 0 |
| ATOM | 5211 | CD1 | ILE | 744 | 49.117 | 25.602 | 52.856 | 1.00 | 2.00 | 0 |
| ATOM | 5212 | C | ILE | 744 | 45.770 | 28.330 | 55.356 | 1.00 | 2.00 | 0 |
| ATOM | 5213 | O | ILE | 744 | 45.830 | 29.423 | 54.788 | 1.00 | 2.00 | 0 |
| ATOM | 5214 | N | CYS | 745 | 45.557 | 28.226 | 56.655 | 1.00 | 71.57 | 0 |
| ATOM | 5216 | CA | CYS | 745 | 45.426 | 29.418 | 57.462 | 1.00 | 66.70 | 0 |
| ATOM | 5217 | CB | CYS | 745 | 44.204 | 29.301 | 58.363 | 1.00 | 17.55 | 0 |
| ATOM | 5218 | SG | CYS | 745 | 43.454 | 30.878 | 58.703 | 1.00 | 23.65 | 0 |
| ATOM | 5219 | C | CYS | 745 | 46.700 | 29.572 | 58.281 | 1.00 | 69.12 | 0 |
| ATOM | 5220 | O | CYS | 745 | 47.093 | 28.667 | 59.017 | 1.00 | 21.37 | 0 |
| ATOM | 5221 | N | ARG | 746 | 47.363 | 30.706 | 58.121 | 1.00 | 2.00 | 0 |
| ATOM | 5223 | CA | ARG | 746 | 48.594 | 30.982 | 58.837 | 1.00 | 2.00 | 0 |
| ATOM | 5224 | CB | ARG | 746 | 49.810 | 30.672 | 57.944 | 1.00 | 2.00 | 0 |
| ATOM | 5225 | CG | ARG | 746 | 49.860 | 31.394 | 56.609 | 1.00 | 2.00 | 0 |
| ATOM | 5226 | CD | ARG | 746 | 50.792 | 32.619 | 56.617 | 1.00 | 2.00 | 0 |
| ATOM | 5227 | NE | ARG | 746 | 52.220 | 32.293 | 56.560 | 1.00 | 2.00 | 0 |
| ATOM | 5229 | CZ | ARG | 746 | 53.212 | 33.184 | 56.626 | 1.00 | 2.00 | 0 |
| ATOM | 5230 | NH1 | ARG | 746 | 52.956 | 34.479 | 56.738 | 1.00 | 2.00 | 0 |
| ATOM | 5233 | NH2 | ARG | 746 | 54.468 | 32.778 | 56.603 | 1.00 | 2.00 | 0 |
| ATOM | 5236 | C | ARG | 746 | 48.597 | 32.439 | 59.271 | 1.00 | 2.00 | 0 |
| ATOM | 5237 | O | ARG | 746 | 47.739 | 33.220 | 58.847 | 1.00 | 2.00 | 0 |
| ATOM | 5238 | N | ALA | 747 | 49.524 | 32.802 | 60.146 | 1.00 | 2.00 | 0 |
| ATOM | 5240 | CA | ALA | 747 | 49.635 | 34.185 | 60.595 | 1.00 | 2.00 | 0 |
| ATOM | 5241 | CB | ALA | 747 | 49.410 | 34.264 | 62.106 | 1.00 | 2.00 | 0 |
| ATOM | 5242 | C | ALA | 747 | 51.073 | 34.588 | 60.193 | 1.00 | 2.00 | 0 |
| ATOM | 5243 | O | ALA | 747 | 51.378 | 34.658 | 58.999 | 1.00 | 2.00 | 0 |
| ATOM | 5244 | N | HIS | 748 | 51.943 | 34.854 | 61.168 | 1.00 | 2.00 | 0 |
| ATOM | 5246 | CA | HIS | 748 | 53.359 | 35.168 | 60.939 | 1.00 | 2.00 | 0 |
| ATOM | 5247 | C | HIS | 748 | 53.812 | 36.462 | 60.309 | 1.00 | 2.00 | 0 |
| ATOM | 5248 | O | HIS | 748 | 54.820 | 37.004 | 60.744 | 1.00 | 2.00 | 0 |
| ATOM | 5249 | CB | HIS | 748 | 54.032 | 34.028 | 60.187 | 1.00 | 2.00 | 0 |
| ATOM | 5250 | CG | HIS | 748 | 55.503 | 33.916 | 60.429 | 1.00 | 2.00 | 0 |
| ATOM | 5251 | ND1 | HIS | 748 | 56.023 | 33.803 | 61.694 | 1.00 | 2.00 | 0 |
| ATOM | 5252 | CE1 | HIS | 748 | 57.308 | 33.548 | 61.526 | 1.00 | 2.00 | 0 |
| ATOM | 5253 | CD2 | HIS | 748 | 56.493 | 33.737 | 59.527 | 1.00 | 2.00 | 0 |
| ATOM | 5254 | NE2 | HIS | 748 | 57.634 | 33.500 | 60.237 | 1.00 | 2.00 | 0 |
| ATOM | 5256 | N | GLN | 749 | 53.116 | 36.962 | 59.302 | 1.00 | 2.00 | 0 |
| ATOM | 5258 | CA | GLN | 749 | 53.556 | 38.197 | 58.677 | 1.00 | 2.00 | 0 |
| ATOM | 5259 | CB | GLN | 749 | 53.964 | 37.940 | 57.249 | 1.00 | 27.13 | 0 |
| ATOM | 5260 | CG | GLN | 749 | 55.257 | 37.222 | 57.143 | 1.00 | 28.03 | 0 |
| ATOM | 5261 | CD | GLN | 749 | 55.586 | 36.915 | 55.720 | 1.00 | 30.37 | 0 |
| ATOM | 5262 | OE1 | GLN | 749 | 56.425 | 37.580 | 55.107 | 1.00 | 30.92 | 0 |
| ATOM | 5263 | NE2 | GLN | 749 | 54.928 | 35.898 | 55.173 | 1.00 | 30.08 | 0 |
| ATOM | 5266 | C | GLN | 749 | 52.556 | 39.310 | 58.708 | 1.00 | 2.00 | 0 |
| ATOM | 5267 | O | GLN | 749 | 51.388 | 39.106 | 58.407 | 1.00 | 25.39 | 0 |
| ATOM | 5268 | N | VAL | 750 | 53.038 | 40.498 | 59.069 | 1.00 | 6.34 | 0 |
| ATOM | 5270 | CA | VAL | 750 | 52.193 | 41.682 | 59.157 | 1.00 | 6.34 | 0 |
| ATOM | 5271 | CB | VAL | 750 | 52.968 | 42.896 | 59.764 | 1.00 | 12.20 | 0 |
| ATOM | 5272 | CG1 | VAL | 750 | 54.183 | 43.216 | 58.935 | 1.00 | 12.20 | 0 |
| ATOM | 5273 | CG2 | VAL | 750 | 52.055 | 44.109 | 59.872 | 1.00 | 12.20 | 0 |
| ATOM | 5274 | C | VAL | 750 | 51.672 | 42.018 | 57.771 | 1.00 | 6.34 | 0 |
| ATOM | 5275 | O | VAL | 750 | 52.471 | 42.219 | 56.850 | 1.00 | 12.20 | 0 |
| ATOM | 5276 | N | VAL | 751 | 50.343 | 42.001 | 57.617 | 1.00 | 25.10 | 0 |
| ATOM | 5278 | CA | VAL | 751 | 49.685 | 42.327 | 56.348 | 1.00 | 25.10 | 0 |
| ATOM | 5279 | CB | VAL | 751 | 48.617 | 41.298 | 55.902 | 1.00 | 2.00 | 0 |
| ATOM | 5280 | CG1 | VAL | 751 | 49.271 | 39.971 | 55.524 | 1.00 | 2.00 | 0 |
| ATOM | 5281 | CG2 | VAL | 751 | 47.570 | 41.138 | 56.976 | 1.00 | 2.00 | 0 |
| ATOM | 5282 | C | VAL | 751 | 48.996 | 43.654 | 56.540 | 1.00 | 25.10 | 0 |
| ATOM | 5283 | O | VAL | 751 | 48.606 | 43.995 | 57.646 | 1.00 | 2.00 | 0 |
| ATOM | 5284 | N | GLU | 752 | 48.820 | 44.389 | 55.453 | 1.00 | 2.00 | 0 |
| ATOM | 5286 | CA | GLU | 752 | 48.219 | 45.709 | 55.526 | 1.00 | 2.00 | 0 |

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|---|---|---|---|---|---|---|---|---|---|---|
| ATOM | 5287 | CB | GLU | 752 | 48.430 | 46.435 | 54.190 | 1.00 | 39.24 | 0 |
| ATOM | 5288 | CG | GLU | 752 | 49.867 | 46.349 | 53.628 | 1.00 | 75.32 | 0 |
| ATOM | 5289 | CD | GLU | 752 | 50.962 | 46.804 | 54.611 | 1.00 | 75.31 | 0 |
| ATOM | 5290 | OE1 | GLU | 752 | 52.007 | 46.121 | 54.687 | 1.00 | 74.90 | 0 |
| ATOM | 5291 | OE2 | GLU | 752 | 50.792 | 47.837 | 55.300 | 1.00 | 91.76 | 0 |
| ATOM | 5292 | C | GLU | 752 | 46.744 | 45.716 | 55.913 | 1.00 | 2.00 | 0 |
| ATOM | 5293 | O | GLU | 752 | 46.326 | 46.469 | 56.796 | 1.00 | 38.94 | 0 |
| ATOM | 5294 | N | ASP | 753 | 45.968 | 44.860 | 55.259 | 1.00 | 31.76 | 0 |
| ATOM | 5296 | CA | ASP | 753 | 44.527 | 44.776 | 55.491 | 1.00 | 34.73 | 0 |
| ATOM | 5297 | CB | ASP | 753 | 43.787 | 44.470 | 54.170 | 1.00 | 79.26 | 0 |
| ATOM | 5298 | CG | ASP | 753 | 44.539 | 43.487 | 53.251 | 1.00 | 85.10 | 0 |
| ATOM | 5299 | OD1 | ASP | 753 | 44.040 | 43.240 | 52.130 | 1.00 | 88.01 | 0 |
| ATOM | 5300 | OD2 | ASP | 753 | 45.613 | 42.960 | 53.619 | 1.00 | 92.40 | 0 |
| ATOM | 5301 | C | ASP | 753 | 44.028 | 43.853 | 56.606 | 1.00 | 31.43 | 0 |
| ATOM | 5302 | O | ASP | 753 | 42.824 | 43.759 | 56.835 | 1.00 | 64.64 | 0 |
| ATOM | 5303 | N | GLY | 754 | 44.940 | 43.188 | 57.309 | 1.00 | 8.60 | 0 |
| ATOM | 5305 | CA | GLY | 754 | 44.535 | 42.309 | 58.393 | 1.00 | 5.10 | 0 |
| ATOM | 5306 | C | GLY | 754 | 44.577 | 40.849 | 58.007 | 1.00 | 3.66 | 0 |
| ATOM | 5307 | O | GLY | 754 | 44.781 | 39.959 | 58.853 | 1.00 | 2.00 | 0 |
| ATOM | 5308 | N | TYR | 755 | 44.361 | 40.611 | 56.718 | 1.00 | 27.09 | 0 |
| ATOM | 5310 | CA | TYR | 755 | 44.388 | 39.282 | 56.129 | 1.00 | 27.09 | 0 |
| ATOM | 5311 | CB | TYR | 755 | 43.004 | 38.632 | 56.128 | 1.00 | 28.14 | 0 |
| ATOM | 5312 | CG | TYR | 755 | 41.976 | 39.338 | 55.279 | 1.00 | 25.47 | 0 |
| ATOM | 5313 | CD1 | TYR | 755 | 41.236 | 40.393 | 55.797 | 1.00 | 23.65 | 0 |
| ATOM | 5314 | CE1 | TYR | 755 | 40.276 | 41.049 | 55.034 | 1.00 | 28.13 | 0 |
| ATOM | 5315 | CD2 | TYR | 755 | 41.736 | 38.949 | 53.964 | 1.00 | 30.24 | 0 |
| ATOM | 5316 | CE2 | TYR | 755 | 40.774 | 39.601 | 53.187 | 1.00 | 27.11 | 0 |
| ATOM | 5317 | CZ | TYR | 755 | 40.046 | 40.653 | 53.732 | 1.00 | 32.27 | 0 |
| ATOM | 5318 | OH | TYR | 755 | 39.086 | 41.311 | 52.996 | 1.00 | 28.90 | 0 |
| ATOM | 5320 | C | TYR | 755 | 44.844 | 39.530 | 54.713 | 1.00 | 27.09 | 0 |
| ATOM | 5321 | O | TYR | 755 | 44.772 | 40.654 | 54.238 | 1.00 | 25.53 | 0 |
| ATOM | 5322 | N | GLU | 756 | 45.288 | 38.483 | 54.035 | 1.00 | 8.71 | 0 |
| ATOM | 5324 | CA | GLU | 756 | 45.787 | 38.617 | 52.676 | 1.00 | 8.71 | 0 |
| ATOM | 5325 | CB | GLU | 756 | 47.170 | 39.251 | 52.740 | 1.00 | 5.76 | 0 |
| ATOM | 5326 | CG | GLU | 756 | 47.832 | 39.557 | 51.436 | 1.00 | 16.72 | 0 |
| ATOM | 5327 | CD | GLU | 756 | 49.127 | 40.303 | 51.671 | 1.00 | 23.34 | 0 |
| ATOM | 5328 | OE1 | GLU | 756 | 49.074 | 41.554 | 51.801 | 1.00 | 25.72 | 0 |
| ATOM | 5329 | OE2 | GLU | 756 | 50.194 | 39.636 | 51.751 | 1.00 | 25.15 | 0 |
| ATOM | 5330 | C | GLU | 756 | 45.853 | 37.240 | 52.044 | 1.00 | 8.71 | 0 |
| ATOM | 5331 | O | GLU | 756 | 46.400 | 36.306 | 52.638 | 1.00 | 6.14 | 0 |
| ATOM | 5332 | N | PHE | 757 | 45.269 | 37.105 | 50.858 | 1.00 | 28.33 | 0 |
| ATOM | 5334 | CA | PHE | 757 | 45.270 | 35.822 | 50.174 | 1.00 | 28.33 | 0 |
| ATOM | 5335 | CB | PHE | 757 | 44.055 | 35.683 | 49.253 | 1.00 | 2.00 | 0 |
| ATOM | 5336 | CG | PHE | 757 | 42.748 | 35.612 | 49.982 | 1.00 | 2.00 | 0 |
| ATOM | 5337 | CD1 | PHE | 757 | 41.961 | 36.747 | 50.137 | 1.00 | 2.00 | 0 |
| ATOM | 5338 | CD2 | PHE | 757 | 42.306 | 34.407 | 50.535 | 1.00 | 2.00 | 0 |
| ATOM | 5339 | CE1 | PHE | 757 | 40.751 | 36.695 | 50.833 | 1.00 | 2.00 | 0 |
| ATOM | 5340 | CE2 | PHE | 757 | 41.092 | 34.337 | 51.238 | 1.00 | 2.00 | 0 |
| ATOM | 5341 | CZ | PHE | 757 | 40.315 | 35.489 | 51.385 | 1.00 | 2.00 | 0 |
| ATOM | 5342 | C | PHE | 757 | 46.547 | 35.639 | 49.387 | 1.00 | 28.33 | 0 |
| ATOM | 5343 | O | PHE | 757 | 47.220 | 36.602 | 49.033 | 1.00 | 2.00 | 0 |
| ATOM | 5344 | N | PHE | 758 | 46.893 | 34.387 | 49.150 | 1.00 | 2.00 | 0 |
| ATOM | 5346 | CA | PHE | 758 | 48.075 | 34.050 | 48.397 | 1.00 | 2.00 | 0 |
| ATOM | 5347 | CB | PHE | 758 | 49.241 | 33.789 | 49.317 | 1.00 | 10.52 | 0 |
| ATOM | 5348 | CG | PHE | 758 | 50.450 | 33.263 | 48.618 | 1.00 | 7.54 | 0 |
| ATOM | 5349 | CD1 | PHE | 758 | 51.404 | 34.131 | 48.100 | 1.00 | 7.91 | 0 |
| ATOM | 5350 | CD2 | PHE | 758 | 50.654 | 31.895 | 48.492 | 1.00 | 7.80 | 0 |
| ATOM | 5351 | CE1 | PHE | 758 | 52.546 | 33.642 | 47.467 | 1.00 | 11.14 | 0 |
| ATOM | 5352 | CE2 | PHE | 758 | 51.796 | 31.398 | 47.858 | 1.00 | 11.57 | 0 |
| ATOM | 5353 | CZ | PHE | 758 | 52.741 | 32.272 | 47.347 | 1.00 | 10.83 | 0 |
| ATOM | 5354 | C | PHE | 758 | 47.725 | 32.786 | 47.636 | 1.00 | 2.00 | 0 |
| ATOM | 5355 | O | PHE | 758 | 46.826 | 32.034 | 48.042 | 1.00 | 13.46 | 0 |
| ATOM | 5356 | N | ALA | 759 | 48.415 | 32.573 | 46.518 | 1.00 | 17.88 | 0 |
| ATOM | 5358 | CA | ALA | 759 | 48.196 | 31.407 | 45.673 | 1.00 | 17.63 | 0 |
| ATOM | 5359 | CB | ALA | 759 | 48.767 | 30.155 | 46.334 | 1.00 | 2.00 | 0 |
| ATOM | 5360 | C | ALA | 759 | 46.733 | 31.180 | 45.314 | 1.00 | 19.54 | 0 |
| ATOM | 5361 | O | ALA | 759 | 46.187 | 30.106 | 45.547 | 1.00 | 2.00 | 0 |
| ATOM | 5362 | N | LYS | 760 | 46.086 | 32.205 | 44.780 | 1.00 | 3.38 | 0 |

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|---|---|---|---|---|---|---|---|---|---|---|
| ATOM | 5364 | CA | LYS | 760 | 44.699 | 32.076 | 44.341 | 1.00 | 3.38 | 0 |
| ATOM | 5365 | CB | LYS | 760 | 44.639 | 31.068 | 43.184 | 1.00 | 64.10 | 0 |
| ATOM | 5366 | CG | LYS | 760 | 45.654 | 31.316 | 42.062 | 1.00 | 64.10 | 0 |
| ATOM | 5367 | CD | LYS | 760 | 45.843 | 30.068 | 41.205 | 1.00 | 64.10 | 0 |
| ATOM | 5368 | CE | LYS | 760 | 44.506 | 29.540 | 40.699 | 1.00 | 64.10 | 0 |
| ATOM | 5369 | NZ | LYS | 760 | 44.621 | 28.293 | 39.896 | 1.00 | 64.10 | 0 |
| ATOM | 5373 | C | LYS | 760 | 43.715 | 31.659 | 45.432 | 1.00 | 3.38 | 0 |
| ATOM | 5374 | O | LYS | 760 | 42.953 | 30.702 | 45.256 | 1.00 | 64.10 | 0 |
| ATOM | 5375 | N | ARG | 761 | 43.751 | 32.376 | 46.557 | 1.00 | 16.83 | 0 |
| ATOM | 5377 | CA | ARG | 761 | 42.869 | 32.139 | 47.721 | 1.00 | 16.83 | 0 |
| ATOM | 5378 | CB | ARG | 761 | 41.399 | 32.154 | 47.274 | 1.00 | 38.86 | 0 |
| ATOM | 5379 | CG | ARG | 761 | 41.012 | 33.375 | 46.458 | 1.00 | 38.86 | 0 |
| ATOM | 5380 | CD | ARG | 761 | 40.550 | 34.493 | 47.334 | 1.00 | 38.86 | 0 |
| ATOM | 5381 | NE | ARG | 761 | 40.635 | 35.785 | 46.669 | 1.00 | 38.86 | 0 |
| ATOM | 5383 | CZ | ARG | 761 | 39.799 | 36.793 | 46.898 | 1.00 | 38.86 | 0 |
| ATOM | 5384 | NH1 | ARG | 761 | 38.798 | 36.642 | 47.767 | 1.00 | 38.86 | 0 |
| ATOM | 5387 | NH2 | ARG | 761 | 39.988 | 37.963 | 46.291 | 1.00 | 38.86 | 0 |
| ATOM | 5390 | C | ARG | 761 | 43.145 | 30.844 | 48.508 | 1.00 | 16.83 | 0 |
| ATOM | 5391 | O | ARG | 761 | 42.596 | 30.639 | 49.585 | 1.00 | 38.86 | 0 |
| ATOM | 5392 | N | GLN | 762 | 44.021 | 30.002 | 47.971 | 1.00 | 24.54 | 0 |
| ATOM | 5394 | CA | GLN | 762 | 44.359 | 28.718 | 48.559 | 1.00 | 24.54 | 0 |
| ATOM | 5395 | CB | GLN | 762 | 45.167 | 27.908 | 47.553 | 1.00 | 19.81 | 0 |
| ATOM | 5396 | CG | GLN | 762 | 44.502 | 27.794 | 46.173 | 1.00 | 19.81 | 0 |
| ATOM | 5397 | CD | GLN | 762 | 45.309 | 26.959 | 45.196 | 1.00 | 19.81 | 0 |
| ATOM | 5398 | OE1 | GLN | 762 | 45.111 | 25.745 | 45.097 | 1.00 | 19.81 | 0 |
| ATOM | 5399 | NE2 | GLN | 762 | 46.230 | 27.596 | 44.476 | 1.00 | 19.81 | 0 |
| ATOM | 5402 | C | GLN | 762 | 45.126 | 28.856 | 49.857 | 1.00 | 24.54 | 0 |
| ATOM | 5403 | O | GLN | 762 | 45.278 | 27.893 | 50.599 | 1.00 | 19.81 | 0 |
| ATOM | 5404 | N | LEU | 763 | 45.631 | 30.053 | 50.119 | 1.00 | 2.00 | 0 |
| ATOM | 5406 | CA | LEU | 763 | 46.354 | 30.326 | 51.353 | 1.00 | 2.00 | 0 |
| ATOM | 5407 | CB | LEU | 763 | 47.882 | 30.319 | 51.127 | 1.00 | 13.68 | 0 |
| ATOM | 5408 | CG | LEU | 763 | 48.847 | 30.427 | 52.335 | 1.00 | 13.68 | 0 |
| ATOM | 5409 | CD1 | LEU | 763 | 50.117 | 29.641 | 52.066 | 1.00 | 13.68 | 0 |
| ATOM | 5410 | CD2 | LEU | 763 | 49.200 | 31.871 | 52.633 | 1.00 | 13.68 | 0 |
| ATOM | 5411 | C | LEU | 763 | 45.893 | 31.705 | 51.809 | 1.00 | 2.00 | 0 |
| ATOM | 5412 | O | LEU | 763 | 45.654 | 32.595 | 50.981 | 1.00 | 13.68 | 0 |
| ATOM | 5413 | N | VAL | 764 | 45.741 | 31.869 | 53.118 | 1.00 | 13.21 | 0 |
| ATOM | 5415 | CA | VAL | 764 | 45.340 | 33.140 | 53.680 | 1.00 | 13.65 | 0 |
| ATOM | 5416 | CB | VAL | 764 | 43.825 | 33.165 | 53.953 | 1.00 | 2.00 | 0 |
| ATOM | 5417 | CG1 | VAL | 764 | 43.452 | 32.097 | 54.933 | 1.00 | 2.00 | 0 |
| ATOM | 5418 | CG2 | VAL | 764 | 43.404 | 34.521 | 54.434 | 1.00 | 2.00 | 0 |
| ATOM | 5419 | C | VAL | 764 | 46.159 | 33.363 | 54.955 | 1.00 | 18.12 | 0 |
| ATOM | 5420 | O | VAL | 764 | 46.396 | 32.437 | 55.737 | 1.00 | 2.00 | 0 |
| ATOM | 5421 | N | THR | 765 | 46.646 | 34.587 | 55.111 | 1.00 | 2.00 | 0 |
| ATOM | 5423 | CA | THR | 765 | 47.453 | 34.992 | 56.254 | 1.00 | 2.00 | 0 |
| ATOM | 5424 | CB | THR | 765 | 48.731 | 35.660 | 55.798 | 1.00 | 2.00 | 0 |
| ATOM | 5425 | OG1 | THR | 765 | 49.474 | 34.740 | 54.991 | 1.00 | 2.00 | 0 |
| ATOM | 5427 | CG2 | THR | 765 | 49.542 | 36.119 | 56.973 | 1.00 | 2.00 | 0 |
| ATOM | 5428 | C | THR | 765 | 46.675 | 36.024 | 57.030 | 1.00 | 2.00 | 0 |
| ATOM | 5429 | O | THR | 765 | 46.201 | 37.016 | 56.454 | 1.00 | 2.00 | 0 |
| ATOM | 5430 | N | LEU | 766 | 46.549 | 35.797 | 58.333 | 1.00 | 5.65 | 0 |
| ATOM | 5432 | CA | LEU | 766 | 45.832 | 36.717 | 59.205 | 1.00 | 5.65 | 0 |
| ATOM | 5433 | CB | LEU | 766 | 44.848 | 35.943 | 60.059 | 1.00 | 2.00 | 0 |
| ATOM | 5434 | CG | LEU | 766 | 43.964 | 34.922 | 59.372 | 1.00 | 2.00 | 0 |
| ATOM | 5435 | CD1 | LEU | 766 | 43.703 | 33.794 | 60.327 | 1.00 | 2.00 | 0 |
| ATOM | 5436 | CD2 | LEU | 766 | 42.672 | 35.581 | 58.943 | 1.00 | 2.00 | 0 |
| ATOM | 5437 | C | LEU | 766 | 46.826 | 37.382 | 60.142 | 1.00 | 5.65 | 0 |
| ATOM | 5438 | O | LEU | 766 | 47.864 | 36.790 | 60.478 | 1.00 | 2.00 | 0 |
| ATOM | 5439 | N | PHE | 767 | 46.520 | 38.605 | 60.554 | 1.00 | 2.00 | 0 |
| ATOM | 5441 | CA | PHE | 767 | 47.342 | 39.320 | 61.530 | 1.00 | 2.00 | 0 |
| ATOM | 5442 | CB | PHE | 767 | 48.259 | 40.328 | 60.864 | 1.00 | 2.00 | 0 |
| ATOM | 5443 | CG | PHE | 767 | 49.494 | 40.612 | 61.649 | 1.00 | 2.00 | 0 |
| ATOM | 5444 | CD1 | PHE | 767 | 50.523 | 39.678 | 61.695 | 1.00 | 2.00 | 0 |
| ATOM | 5445 | CD2 | PHE | 767 | 49.647 | 41.811 | 62.317 | 1.00 | 2.00 | 0 |
| ATOM | 5446 | CE1 | PHE | 767 | 51.689 | 39.935 | 62.389 | 1.00 | 2.00 | 0 |
| ATOM | 5447 | CE2 | PHE | 767 | 50.813 | 42.078 | 63.018 | 1.00 | 2.00 | 0 |
| ATOM | 5448 | CZ | PHE | 767 | 51.838 | 41.134 | 63.050 | 1.00 | 2.00 | 0 |
| ATOM | 5449 | C | PHE | 767 | 46.325 | 40.033 | 62.418 | 1.00 | 2.00 | 0 |

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|---|---|---|---|---|---|---|---|---|---|---|
| ATOM | 5450 | O | PHE | 767 | 45.957 | 41.184 | 62.171 | 1.00 | 2.00 | 0 |
| ATOM | 5451 | N | SER | 768 | 45.850 | 39.317 | 63.432 | 1.00 | 2.00 | 0 |
| ATOM | 5453 | CA | SER | 768 | 44.833 | 39.819 | 64.334 | 1.00 | 2.00 | 0 |
| ATOM | 5454 | CB | SER | 768 | 44.247 | 38.645 | 65.091 | 1.00 | 2.00 | 0 |
| ATOM | 5455 | OG | SER | 768 | 43.903 | 37.635 | 64.175 | 1.00 | 2.00 | 0 |
| ATOM | 5457 | C | SER | 768 | 45.261 | 40.872 | 65.336 | 1.00 | 2.00 | 0 |
| ATOM | 5458 | O | SER | 768 | 46.297 | 40.731 | 65.973 | 1.00 | 2.00 | 0 |
| ATOM | 5459 | N | ALA | 769 | 44.435 | 41.911 | 65.474 | 1.00 | 30.20 | 0 |
| ATOM | 5461 | CA | ALA | 769 | 44.619 | 43.009 | 66.428 | 1.00 | 27.69 | 0 |
| ATOM | 5462 | CB | ALA | 769 | 45.142 | 42.454 | 67.786 | 1.00 | 4.86 | 0 |
| ATOM | 5463 | C | ALA | 769 | 45.410 | 44.253 | 66.018 | 1.00 | 31.35 | 0 |
| ATOM | 5464 | O | ALA | 769 | 44.855 | 45.347 | 65.940 | 1.00 | 11.84 | 0 |
| ATOM | 5465 | N | PRO | 770 | 46.717 | 44.109 | 65.786 | 1.00 | 14.07 | 0 |
| ATOM | 5466 | CD | PRO | 770 | 47.556 | 42.904 | 65.939 | 1.00 | 2.00 | 0 |
| ATOM | 5467 | CA | PRO | 770 | 47.578 | 45.209 | 65.398 | 1.00 | 14.07 | 0 |
| ATOM | 5468 | CB | PRO | 770 | 48.615 | 44.494 | 64.540 | 1.00 | 2.00 | 0 |
| ATOM | 5469 | CG | PRO | 770 | 48.913 | 43.329 | 65.392 | 1.00 | 2.00 | 0 |
| ATOM | 5470 | C | PRO | 770 | 47.227 | 46.584 | 64.825 | 1.00 | 14.07 | 0 |
| ATOM | 5471 | O | PRO | 770 | 46.081 | 47.016 | 64.640 | 1.00 | 2.00 | 0 |
| ATOM | 5472 | N | ASN | 771 | 48.363 | 47.259 | 64.718 | 1.00 | 2.00 | 0 |
| ATOM | 5474 | CA | ASN | 771 | 48.703 | 48.578 | 64.220 | 1.00 | 2.00 | 0 |
| ATOM | 5475 | CB | ASN | 771 | 48.014 | 49.664 | 65.022 | 1.00 | 40.66 | 0 |
| ATOM | 5476 | CG | ASN | 771 | 48.270 | 51.032 | 64.457 | 1.00 | 47.17 | 0 |
| ATOM | 5477 | OD1 | ASN | 771 | 49.382 | 51.557 | 64.550 | 1.00 | 40.36 | 0 |
| ATOM | 5478 | ND2 | ASN | 771 | 47.249 | 51.617 | 63.841 | 1.00 | 43.79 | 0 |
| ATOM | 5481 | C | ASN | 771 | 50.174 | 48.414 | 64.666 | 1.00 | 2.00 | 0 |
| ATOM | 5482 | O | ASN | 771 | 50.811 | 49.318 | 65.208 | 1.00 | 50.90 | 0 |
| ATOM | 5483 | N | TYR | 772 | 50.657 | 47.191 | 64.417 | 1.00 | 6.11 | 0 |
| ATOM | 5485 | CA | TYR | 772 | 51.955 | 46.645 | 64.768 | 1.00 | 6.11 | 0 |
| ATOM | 5486 | CB | TYR | 772 | 52.366 | 45.641 | 63.705 | 1.00 | 8.06 | 0 |
| ATOM | 5487 | CG | TYR | 772 | 53.253 | 44.546 | 64.228 | 1.00 | 8.06 | 0 |
| ATOM | 5488 | CD1 | TYR | 772 | 52.992 | 43.949 | 65.453 | 1.00 | 8.06 | 0 |
| ATOM | 5489 | CE1 | TYR | 772 | 53.781 | 42.910 | 65.929 | 1.00 | 8.06 | 0 |
| ATOM | 5490 | CD2 | TYR | 772 | 54.335 | 44.084 | 63.487 | 1.00 | 8.06 | 0 |
| ATOM | 5491 | CE2 | TYR | 772 | 55.135 | 43.048 | 63.945 | 1.00 | 8.06 | 0 |
| ATOM | 5492 | CZ | TYR | 772 | 54.854 | 42.459 | 65.170 | 1.00 | 8.06 | 0 |
| ATOM | 5493 | OH | TYR | 772 | 55.634 | 41.403 | 65.632 | 1.00 | 8.06 | 0 |
| ATOM | 5495 | C | TYR | 772 | 53.130 | 47.557 | 65.074 | 1.00 | 6.11 | 0 |
| ATOM | 5496 | O | TYR | 772 | 53.499 | 48.428 | 64.271 | 1.00 | 19.22 | 0 |
| ATOM | 5497 | N | CYS | 773 | 53.724 | 47.335 | 66.244 | 1.00 | 15.64 | 0 |
| ATOM | 5499 | CA | CYS | 773 | 54.868 | 48.107 | 66.681 | 1.00 | 13.08 | 0 |
| ATOM | 5500 | CB | CYS | 773 | 56.059 | 47.798 | 65.777 | 1.00 | 21.47 | 0 |
| ATOM | 5501 | SG | CYS | 773 | 56.646 | 46.112 | 65.891 | 1.00 | 23.28 | 0 |
| ATOM | 5502 | C | CYS | 773 | 54.624 | 49.617 | 66.685 | 1.00 | 16.93 | 0 |
| ATOM | 5503 | O | CYS | 773 | 55.573 | 50.398 | 66.832 | 1.00 | 20.82 | 0 |
| ATOM | 5504 | N | GLY | 774 | 53.362 | 50.031 | 66.545 | 1.00 | 2.00 | 0 |
| ATOM | 5506 | CA | GLY | 774 | 53.059 | 51.452 | 66.482 | 1.00 | 2.00 | 0 |
| ATOM | 5507 | C | GLY | 774 | 53.821 | 52.023 | 65.288 | 1.00 | 2.00 | 0 |
| ATOM | 5508 | O | GLY | 774 | 54.051 | 53.233 | 65.188 | 1.00 | 60.37 | 0 |
| ATOM | 5509 | N | GLU | 775 | 54.219 | 51.130 | 64.383 | 1.00 | 22.26 | 0 |
| ATOM | 5511 | CA | GLU | 775 | 54.973 | 51.500 | 63.211 | 1.00 | 18.01 | 0 |
| ATOM | 5512 | CB | GLU | 775 | 56.253 | 50.683 | 63.133 | 1.00 | 40.50 | 0 |
| ATOM | 5513 | CG | GLU | 775 | 57.103 | 50.811 | 64.357 | 1.00 | 44.10 | 0 |
| ATOM | 5514 | CD | GLU | 775 | 58.496 | 50.246 | 64.190 | 1.00 | 42.58 | 0 |
| ATOM | 5515 | OE1 | GLU | 775 | 59.404 | 50.734 | 64.894 | 1.00 | 46.10 | 0 |
| ATOM | 5516 | OE2 | GLU | 775 | 58.687 | 49.324 | 63.367 | 1.00 | 44.55 | 0 |
| ATOM | 5517 | C | GLU | 775 | 54.181 | 51.268 | 61.945 | 1.00 | 16.06 | 0 |
| ATOM | 5518 | O | GLU | 775 | 54.133 | 52.118 | 61.051 | 1.00 | 34.47 | 0 |
| ATOM | 5519 | N | PHE | 776 | 53.530 | 50.125 | 61.874 | 1.00 | 21.64 | 0 |
| ATOM | 5521 | CA | PHE | 776 | 52.809 | 49.796 | 60.667 | 1.00 | 19.45 | 0 |
| ATOM | 5522 | CB | PHE | 776 | 52.828 | 48.279 | 60.517 | 1.00 | 7.64 | 0 |
| ATOM | 5523 | CG | PHE | 776 | 54.213 | 47.739 | 60.363 | 1.00 | 6.06 | 0 |
| ATOM | 5524 | CD1 | PHE | 776 | 55.056 | 47.656 | 61.452 | 1.00 | 6.54 | 0 |
| ATOM | 5525 | CD2 | PHE | 776 | 54.692 | 47.363 | 59.122 | 1.00 | 10.09 | 0 |
| ATOM | 5526 | CE1 | PHE | 776 | 56.370 | 47.206 | 61.313 | 1.00 | 6.06 | 0 |
| ATOM | 5527 | CE2 | PHE | 776 | 56.005 | 46.910 | 58.969 | 1.00 | 9.96 | 0 |
| ATOM | 5528 | CZ | PHE | 776 | 56.845 | 46.833 | 60.071 | 1.00 | 6.06 | 0 |
| ATOM | 5529 | C | PHE | 776 | 51.424 | 50.402 | 60.480 | 1.00 | 21.71 | 0 |

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|---|---|---|---|---|---|---|---|---|---|---|
| ATOM | 5530 | O | PHE | 776 | 50.979 | 50.601 | 59.346 | 1.00 | 9.78 | 0 |
| ATOM | 5531 | N | ASP | 777 | 50.757 | 50.720 | 61.584 | 1.00 | 47.34 | 0 |
| ATOM | 5533 | CA | ASP | 777 | 49.427 | 51.322 | 61.532 | 1.00 | 47.73 | 0 |
| ATOM | 5534 | CB | ASP | 777 | 49.526 | 52.790 | 61.071 | 1.00 | 36.82 | 0 |
| ATOM | 5535 | CG | ASP | 777 | 50.299 | 53.677 | 62.059 | 1.00 | 86.03 | 0 |
| ATOM | 5536 | OD1 | ASP | 777 | 51.519 | 53.464 | 62.246 | 1.00 | 85.84 | 0 |
| ATOM | 5537 | OD2 | ASP | 777 | 49.685 | 54.595 | 62.644 | 1.00 | 85.92 | 0 |
| ATOM | 5538 | C | ASP | 777 | 48.456 | 50.547 | 60.632 | 1.00 | 47.70 | 0 |
| ATOM | 5539 | O | ASP | 777 | 47.458 | 51.095 | 60.164 | 1.00 | 37.69 | 0 |
| ATOM | 5540 | N | ASN | 778 | 48.756 | 49.268 | 60.419 | 1.00 | 12.97 | 0 |
| ATOM | 5542 | CA | ASN | 778 | 47.948 | 48.373 | 59.584 | 1.00 | 3.97 | 0 |
| ATOM | 5543 | CB | ASN | 778 | 48.760 | 47.123 | 59.221 | 1.00 | 17.34 | 0 |
| ATOM | 5544 | CG | ASN | 778 | 49.081 | 46.258 | 60.435 | 1.00 | 11.19 | 0 |
| ATOM | 5545 | OD1 | ASN | 778 | 49.928 | 46.613 | 61.275 | 1.00 | 10.18 | 0 |
| ATOM | 5546 | ND2 | ASN | 778 | 48.404 | 45.120 | 60.538 | 1.00 | 7.69 | 0 |
| ATOM | 5549 | C | ASN | 778 | 46.672 | 47.945 | 60.296 | 1.00 | 4.32 | 0 |
| ATOM | 5550 | O | ASN | 778 | 46.497 | 48.227 | 61.481 | 1.00 | 21.92 | 0 |
| ATOM | 5551 | N | ALA | 779 | 45.783 | 47.267 | 59.578 | 1.00 | 6.26 | 0 |
| ATOM | 5553 | CA | ALA | 779 | 44.537 | 46.799 | 60.168 | 1.00 | 6.26 | 0 |
| ATOM | 5554 | CB | ALA | 779 | 43.404 | 46.923 | 59.174 | 1.00 | 78.54 | 0 |
| ATOM | 5555 | C | ALA | 779 | 44.727 | 45.344 | 60.580 | 1.00 | 6.26 | 0 |
| ATOM | 5556 | O | ALA | 779 | 45.537 | 44.626 | 59.988 | 1.00 | 86.19 | 0 |
| ATOM | 5557 | N | GLY | 780 | 43.998 | 44.925 | 61.606 | 1.00 | 2.00 | 0 |
| ATOM | 5559 | CA | GLY | 780 | 44.091 | 43.560 | 62.077 | 1.00 | 2.00 | 0 |
| ATOM | 5560 | C | GLY | 780 | 42.800 | 42.848 | 61.747 | 1.00 | 2.00 | 0 |
| ATOM | 5561 | O | GLY | 780 | 41.725 | 43.433 | 61.869 | 1.00 | 21.77 | 0 |
| ATOM | 5562 | N | ALA | 781 | 42.880 | 41.587 | 61.345 | 1.00 | 2.00 | 0 |
| ATOM | 5564 | CA | ALA | 781 | 41.670 | 40.870 | 60.984 | 1.00 | 2.00 | 0 |
| ATOM | 5565 | CB | ALA | 781 | 41.671 | 40.567 | 59.492 | 1.00 | 14.58 | 0 |
| ATOM | 5566 | C | ALA | 781 | 41.474 | 39.587 | 61.763 | 1.00 | 2.00 | 0 |
| ATOM | 5567 | O | ALA | 781 | 42.396 | 39.076 | 62.398 | 1.00 | 14.58 | 0 |
| ATOM | 5568 | N | MET | 782 | 40.263 | 39.061 | 61.660 | 1.00 | 2.00 | 0 |
| ATOM | 5570 | CA | MET | 782 | 39.857 | 37.833 | 62.319 | 1.00 | 2.00 | 0 |
| ATOM | 5571 | CB | MET | 782 | 39.037 | 38.204 | 63.554 | 1.00 | 2.00 | 0 |
| ATOM | 5572 | CG | MET | 782 | 38.736 | 37.067 | 64.502 | 1.00 | 2.00 | 0 |
| ATOM | 5573 | SD | MET | 782 | 37.743 | 37.608 | 65.912 | 1.00 | 2.00 | 0 |
| ATOM | 5574 | CE | MET | 782 | 37.595 | 39.370 | 65.621 | 1.00 | 2.00 | 0 |
| ATOM | 5575 | C | MET | 782 | 39.010 | 37.029 | 61.306 | 1.00 | 2.00 | 0 |
| ATOM | 5576 | O | MET | 782 | 38.090 | 37.570 | 60.688 | 1.00 | 2.00 | 0 |
| ATOM | 5577 | N | MET | 783 | 39.325 | 35.752 | 61.116 | 1.00 | 2.00 | 0 |
| ATOM | 5579 | CA | MET | 783 | 38.570 | 34.955 | 60.165 | 1.00 | 2.00 | 0 |
| ATOM | 5580 | CB | MET | 783 | 39.482 | 34.182 | 59.209 | 1.00 | 16.43 | 0 |
| ATOM | 5581 | CG | MET | 783 | 38.688 | 33.363 | 58.165 | 1.00 | 19.34 | 0 |
| ATOM | 5582 | SD | MET | 783 | 39.689 | 32.337 | 57.060 | 1.00 | 18.69 | 0 |
| ATOM | 5583 | CE | MET | 783 | 39.780 | 30.793 | 57.975 | 1.00 | 21.53 | 0 |
| ATOM | 5584 | C | MET | 783 | 37.608 | 33.976 | 60.794 | 1.00 | 2.00 | 0 |
| ATOM | 5585 | O | MET | 783 | 38.004 | 33.010 | 61.447 | 1.00 | 10.33 | 0 |
| ATOM | 5586 | N | SER | 784 | 36.335 | 34.221 | 60.542 | 1.00 | 2.00 | 0 |
| ATOM | 5588 | CA | SER | 784 | 35.276 | 33.374 | 61.034 | 1.00 | 2.00 | 0 |
| ATOM | 5589 | CB | SER | 784 | 34.033 | 34.220 | 61.308 | 1.00 | 16.25 | 0 |
| ATOM | 5590 | OG | SER | 784 | 34.385 | 35.392 | 62.020 | 1.00 | 16.25 | 0 |
| ATOM | 5592 | C | SER | 784 | 34.953 | 32.301 | 59.990 | 1.00 | 2.00 | 0 |
| ATOM | 5593 | O | SER | 784 | 34.672 | 32.611 | 58.839 | 1.00 | 19.28 | 0 |
| ATOM | 5594 | N | VAL | 785 | 35.033 | 31.045 | 60.401 | 1.00 | 10.88 | 0 |
| ATOM | 5596 | CA | VAL | 785 | 34.706 | 29.907 | 59.557 | 1.00 | 16.53 | 0 |
| ATOM | 5597 | CB | VAL | 785 | 35.649 | 28.739 | 59.792 | 1.00 | 11.43 | 0 |
| ATOM | 5598 | CG1 | VAL | 785 | 35.183 | 27.538 | 58.975 | 1.00 | 11.43 | 0 |
| ATOM | 5599 | CG2 | VAL | 785 | 37.082 | 29.153 | 59.477 | 1.00 | 11.43 | 0 |
| ATOM | 5600 | C | VAL | 785 | 33.357 | 29.465 | 60.083 | 1.00 | 12.38 | 0 |
| ATOM | 5601 | O | VAL | 785 | 33.254 | 28.998 | 61.225 | 1.00 | 11.43 | 0 |
| ATOM | 5602 | N | ASP | 786 | 32.307 | 29.613 | 59.291 | 1.00 | 2.00 | 0 |
| ATOM | 5604 | CA | ASP | 786 | 31.024 | 29.200 | 59.807 | 1.00 | 2.00 | 0 |
| ATOM | 5605 | CB | ASP | 786 | 29.874 | 30.008 | 59.171 | 1.00 | 24.90 | 0 |
| ATOM | 5606 | CG | ASP | 786 | 29.403 | 29.458 | 57.842 | 1.00 | 30.71 | 0 |
| ATOM | 5607 | OD1 | ASP | 786 | 28.245 | 29.765 | 57.474 | 1.00 | 33.80 | 0 |
| ATOM | 5608 | OD2 | ASP | 786 | 30.165 | 28.737 | 57.163 | 1.00 | 32.56 | 0 |
| ATOM | 5609 | C | ASP | 786 | 30.860 | 27.699 | 59.656 | 1.00 | 2.00 | 0 |
| ATOM | 5610 | O | ASP | 786 | 31.677 | 27.025 | 59.031 | 1.00 | 23.30 | 0 |

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|---|---|---|---|---|---|---|---|---|---|---|
| ATOM | 5611 | N | GLU | 787 | 29.803 | 27.195 | 60.268 | 1.00 | 7.48 | 0 |
| ATOM | 5613 | CA | GLU | 787 | 29.447 | 25.782 | 60.270 | 1.00 | 13.41 | 0 |
| ATOM | 5614 | CB | GLU | 787 | 27.983 | 25.636 | 60.696 | 1.00 | 2.00 | 0 |
| ATOM | 5615 | CG | GLU | 787 | 27.174 | 26.963 | 60.747 | 1.00 | 2.00 | 0 |
| ATOM | 5616 | CD | GLU | 787 | 27.384 | 27.758 | 62.053 | 1.00 | 2.00 | 0 |
| ATOM | 5617 | OE1 | GLU | 787 | 26.858 | 27.319 | 63.117 | 1.00 | 2.00 | 0 |
| ATOM | 5618 | OE2 | GLU | 787 | 28.070 | 28.817 | 62.024 | 1.00 | 2.00 | 0 |
| ATOM | 5619 | C | GLU | 787 | 29.665 | 25.015 | 58.965 | 1.00 | 11.86 | 0 |
| ATOM | 5620 | O | GLU | 787 | 30.002 | 23.830 | 58.994 | 1.00 | 2.00 | 0 |
| ATOM | 5621 | N | THR | 788 | 29.492 | 25.698 | 57.836 | 1.00 | 56.74 | 0 |
| ATOM | 5623 | CA | THR | 788 | 29.616 | 25.092 | 56.513 | 1.00 | 52.70 | 0 |
| ATOM | 5624 | CB | THR | 788 | 28.369 | 25.402 | 55.700 | 1.00 | 6.46 | 0 |
| ATOM | 5625 | OG1 | THR | 788 | 28.317 | 26.819 | 55.467 | 1.00 | 4.65 | 0 |
| ATOM | 5627 | CG2 | THR | 788 | 27.101 | 24.968 | 56.457 | 1.00 | 10.48 | 0 |
| ATOM | 5628 | C | THR | 788 | 30.835 | 25.536 | 55.683 | 1.00 | 51.86 | 0 |
| ATOM | 5629 | O | THR | 788 | 30.751 | 25.628 | 54.449 | 1.00 | 12.46 | 0 |
| ATOM | 5630 | N | LEU | 789 | 31.946 | 25.823 | 56.364 | 1.00 | 10.40 | 0 |
| ATOM | 5632 | CA | LEU | 789 | 33.194 | 26.245 | 55.734 | 1.00 | 6.34 | 0 |
| ATOM | 5633 | CB | LEU | 789 | 33.670 | 25.165 | 54.775 | 1.00 | 8.80 | 0 |
| ATOM | 5634 | CG | LEU | 789 | 34.458 | 24.017 | 55.405 | 1.00 | 15.93 | 0 |
| ATOM | 5635 | CD1 | LEU | 789 | 35.879 | 24.487 | 55.677 | 1.00 | 11.55 | 0 |
| ATOM | 5636 | CD2 | LEU | 789 | 33.785 | 23.525 | 56.682 | 1.00 | 14.98 | 0 |
| ATOM | 5637 | C | LEU | 789 | 33.173 | 27.619 | 55.042 | 1.00 | 4.53 | 0 |
| ATOM | 5638 | O | LEU | 789 | 34.065 | 27.948 | 54.248 | 1.00 | 8.97 | 0 |
| ATOM | 5639 | N | MET | 790 | 32.165 | 28.430 | 55.336 | 1.00 | 2.00 | 0 |
| ATOM | 5641 | CA | MET | 790 | 32.126 | 29.748 | 54.743 | 1.00 | 2.00 | 0 |
| ATOM | 5642 | CB | MET | 790 | 30.698 | 30.267 | 54.636 | 1.00 | 19.79 | 0 |
| ATOM | 5643 | CG | MET | 790 | 30.588 | 31.572 | 53.882 | 1.00 | 19.37 | 0 |
| ATOM | 5644 | SD | MET | 790 | 28.979 | 31.708 | 53.134 | 1.00 | 18.51 | 0 |
| ATOM | 5645 | CE | MET | 790 | 28.359 | 33.110 | 53.992 | 1.00 | 23.23 | 0 |
| ATOM | 5646 | C | MET | 790 | 32.945 | 30.667 | 55.627 | 1.00 | 2.00 | 0 |
| ATOM | 5647 | O | MET | 790 | 32.615 | 30.857 | 56.799 | 1.00 | 23.79 | 0 |
| ATOM | 5648 | N | CYS | 791 | 34.014 | 31.228 | 55.067 | 1.00 | 2.00 | 0 |
| ATOM | 5650 | CA | CYS | 791 | 34.882 | 32.133 | 55.803 | 1.00 | 2.00 | 0 |
| ATOM | 5651 | CB | CYS | 791 | 36.325 | 31.793 | 55.516 | 1.00 | 14.83 | 0 |
| ATOM | 5652 | SG | CYS | 791 | 36.570 | 30.052 | 55.766 | 1.00 | 15.43 | 0 |
| ATOM | 5653 | C | CYS | 791 | 34.616 | 33.591 | 55.502 | 1.00 | 2.00 | 0 |
| ATOM | 5654 | O | CYS | 791 | 34.314 | 33.961 | 54.371 | 1.00 | 21.84 | 0 |
| ATOM | 5655 | N | SER | 792 | 34.697 | 34.412 | 56.540 | 1.00 | 2.00 | 0 |
| ATOM | 5657 | CA | SER | 792 | 34.480 | 35.849 | 56.430 | 1.00 | 2.00 | 0 |
| ATOM | 5658 | CB | SER | 792 | 33.073 | 36.221 | 56.903 | 1.00 | 2.93 | 0 |
| ATOM | 5659 | OG | SER | 792 | 32.887 | 35.867 | 58.256 | 1.00 | 3.41 | 0 |
| ATOM | 5661 | C | SER | 792 | 35.539 | 36.518 | 57.303 | 1.00 | 2.00 | 0 |
| ATOM | 5662 | O | SER | 792 | 36.290 | 35.826 | 57.994 | 1.00 | 2.56 | 0 |
| ATOM | 5663 | N | PHE | 793 | 35.609 | 37.842 | 57.270 | 1.00 | 2.00 | 0 |
| ATOM | 5665 | CA | PHE | 793 | 36.617 | 38.558 | 58.039 | 1.00 | 2.00 | 0 |
| ATOM | 5666 | CB | PHE | 793 | 37.765 | 39.025 | 57.129 | 1.00 | 38.05 | 0 |
| ATOM | 5667 | CG | PHE | 793 | 38.531 | 37.913 | 56.469 | 1.00 | 24.74 | 0 |
| ATOM | 5668 | CD1 | PHE | 793 | 38.055 | 37.314 | 55.306 | 1.00 | 28.08 | 0 |
| ATOM | 5669 | CD2 | PHE | 793 | 39.741 | 37.474 | 57.002 | 1.00 | 26.11 | 0 |
| ATOM | 5670 | CE1 | PHE | 793 | 38.774 | 36.295 | 54.680 | 1.00 | 27.84 | 0 |
| ATOM | 5671 | CE2 | PHE | 793 | 40.466 | 36.460 | 56.389 | 1.00 | 27.16 | 0 |
| ATOM | 5672 | CZ | PHE | 793 | 39.983 | 35.868 | 55.225 | 1.00 | 29.41 | 0 |
| ATOM | 5673 | C | PHE | 793 | 36.101 | 39.782 | 58.784 | 1.00 | 2.00 | 0 |
| ATOM | 5674 | O | PHE | 793 | 35.362 | 40.599 | 58.233 | 1.00 | 23.22 | 0 |
| ATOM | 5675 | N | GLN | 794 | 36.480 | 39.893 | 60.051 | 1.00 | 67.38 | 0 |
| ATOM | 5677 | CA | GLN | 794 | 36.128 | 41.064 | 60.837 | 1.00 | 63.52 | 0 |
| ATOM | 5678 | CB | GLN | 794 | 35.608 | 40.713 | 62.238 | 1.00 | 31.74 | 0 |
| ATOM | 5679 | CG | GLN | 794 | 34.294 | 39.954 | 62.289 | 1.00 | 36.03 | 0 |
| ATOM | 5680 | CD | GLN | 794 | 34.506 | 38.455 | 62.252 | 1.00 | 39.99 | 0 |
| ATOM | 5681 | OE1 | GLN | 794 | 34.622 | 37.858 | 61.179 | 1.00 | 39.14 | 0 |
| ATOM | 5682 | NE2 | GLN | 794 | 34.575 | 37.838 | 63.425 | 1.00 | 44.72 | 0 |
| ATOM | 5685 | C | GLN | 794 | 37.471 | 41.760 | 60.958 | 1.00 | 65.96 | 0 |
| ATOM | 5686 | O | GLN | 794 | 38.486 | 41.132 | 61.272 | 1.00 | 37.24 | 0 |
| ATOM | 5687 | N | ILE | 795 | 37.498 | 43.045 | 60.658 | 1.00 | 53.07 | 0 |
| ATOM | 5689 | CA | ILE | 795 | 38.732 | 43.790 | 60.748 | 1.00 | 54.05 | 0 |
| ATOM | 5690 | CB | ILE | 795 | 39.084 | 44.483 | 59.392 | 1.00 | 26.19 | 0 |
| ATOM | 5691 | CG2 | ILE | 795 | 40.115 | 45.589 | 59.608 | 1.00 | 28.70 | 0 |

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|---|---|---|---|---|---|---|---|---|---|---|
| ATOM | 5692 | CG1 | ILE | 795 | 39.643 | 43.467 | 58.390 | 1.00 | 30.47 | 0 |
| ATOM | 5693 | CD1 | ILE | 795 | 38.659 | 42.449 | 57.906 | 1.00 | 28.83 | 0 |
| ATOM | 5694 | C | ILE | 795 | 38.543 | 44.847 | 61.817 | 1.00 | 53.94 | 0 |
| ATOM | 5695 | O | ILE | 795 | 37.476 | 45.452 | 61.903 | 1.00 | 27.08 | 0 |
| ATOM | 5696 | N | LEU | 796 | 39.544 | 45.008 | 62.674 | 1.00 | 30.60 | 0 |
| ATOM | 5698 | CA | LEU | 796 | 39.521 | 46.054 | 63.686 | 1.00 | 34.91 | 0 |
| ATOM | 5699 | CB | LEU | 796 | 39.839 | 45.528 | 65.089 | 1.00 | 41.88 | 0 |
| ATOM | 5700 | CG | LEU | 796 | 40.368 | 44.121 | 65.308 | 1.00 | 41.67 | 0 |
| ATOM | 5701 | CD1 | LEU | 796 | 40.976 | 44.038 | 66.702 | 1.00 | 39.26 | 0 |
| ATOM | 5702 | CD2 | LEU | 796 | 39.242 | 43.114 | 65.119 | 1.00 | 42.51 | 0 |
| ATOM | 5703 | C | LEU | 796 | 40.637 | 46.977 | 63.206 | 1.00 | 33.78 | 0 |
| ATOM | 5704 | O | LEU | 796 | 41.649 | 46.510 | 62.667 | 1.00 | 34.59 | 0 |
| ATOM | 5705 | N | LYS | 797 | 40.454 | 48.280 | 63.356 | 1.00 | 37.84 | 0 |
| ATOM | 5707 | CA | LYS | 797 | 41.475 | 49.207 | 62.902 | 1.00 | 40.12 | 0 |
| ATOM | 5708 | CB | LYS | 797 | 40.805 | 50.354 | 62.154 | 1.00 | 0.26 | 0 |
| ATOM | 5709 | CG | LYS | 797 | 39.959 | 49.929 | 60.932 | 1.00 | 0.34 | 0 |
| ATOM | 5710 | CD | LYS | 797 | 39.456 | 51.183 | 60.151 | 1.00 | 0.65 | 0 |
| ATOM | 5711 | CE | LYS | 797 | 39.134 | 50.875 | 58.662 | 1.00 | 0.12 | 0 |
| ATOM | 5712 | NZ | LYS | 797 | 38.852 | 52.117 | 57.851 | 1.00 | 0.70 | 0 |
| ATOM | 5716 | C | LYS | 797 | 42.356 | 49.727 | 64.053 | 1.00 | 50.42 | 0 |
| ATOM | 5717 | O | LYS | 797 | 42.961 | 50.809 | 63.985 | 1.00 | 0.89 | 0 |
| ATOM | 5718 | N | ALA | 400 | -8.399 | 33.628 | 131.469 | 1.00 | 75.56 | 0 |
| ATOM | 5720 | CA | ALA | 400 | -6.981 | 33.565 | 131.818 | 1.00 | 75.56 | 0 |
| ATOM | 5721 | CB | ALA | 400 | -6.134 | 33.160 | 130.576 | 1.00 | 21.27 | 0 |
| ATOM | 5722 | C | ALA | 400 | -6.530 | 34.922 | 132.352 | 1.00 | 75.56 | 0 |
| ATOM | 5723 | O | ALA | 400 | -7.350 | 35.762 | 132.744 | 1.00 | 21.27 | 0 |
| ATOM | 5724 | N | ARG | 401 | -5.218 | 35.116 | 132.374 | 1.00 | 2.00 | 0 |
| ATOM | 5726 | CA | ARG | 401 | -4.619 | 36.351 | 132.833 | 1.00 | 2.00 | 0 |
| ATOM | 5727 | CB | ARG | 401 | -4.586 | 36.395 | 134.359 | 1.00 | 2.00 | 0 |
| ATOM | 5728 | CG | ARG | 401 | -5.638 | 37.360 | 134.956 | 1.00 | 2.00 | 0 |
| ATOM | 5729 | CD | ARG | 401 | -5.639 | 37.340 | 136.471 | 1.00 | 2.00 | 0 |
| ATOM | 5730 | NE | ARG | 401 | -6.285 | 38.512 | 137.058 | 1.00 | 2.00 | 0 |
| ATOM | 5732 | CZ | ARG | 401 | -5.730 | 39.260 | 138.022 | 1.00 | 2.00 | 0 |
| ATOM | 5733 | NH1 | ARG | 401 | -6.338 | 40.369 | 138.457 | 1.00 | 2.00 | 0 |
| ATOM | 5736 | NH2 | ARG | 401 | -4.527 | 38.949 | 138.511 | 1.00 | 2.00 | 0 |
| ATOM | 5739 | C | ARG | 401 | -3.216 | 36.446 | 132.267 | 1.00 | 2.00 | 0 |
| ATOM | 5740 | O | ARG | 401 | -2.505 | 35.443 | 132.150 | 1.00 | 2.00 | 0 |
| ATOM | 5741 | N | VAL | 402 | -2.822 | 37.655 | 131.898 | 1.00 | 2.00 | 0 |
| ATOM | 5743 | CA | VAL | 402 | -1.516 | 37.882 | 131.311 | 1.00 | 2.00 | 0 |
| ATOM | 5744 | CB | VAL | 402 | -1.331 | 39.379 | 131.042 | 1.00 | 2.00 | 0 |
| ATOM | 5745 | CG1 | VAL | 402 | -0.063 | 39.632 | 130.283 | 1.00 | 2.00 | 0 |
| ATOM | 5746 | CG2 | VAL | 402 | -2.503 | 39.889 | 130.282 | 1.00 | 2.00 | 0 |
| ATOM | 5747 | C | VAL | 402 | -0.398 | 37.376 | 132.223 | 1.00 | 2.00 | 0 |
| ATOM | 5748 | O | VAL | 402 | -0.548 | 37.369 | 133.444 | 1.00 | 2.00 | 0 |
| ATOM | 5749 | N | SER | 403 | 0.701 | 36.920 | 131.625 | 1.00 | 19.26 | 0 |
| ATOM | 5751 | CA | SER | 403 | 1.882 | 36.461 | 132.361 | 1.00 | 23.92 | 0 |
| ATOM | 5752 | CB | SER | 403 | 1.894 | 34.942 | 132.528 | 1.00 | 22.54 | 0 |
| ATOM | 5753 | OG | SER | 403 | 1.503 | 34.298 | 131.333 | 1.00 | 14.30 | 0 |
| ATOM | 5755 | C | SER | 403 | 3.070 | 36.913 | 131.514 | 1.00 | 21.44 | 0 |
| ATOM | 5756 | O | SER | 403 | 2.890 | 37.720 | 130.595 | 1.00 | 23.72 | 0 |
| ATOM | 5757 | N | PHE | 404 | 4.271 | 36.415 | 131.793 | 1.00 | 13.47 | 0 |
| ATOM | 5759 | CA | PHE | 404 | 5.439 | 36.827 | 131.013 | 1.00 | 13.06 | 0 |
| ATOM | 5760 | CB | PHE | 404 | 6.101 | 38.060 | 131.647 | 1.00 | 2.00 | 0 |
| ATOM | 5761 | CG | PHE | 404 | 5.228 | 39.270 | 131.627 | 1.00 | 2.00 | 0 |
| ATOM | 5762 | CD1 | PHE | 404 | 4.421 | 39.574 | 132.711 | 1.00 | 2.00 | 0 |
| ATOM | 5763 | CD2 | PHE | 404 | 5.171 | 40.080 | 130.505 | 1.00 | 2.00 | 0 |
| ATOM | 5764 | CE1 | PHE | 404 | 3.560 | 40.668 | 132.677 | 1.00 | 2.00 | 0 |
| ATOM | 5765 | CE2 | PHE | 404 | 4.313 | 41.178 | 130.463 | 1.00 | 2.00 | 0 |
| ATOM | 5766 | CZ | PHE | 404 | 3.507 | 41.472 | 131.549 | 1.00 | 2.00 | 0 |
| ATOM | 5767 | C | PHE | 404 | 6.476 | 35.735 | 130.791 | 1.00 | 16.54 | 0 |
| ATOM | 5768 | O | PHE | 404 | 6.472 | 34.720 | 131.489 | 1.00 | 2.00 | 0 |
| ATOM | 5769 | N | ALA | 405 | 7.341 | 35.960 | 129.802 | 1.00 | 2.00 | 0 |
| ATOM | 5771 | CA | ALA | 405 | 8.420 | 35.054 | 129.414 | 1.00 | 2.00 | 0 |
| ATOM | 5772 | CB | ALA | 405 | 9.762 | 35.742 | 129.619 | 1.00 | 85.03 | 0 |
| ATOM | 5773 | C | ALA | 405 | 8.434 | 33.682 | 130.078 | 1.00 | 2.00 | 0 |
| ATOM | 5774 | O | ALA | 405 | 8.380 | 32.654 | 129.401 | 1.00 | 85.03 | 0 |
| ATOM | 5775 | N | GLY | 899 | 32.968 | 17.226 | 49.661 | 1.00 | 95.94 | 0 |
| ATOM | 5777 | CA | GLY | 899 | 31.781 | 16.989 | 50.464 | 1.00 | 95.94 | 0 |

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|---|---|---|---|---|---|---|---|---|---|---|
| ATOM | 5778 | C | GLY | 899 | 31.215 | 18.274 | 51.038 | 1.00 | 95.94 | 0 |
| ATOM | 5779 | O | GLY | 899 | 30.022 | 18.368 | 51.338 | 1.00 | 32.75 | 0 |
| ATOM | 5780 | N | ARG | 900 | 32.090 | 19.260 | 51.193 | 1.00 | 42.23 | 0 |
| ATOM | 5782 | CA | ARG | 900 | 31.732 | 20.569 | 51.722 | 1.00 | 42.23 | 0 |
| ATOM | 5783 | CB | ARG | 900 | 31.110 | 20.432 | 53.110 | 1.00 | 22.01 | 0 |
| ATOM | 5784 | CG | ARG | 900 | 30.578 | 21.718 | 53.694 | 1.00 | 22.01 | 0 |
| ATOM | 5785 | CD | ARG | 900 | 30.080 | 21.488 | 55.120 | 1.00 | 22.01 | 0 |
| ATOM | 5786 | NE | ARG | 900 | 31.005 | 20.664 | 55.909 | 1.00 | 22.01 | 0 |
| ATOM | 5788 | CZ | ARG | 900 | 31.111 | 20.691 | 57.237 | 1.00 | 22.01 | 0 |
| ATOM | 5789 | NH1 | ARG | 900 | 30.361 | 21.512 | 57.963 | 1.00 | 22.01 | 0 |
| ATOM | 5792 | NH2 | ARG | 900 | 31.957 | 19.865 | 57.839 | 1.00 | 22.01 | 0 |
| ATOM | 5795 | C | ARG | 900 | 33.034 | 21.365 | 51.774 | 1.00 | 42.23 | 0 |
| ATOM | 5796 | O | ARG | 900 | 33.795 | 21.309 | 52.735 | 1.00 | 22.01 | 0 |
| ATOM | 5797 | N | ARG | 901 | 33.284 | 22.091 | 50.697 | 1.00 | 8.39 | 0 |
| ATOM | 5799 | CA | ARG | 901 | 34.490 | 22.880 | 50.542 | 1.00 | 8.39 | 0 |
| ATOM | 5800 | CB | ARG | 901 | 34.793 | 23.036 | 49.045 | 1.00 | 2.00 | 0 |
| ATOM | 5801 | CG | ARG | 901 | 34.504 | 21.810 | 48.186 | 1.00 | 2.00 | 0 |
| ATOM | 5802 | CD | ARG | 901 | 34.584 | 22.175 | 46.699 | 1.00 | 2.00 | 0 |
| ATOM | 5803 | NE | ARG | 901 | 34.278 | 21.012 | 45.863 | 1.00 | 2.00 | 0 |
| ATOM | 5805 | CZ | ARG | 901 | 35.190 | 20.195 | 45.327 | 1.00 | 2.00 | 0 |
| ATOM | 5806 | NH1 | ARG | 901 | 36.498 | 20.416 | 45.509 | 1.00 | 2.00 | 0 |
| ATOM | 5809 | NH2 | ARG | 901 | 34.791 | 19.114 | 44.649 | 1.00 | 2.00 | 0 |
| ATOM | 5812 | C | ARG | 901 | 34.327 | 24.259 | 51.158 | 1.00 | 8.39 | 0 |
| ATOM | 5813 | O | ARG | 901 | 33.241 | 24.629 | 51.607 | 1.00 | 2.00 | 0 |
| ATOM | 5814 | N | VAL | 902 | 35.393 | 25.005 | 51.149 | 1.00 | 2.00 | 0 |
| ATOM | 5816 | CA | VAL | 902 | 35.425 | 26.384 | 51.650 | 1.00 | 2.00 | 0 |
| ATOM | 5817 | CB | VAL | 902 | 36.880 | 26.814 | 51.869 | 1.00 | 12.90 | 0 |
| ATOM | 5818 | CG1 | VAL | 902 | 37.039 | 28.332 | 51.992 | 1.00 | 12.90 | 0 |
| ATOM | 5819 | CG2 | VAL | 902 | 37.492 | 26.219 | 53.139 | 1.00 | 12.90 | 0 |
| ATOM | 5820 | C | VAL | 902 | 34.782 | 27.324 | 50.627 | 1.00 | 2.00 | 0 |
| ATOM | 5821 | O | VAL | 902 | 34.737 | 27.031 | 49.435 | 1.00 | 12.90 | 0 |
| ATOM | 5822 | N | SER | 903 | 34.288 | 28.438 | 51.120 | 1.00 | 2.00 | 0 |
| ATOM | 5824 | CA | SER | 903 | 33.673 | 29.487 | 50.271 | 1.00 | 2.00 | 0 |
| ATOM | 5825 | CB | SER | 903 | 32.173 | 29.205 | 50.008 | 1.00 | 2.00 | 0 |
| ATOM | 5826 | OG | SER | 903 | 31.477 | 28.917 | 51.209 | 1.00 | 2.00 | 0 |
| ATOM | 5828 | C | SER | 903 | 33.871 | 30.814 | 50.991 | 1.00 | 2.00 | 0 |
| ATOM | 5829 | O | SER | 903 | 34.386 | 30.866 | 52.115 | 1.00 | 2.00 | 0 |
| ATOM | 5830 | N | PHE | 904 | 33.482 | 31.903 | 50.376 | 1.00 | 2.00 | 0 |
| ATOM | 5832 | CA | PHE | 904 | 33.683 | 33.188 | 51.034 | 1.00 | 2.00 | 0 |
| ATOM | 5833 | CB | PHE | 904 | 34.894 | 33.898 | 50.455 | 1.00 | 17.14 | 0 |
| ATOM | 5834 | CG | PHE | 904 | 36.184 | 33.109 | 50.672 | 1.00 | 17.14 | 0 |
| ATOM | 5835 | CD1 | PHE | 904 | 36.511 | 32.067 | 49.805 | 1.00 | 17.14 | 0 |
| ATOM | 5836 | CD2 | PHE | 904 | 37.034 | 33.426 | 51.738 | 1.00 | 17.14 | 0 |
| ATOM | 5837 | CE1 | PHE | 904 | 37.690 | 31.343 | 49.994 | 1.00 | 17.14 | 0 |
| ATOM | 5838 | CE2 | PHE | 904 | 38.216 | 32.704 | 51.927 | 1.00 | 17.14 | 0 |
| ATOM | 5839 | CZ | PHE | 904 | 38.544 | 31.662 | 51.054 | 1.00 | 17.14 | 0 |
| ATOM | 5840 | C | PHE | 904 | 32.491 | 34.080 | 50.894 | 1.00 | 2.00 | 0 |
| ATOM | 5841 | O | PHE | 904 | 31.716 | 33.994 | 49.926 | 1.00 | 17.14 | 0 |
| ATOM | 5842 | N | ALA | 905 | 32.386 | 34.912 | 51.874 | 1.00 | 70.83 | 0 |
| ATOM | 5844 | CA | ALA | 905 | 31.311 | 35.857 | 51.949 | 1.00 | 69.99 | 0 |
| ATOM | 5845 | CB | ALA | 905 | 30.042 | 35.128 | 52.370 | 1.00 | 2.00 | 0 |
| ATOM | 5846 | C | ALA | 905 | 31.646 | 36.940 | 52.962 | 1.00 | 69.85 | 0 |
| ATOM | 5847 | O | ALA | 905 | 30.981 | 37.068 | 53.993 | 1.00 | 2.00 | 0 |
| ATOM | 5848 | N | ALA | 907 | 37.374 | 34.312 | 47.285 | 1.00 | 23.39 | 0 |
| ATOM | 5850 | CA | ALA | 907 | 36.215 | 33.651 | 46.695 | 1.00 | 23.39 | 0 |
| ATOM | 5851 | CB | ALA | 907 | 35.317 | 34.681 | 46.008 | 1.00 | 41.64 | 0 |
| ATOM | 5852 | C | ALA | 907 | 36.637 | 32.568 | 45.699 | 1.00 | 23.39 | 0 |
| ATOM | 5853 | O | ALA | 907 | 35.850 | 31.680 | 45.370 | 1.00 | 41.64 | 0 |
| ATOM | 5854 | N | ALA | 908 | 37.875 | 32.643 | 45.215 | 1.00 | 83.90 | 0 |
| ATOM | 5856 | CA | ALA | 908 | 38.378 | 31.663 | 44.253 | 1.00 | 83.90 | 0 |
| ATOM | 5857 | CB | ALA | 908 | 39.439 | 32.296 | 43.337 | 1.00 | 22.84 | 0 |
| ATOM | 5858 | C | ALA | 908 | 38.961 | 30.466 | 44.992 | 1.00 | 83.90 | 0 |
| ATOM | 5859 | O | ALA | 908 | 38.459 | 30.074 | 46.046 | 1.00 | 22.84 | 0 |
| ATOM | 5860 | OW | WAT | 1 | 62.869 | 37.982 | 63.341 | 1.00 | 20.00 | 0 |
| ATOM | 5863 | OW | WAT | 103 | 57.039 | 39.062 | 61.228 | 1.00 | 20.00 | 0 |
| ATOM | 5866 | OW | WAT | 101 | 7.257 | 66.194 | 118.365 | 1.00 | 20.00 | 0 |
| ATOM | 5869 | OW | WAT | 2 | 12.341 | 60.209 | 123.464 | 1.00 | 20.00 | 0 |
| ATOM | 5872 | OW | WAT | 3 | 10.655 | 60.748 | 120.833 | 1.00 | 20.00 | 0 |

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|---|---|---|---|---|---|---|---|---|---|---|
| ATOM | 5875 | OW | WAT | 104 | 55.432 | 36.306 | 63.901 | 1.00 | 20.00 | 0 |
| ATOM | 5878 | OW | WAT | 102 | 56.782 | 40.457 | 58.333 | 1.00 | 20.00 | 0 |
| ATOM | 5881 | OW | WAT | 4 | 5.787 | 57.856 | 118.686 | 1.00 | 20.00 | 0 |
| ATOM | 5884 | OW | WAT | 105 | 54.382 | 39.155 | 63.734 | 1.00 | 20.00 | 0 |
| ATOM | 5887 | OW | WAT | 5 | 8.964 | 57.595 | 118.151 | 1.00 | 20.00 | 0 |
| ATOM | 5890 | OW | WAT | 106 | 38.565 | 47.423 | 74.959 | 1.00 | 20.00 | 0 |
| ATOM | 5893 | OW | WAT | 6 | 16.086 | 42.169 | 105.289 | 1.00 | 20.00 | 0 |
| ATOM | 5896 | OW | WAT | 107 | 31.158 | 26.414 | 51.913 | 1.00 | 20.00 | 0 |
| ATOM | 5899 | OW | WAT | 7 | -0.781 | 32.787 | 131.574 | 1.00 | 20.00 | 0 |
| ATOM | 5902 | MN | MN2 | 430 | 4.422 | 59.061 | 119.360 | 1.00 | 15.61 | 0 |
| ATOM | 5903 | MN | MN2 | 431 | 7.458 | 57.875 | 117.661 | 1.00 | 16.53 | 0 |
| ATOM | 5904 | MN | MN2 | 930 | 56.038 | 34.500 | 63.727 | 1.00 | 16.67 | 0 |
| ATOM | 5905 | MN | MN2 | 931 | 54.402 | 37.798 | 64.756 | 1.00 | 15.40 | 0 |
| ATOM | 5906 | S | SO4 | 801 | 57.551 | 37.278 | 64.009 | 1.00 | 37.87 | 0 |
| ATOM | 5907 | O1 | SO4 | 801 | 57.600 | 35.852 | 63.897 | 1.00 | 42.46 | 0 |
| ATOM | 5908 | O2 | SO4 | 801 | 58.690 | 37.740 | 64.722 | 1.00 | 42.01 | 0 |
| ATOM | 5909 | O3 | SO4 | 801 | 56.355 | 37.648 | 64.705 | 1.00 | 45.08 | 0 |
| ATOM | 5910 | O4 | SO4 | 801 | 57.520 | 37.854 | 62.725 | 1.00 | 41.40 | 0 |
| ATOM | 5911 | S | SO4 | 800 | 6.866 | 60.776 | 118.643 | 1.00 | 37.87 | 0 |
| ATOM | 5912 | O1 | SO4 | 800 | 7.710 | 60.635 | 119.773 | 1.00 | 42.46 | 0 |
| ATOM | 5913 | O2 | SO4 | 800 | 7.044 | 62.063 | 118.053 | 1.00 | 42.01 | 0 |
| ATOM | 5914 | O3 | SO4 | 800 | 5.496 | 60.612 | 119.046 | 1.00 | 45.08 | 0 |
| ATOM | 5915 | O4 | SO4 | 800 | 7.194 | 59.728 | 117.703 | 1.00 | 41.40 | 0 |

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## CLAIMS

1. A method of identifying a compound which modulates the interaction between a PP1c and a regulatory subunit thereof, the method comprising determining whether a compound enhances or disrupts the interaction between (a) a PP1c or a fragment, variant, derivative or fusion thereof or a fusion of a fragment, variant or derivative and (b) a regulatory subunit which is able to bind to PP1c or a PP1c-binding fragment, variant, derivative or fusion of said subunit or a fusion of said fragment, variant or derivative.

2. A method of identifying a compound which mimics the effect of a regulatory subunit of PP1c, the method comprising contacting said compound with PP1c and determining whether, in the presence of the compound, PP1c adopts the function of properties of a PP1c in the presence of a given regulatory subunit.

3. A method according to Claim 1 or 2 wherein said regulatory subunit of PP1c is any one of $M_{110}$, $G_L$, $G_M$, M-complexes, p53 BP2, sds22, NIPPI, L5, Inhibitor-1, Inhibitor-2, or DARPP.

4. A method according to Claim 3 wherein the regulatory subunit of PP1c is any one of $M_{110}$, $G_L$, $G_M$, M-complexes or p53BP2.

5. A method according to Claim 4 wherein the regulatory subunit of PP1c is $M_{110}$ or $G_M$.

6. A method according to Claim 1 wherein the fragment of a regulatory subunit which is able to bind to PP1c is any of the peptides [G63-T93], [G63-N75], [E2-P243], [E2-D118], and peptide 63-80 of $G_M$ or

functional equivalents thereof or peptides comprising said peptide sequences provided that they are not the complete $G_M$ regulatory subunit.

7. A method according to Claim 1 wherein the fragment of a regulatory subunit which is able to bind to PP1c is any of the peptides [M1-E309], [M1-F38], [M1-A150] or [L24-Y496] of $M_{110}$ or functional equivalents thereof or peptides comprising said peptide sequences provided that they are not the complete $M_{110}$ regulatory subunit.

8. A method according to Claim 1 wherein the PP1c-binding fragment, variant or derivative of said regulatory subunit or a fusion of said fragment, variant or derivative comprises the consensus peptide sequence Arg/Lys-Val/Ile-Xaa-Phe wherein Xaa is any amino acid.

9. A method according to Claim 8 wherein the PP1c-binding fragment, variant or derivative comprises, in addition to the said consensus peptide sequence, at least one basic residue in the four residues N-terminal of the consensus peptide sequence.

10. A method according to Claim 8 wherein in the consensus peptide sequence Xaa is not Asp or Glu or a large hydrophobic residue.

11. A method according to Claim 8 wherein the PP1c-binding fragment is a fragment of a regulatory subunit comprising the said consensus peptide sequence.

12. A method according to Claim 10 wherein the PP1c-binding fragment is a fragment of any of the $M_{110}$, $G_L$, $G_M$, M-complexes, p53BP2, sds22, NIPPI, L5, Inhibitor-1, Inhibitor-2 or DARPP regulatory subunits comprising said consensus sequence.

13. A method according to any one of the preceding claims wherein the compound binds to a PP1c.

14. A method according to Claim 1 wherein the compound binds to a regulatory subunit of PP1c.

15. A compound identifiable by the method of any one of Claims 1 to 14.

16. A compound which modulates the interaction between a PP1c and a regulatory subunit thereof said compound comprising any of the peptides [G63-T93], [G63-N75], [E2-P243], [E2-D118], and peptide 63 to 80 of $G_M$ or functional equivalents or said compound comprising any of the peptides [M1-E309], [M1-F38], [M1-A150] or [L24-Y496] of $M_{110}$ or functional equivalents thereof or said compound comprising the consensus peptide sequence Arg/Lys-Val/Ile-Xaa-Phe wherein Xaa is any naturally occurring amino acid or functional equivalents thereof, provided that the said compound is not a complete regulatory subunit of PP1c.

17. A compound according to Claim 16 consisting of the peptides [G63-T93], [G63-N75], [E2-P243], [E2-D118], or peptide 63 to 80 of $G_M$ or functional equivalents thereof or consisting of the peptides [M1-E309], [M1-F38], [M1-A150] or [L24-Y496] of $M_{110}$ or functional equivalents thereof.

18. A peptide capable of binding a PP1c and which affects the ability of PP1c to bind to a particular target and/or affects the regulation of PP1c activity, or a functional equivalent thereof.

19. A method of identifying a compound which modulates the interaction

between a PP1c and a regulatory subunit thereof, or binds PP1c or mimics the effect of a regulatory subunit, the method comprising selecting a compound which is capable of adopting the same or substantially the same conformation as a peptide bound to the regulatory subunit-binding site of PP1c or the same or substantially the same conformation as the portion of PP1c which binds to said peptide.

20. A method according to Claim 19 wherein said peptide comprises the consensus peptide sequence Arg/Lys-Val/Ile-Xaa-Phe wherein Xaa is any amino acid.

21. A method according to Claim 20 wherein said peptide consists of residues 63 to 75 of $G_M$.

22. A method according to Claim 21 wherein the conformation of the said peptide and the conformation of the said portion of PP1c is as defined by reference to the coordinates in Table A.

23. A compound identifiable by the method of any one of Claims 19 to 22.

24. A compound according to any one of Claims 15 to 18 or 23 for use in medicine.

25. A pharmaceutical composition comprising a compound according to any one of Claims 15 to 18 or 23 and a pharmaceutically acceptable carrier.

26. A method of affecting cellular metabolism or function, the method comprising administering to a cell (a) a compound which modulates the interaction between a PP1c and a regulatory subunit thereof or (b) a compound which mimics the effect of a regulatory subunit of PP1c or

(c) a peptide capable of binding a PP1c and which affects the ability of PP1c to bind to a particular target and/or affects the regulation of PP1c activity, or a functional equivalent thereof.

27. A method according to Claim 26 wherein any one or more of the peptides [G63-T93], [G63-N75], [E2-P243], [E2-D118], and peptide 63-80 of $G_M$ or functional equivalents thereof or peptides comprising said peptide sequences are administered.

28. A method according to Claim 26 wherein any one or more of the peptides [M1-E309], [M1-F38], [M1-A150] or [L24-Y496] of $M_{110}$ or functional equivalents thereof or peptides comprising said peptide sequences are administered.

29. A method according to Claim 26 wherein a compound according to any one of Claims 15 to 18 or 23 are administered to the cell.

30. A method according to any one of Claims 26 to 29 wherein the cell is in a mammalian body.

31. A method of treating a patient in need of modulation of PP1c activity or function the method comprising administering to the patient an effective amount of a compound which modulates the interaction between a PP1c and a regulatory subunit thereof or (b) a compound which mimics the effect of a regulatory subunit of PP1c or (c) a peptide capable of binding a PP1c and which affects the ability of PP1c to bind to a particular target and/or affects the regulation of PP1c activity, or a functional equivalent thereof.

32. Use of peptides derived from targeting subunits of PP1c, functional

equivalents or portions thereof to affect cellular metabolism.

33. A method of treatment of a mammal said method comprising altering levels of peptides derived from a targeting subunit of PP1c, functional equivalents or portions thereof to an extent that cellular metabolism or function is affected.

34. A PP1c-regulating subunit that is modified so that it cannot interact with PP1c.

35. A PP1c-regulator subunit according to Claim 34 wherein the consensus peptide sequence Arg/Lys-Val/Ile-Xaa-Phe is missing or modified.

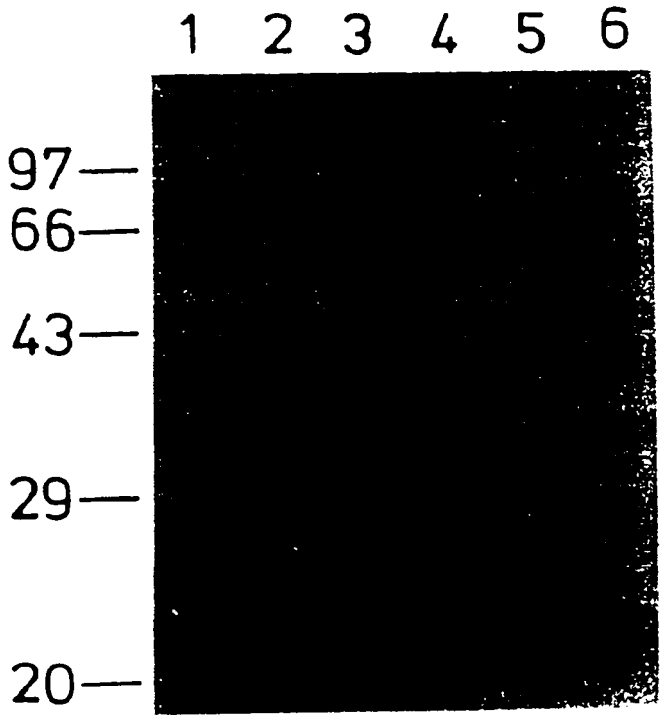



*Fig. 1*

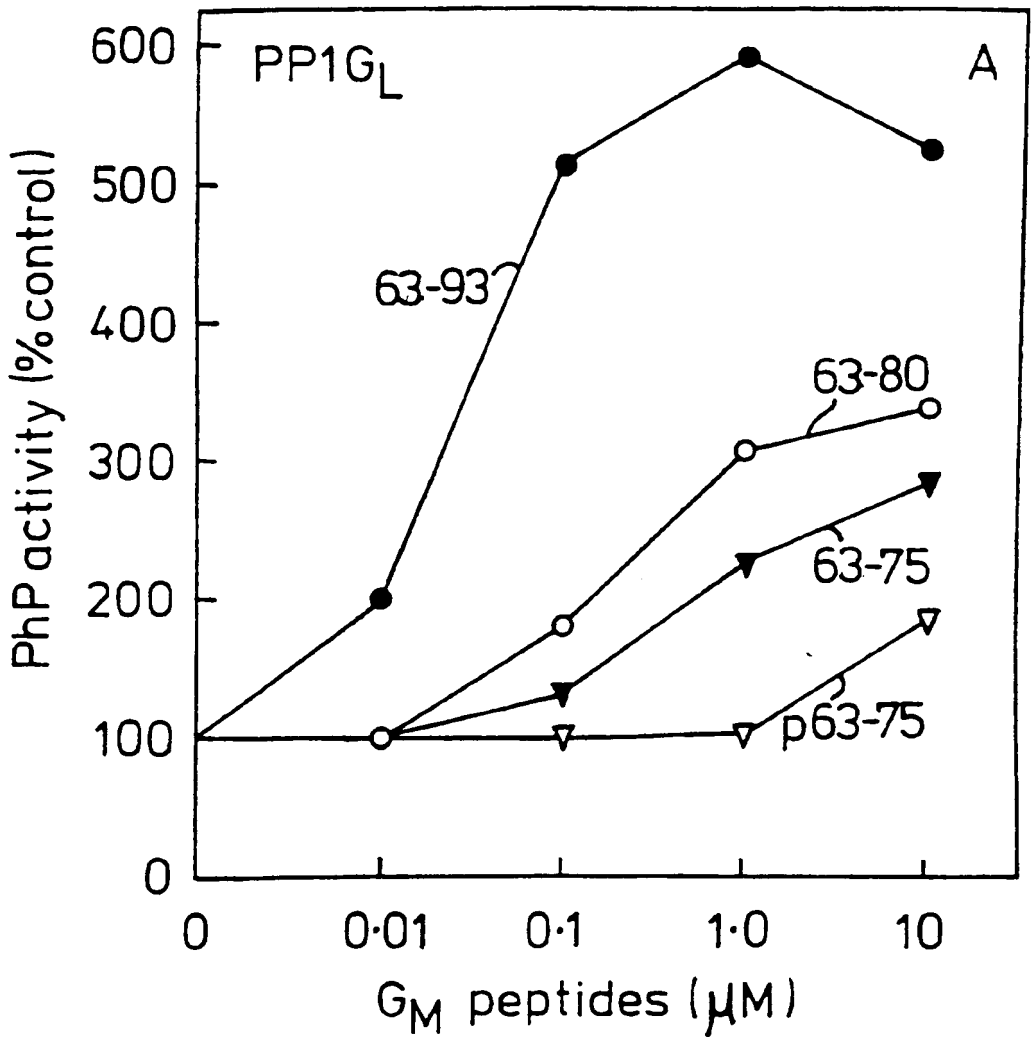

PP1G$_L$
A
600
500
400
300
200
100
0
PhP activity (% control)
63-93
63-80
63-75
p63-75
0
0·01
0·1
1·0
10
G$_M$ peptides (μM)

*Fig. 2*

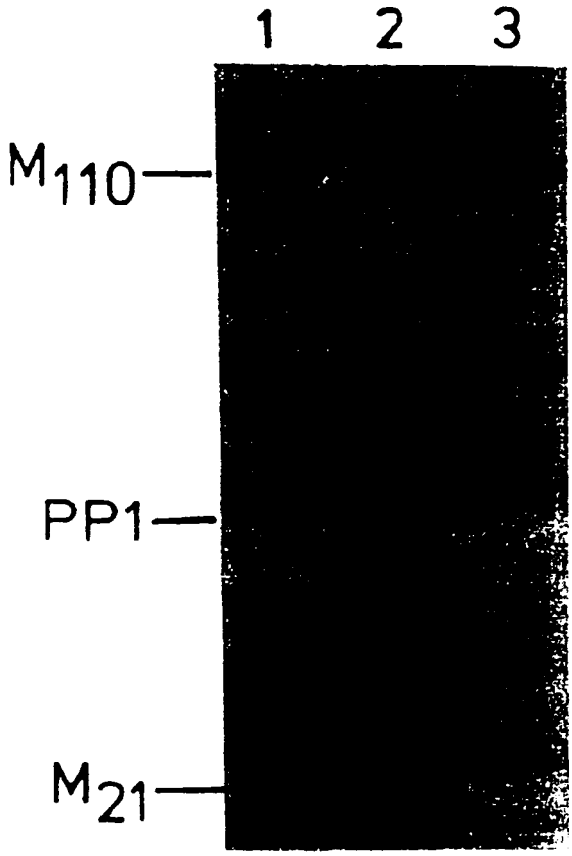



*Fig. 3A*


*Fig. 3B*

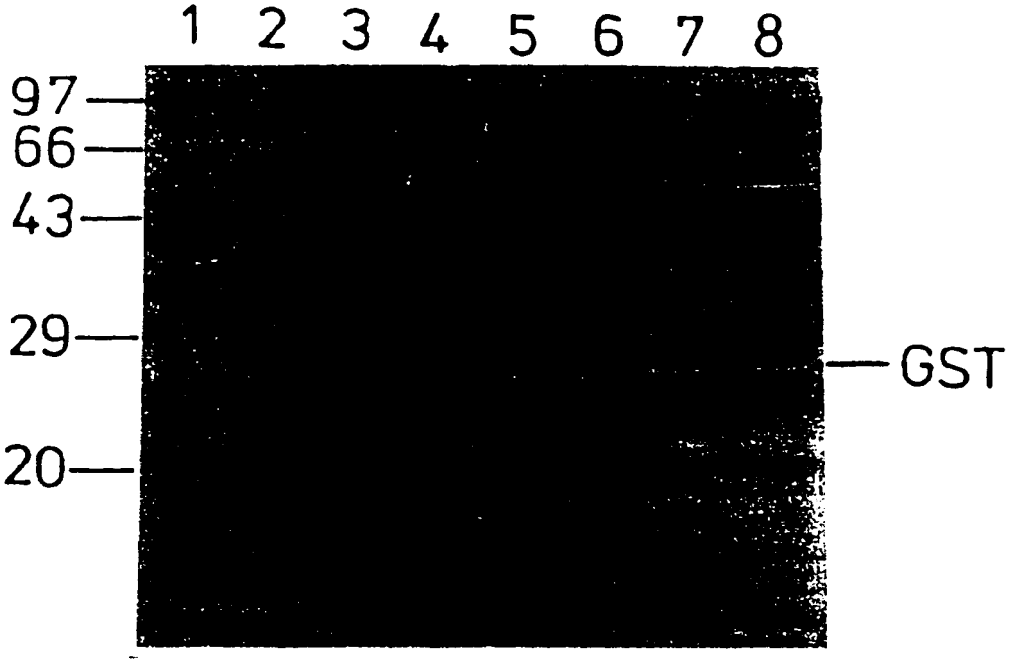



*Fig. 4*

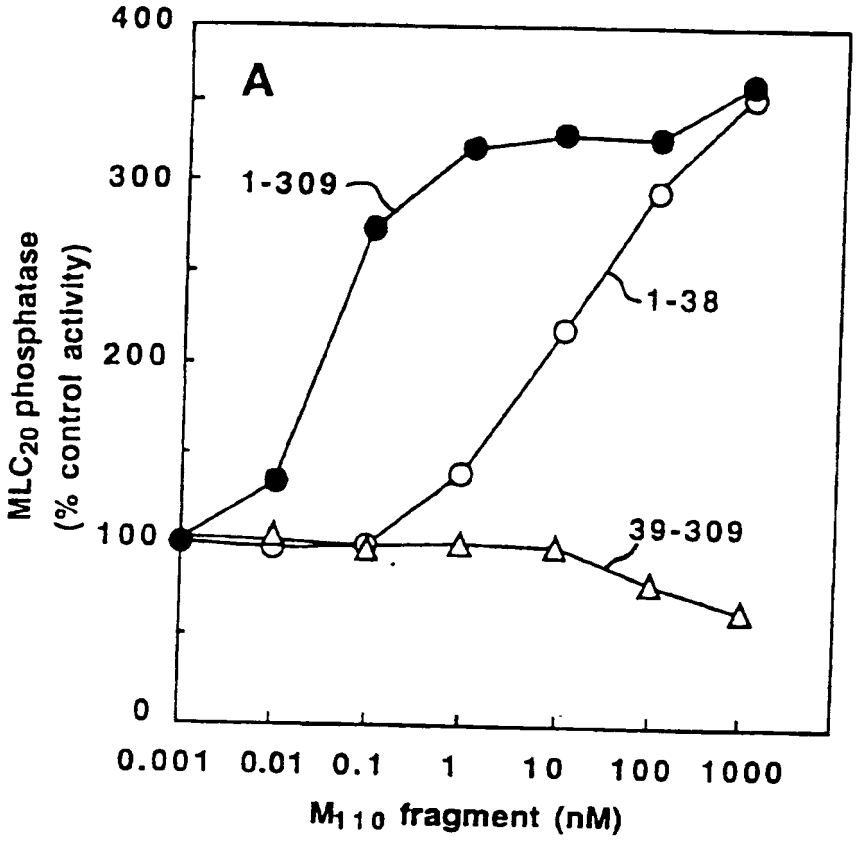

A
400
300
200
100
0
1-309
1-38
39-309
MLC20 phosphatase (% control activity)
0.001 0.01 0.1 1 10 100 1000
M110 fragment (nM)

Fig. 5A

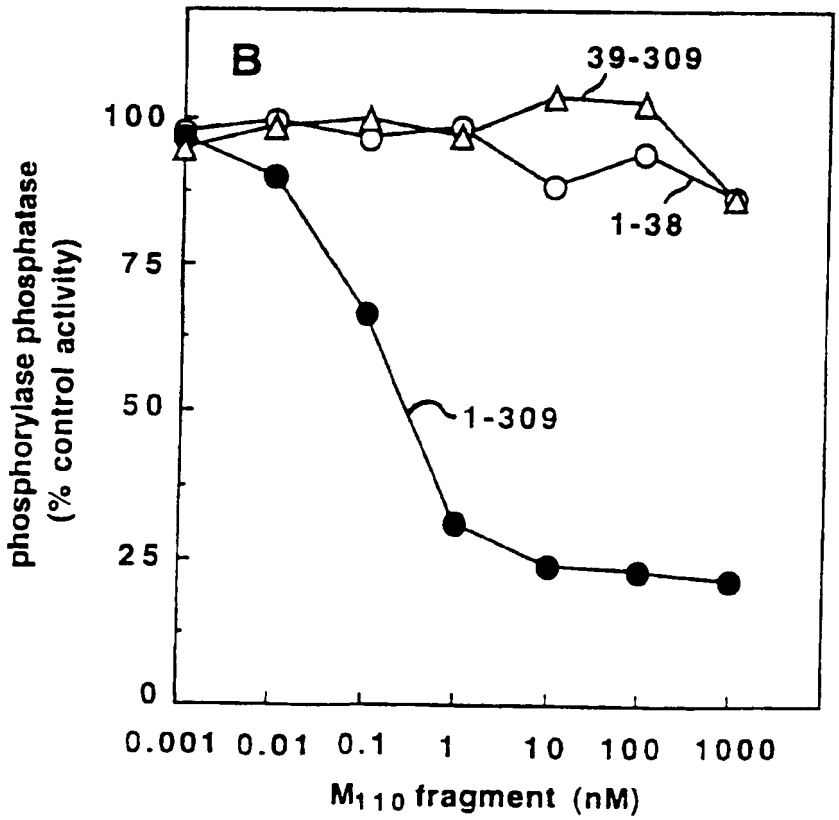

B
100
75
50
25
0
39-309
1-38
1-309
phosphorylase phosphatase (% control activity)
0.001 0.01 0.1 1 10 100 1000
M110 fragment (nM)

Fig. 5B

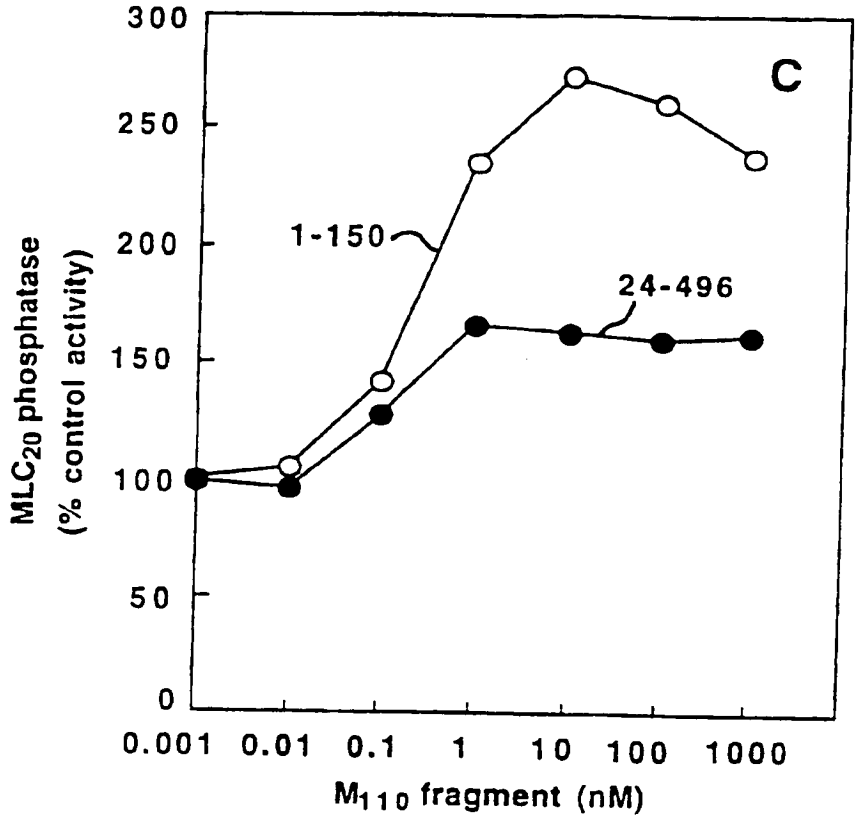

C
300
250
200
150
100
50
0
1-150
24-496
MLC20 phosphatase
(% control activity)
0.001 0.01 0.1 1 10 100 1000
M110 fragment (nM)

Fig. 5C

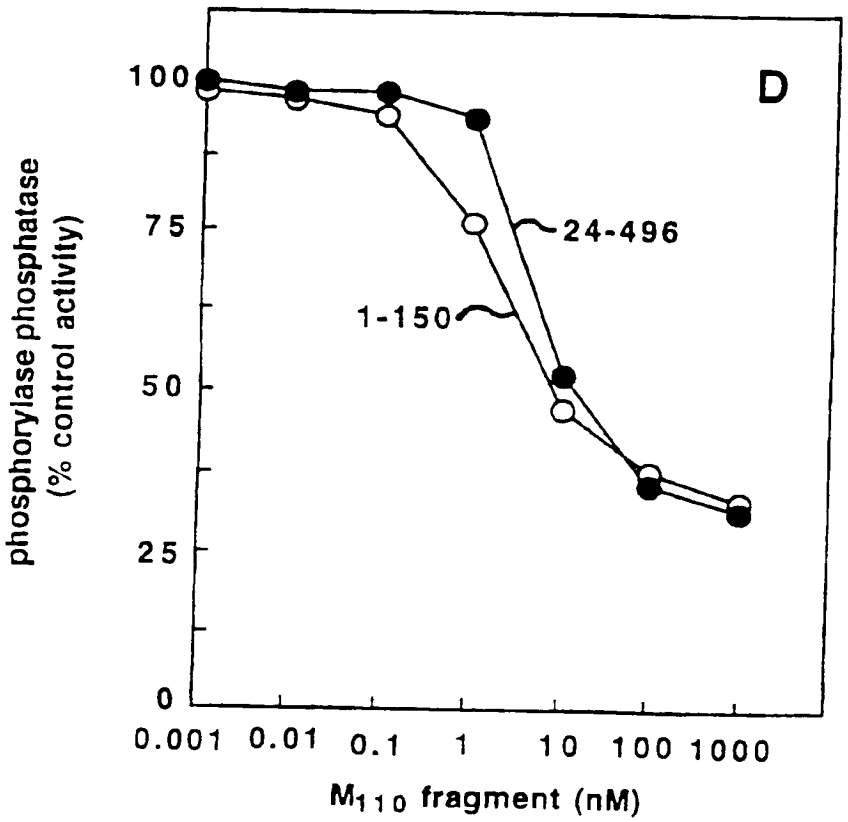

D
100
75
50
25
0
24-496
1-150
phosphorylase phosphatase
(% control activity)
0.001 0.01 0.1 1 10 100 1000
M110 fragment (nM)

Fig. 5D

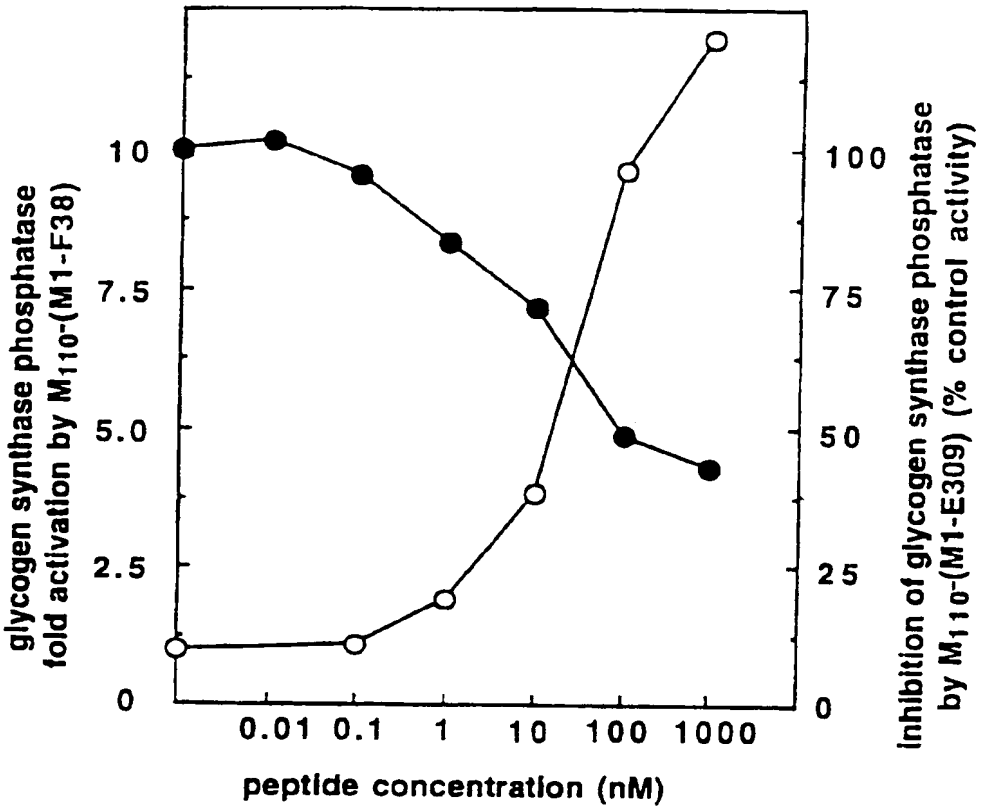

glycogen synthase phosphatase
fold activation by M110-(M1-F38)
10
7.5
5.0
2.5
0
0.01 0.1 1 10 100 1000
peptide concentration (nM)
100
75
50
25
0
inhibition of glycogen synthase phosphatase
by M110-(M1-E309) (% control activity)

*Fig. 6*

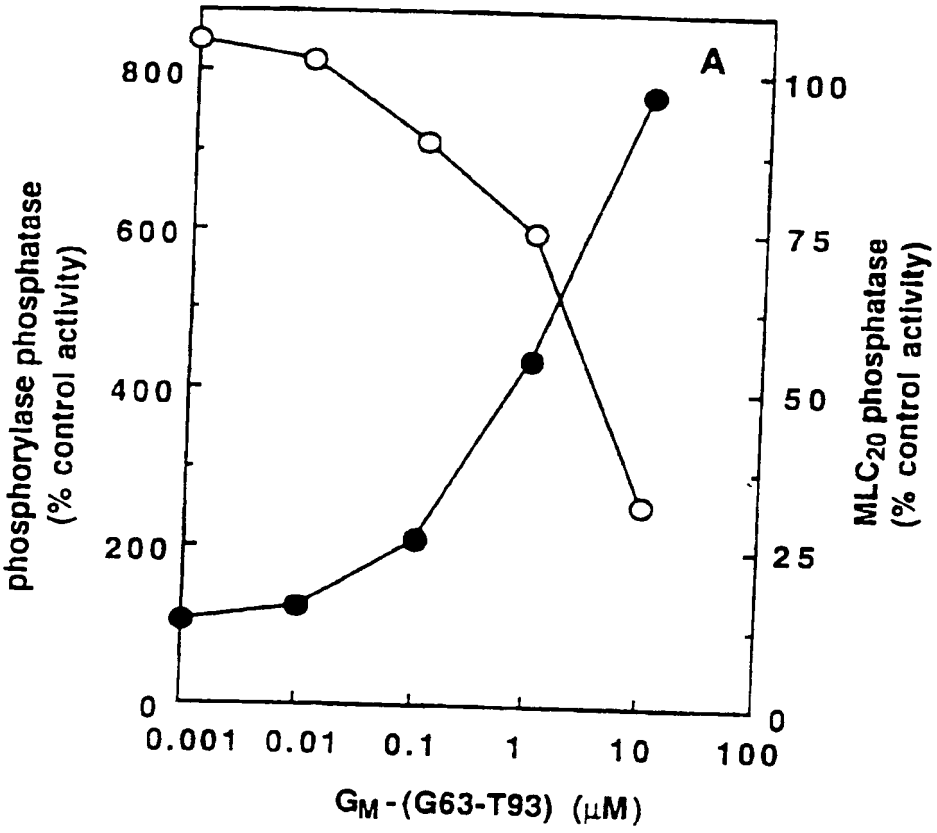

A
800
600
400
200
0
100
75
50
25
0
0.001
0.01
0.1
1
10
100
phosphorylase phosphatase (% control activity)
MLC20 phosphatase (% control activity)
GM-(G63-T93) (μM)

*Fig. 7A*

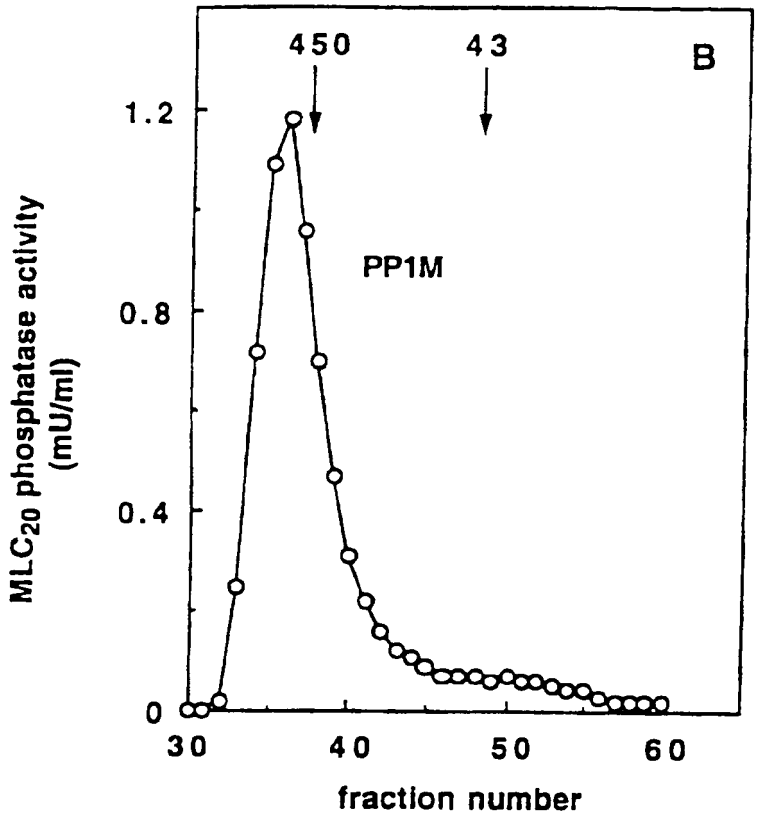

450
43
B
1.2
0.8
0.4
0
PP1M
MLC20 phosphatase activity (mU/ml)
30
40
50
60
fraction number

Fig. 7B

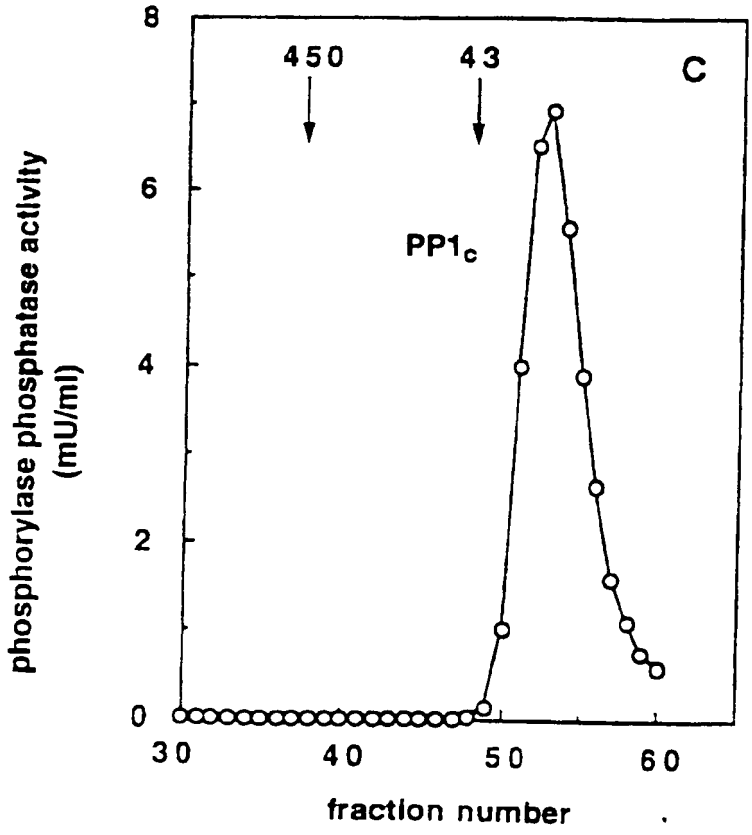
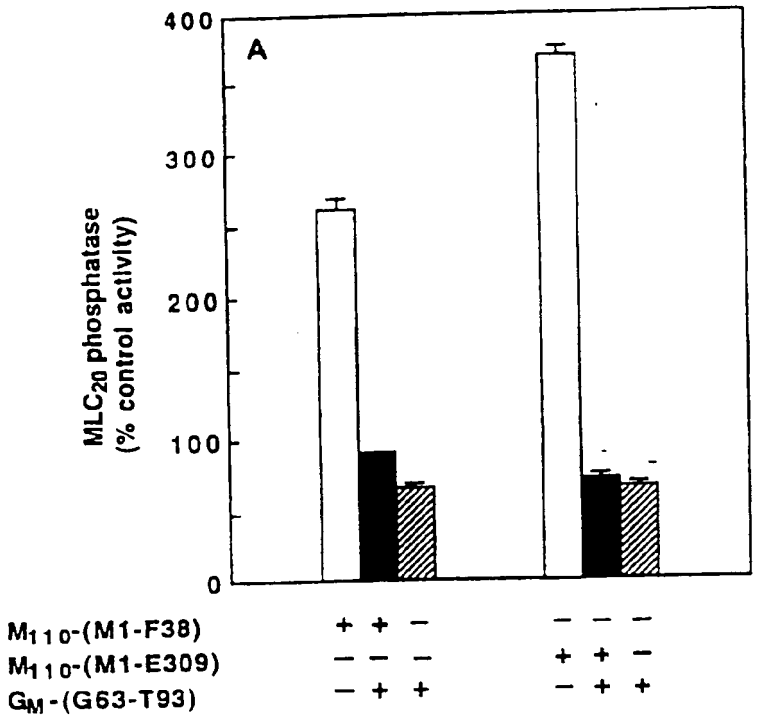

8
450
43
C
6
4
2
0
PP1c
phosphorylase phosphatase activity (mU/ml)
30
40
50
60
fraction number

Fig. 7C


A
400
300
200
100
0
MLC20 phosphatase
(% control activity)
M110-(M1-F38) + + − − − −
M110-(M1-E309) − − − + + −
GM-(G63-T93) − + + − + +

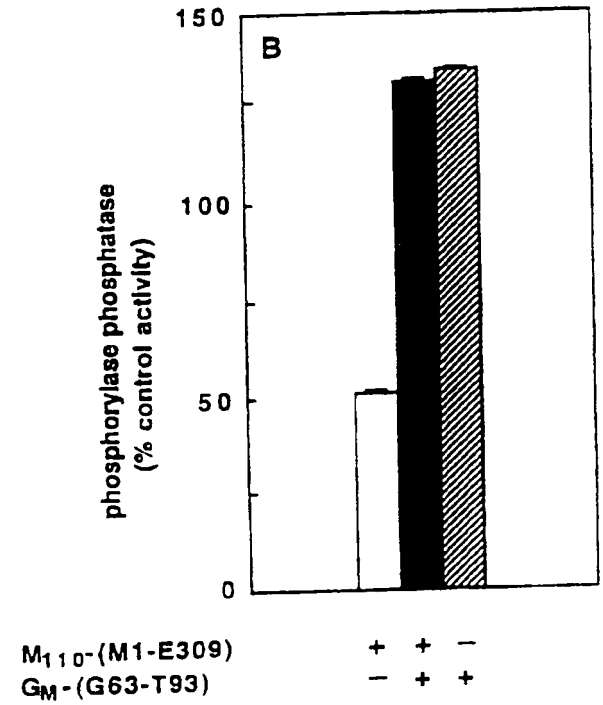

B
150
100
50
0
phosphorylase phosphatase
(% control activity)
M110-(M1-E309) + + −
GM-(G63-T93) − + +

*Fig. 8*

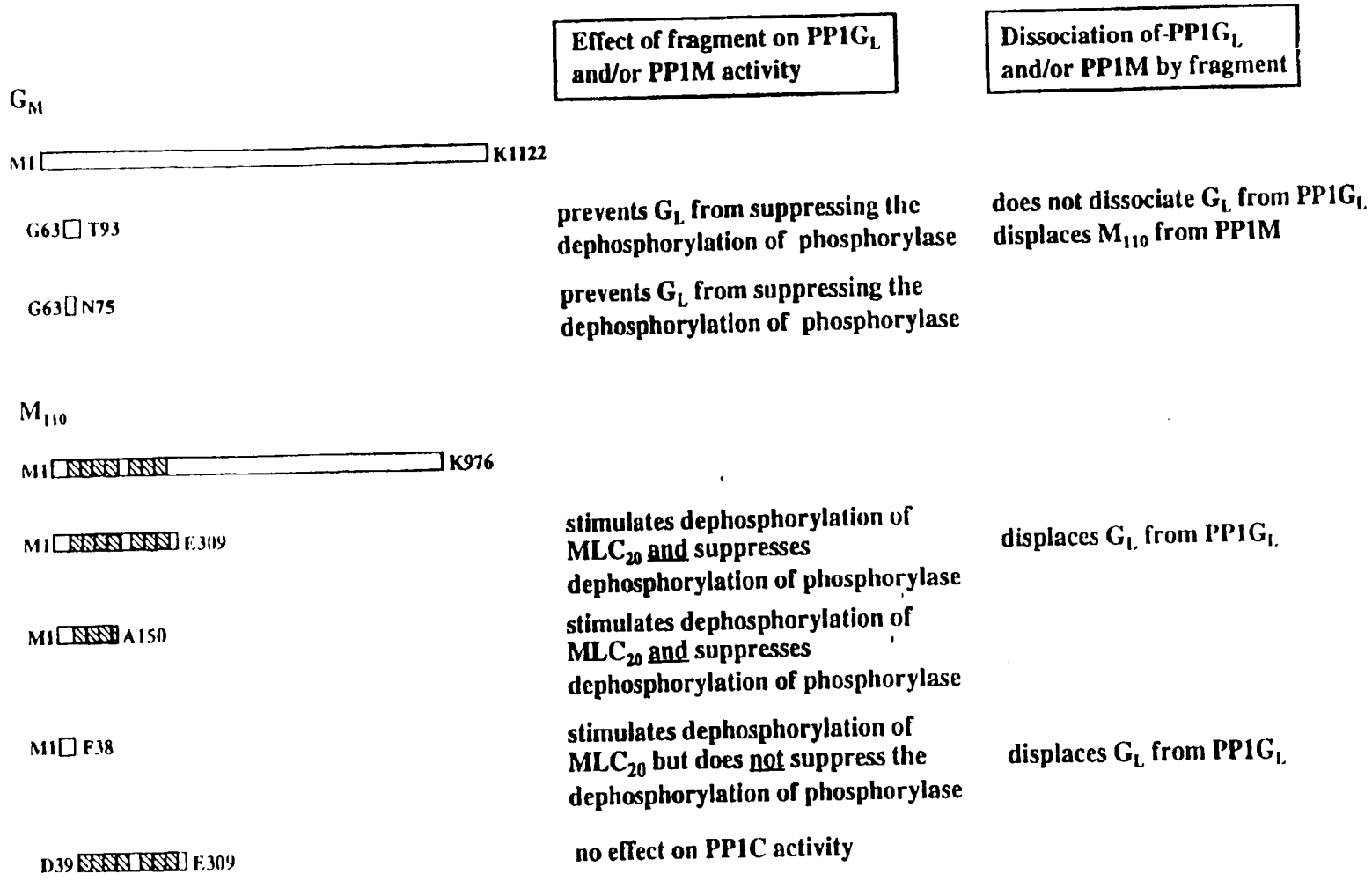

Effect of fragment on PP1G$_L$ and/or PP1M activity
Dissociation of PP1G$_L$ and/or PP1M by fragment
G$_M$
M1
K1122
G63
T93
prevents G$_L$ from suppressing the dephosphorylation of phosphorylase
does not dissociate G$_L$ from PP1G$_L$
displaces M$_{110}$ from PP1M
G63
N75
prevents G$_L$ from suppressing the dephosphorylation of phosphorylase
M$_{110}$
M1
K976
M1
E309
stimulates dephosphorylation of MLC$_{20}$ and suppresses dephosphorylation of phosphorylase
displaces G$_L$ from PP1G$_L$
M1
A150
stimulates dephosphorylation of MLC$_{20}$ and suppresses dephosphorylation of phosphorylase
M1
F38
stimulates dephosphorylation of MLC$_{20}$ but does not suppress the dephosphorylation of phosphorylase
displaces G$_L$ from PP1G$_L$
D39
E309
no effect on PP1C activity

*Fig. 9*

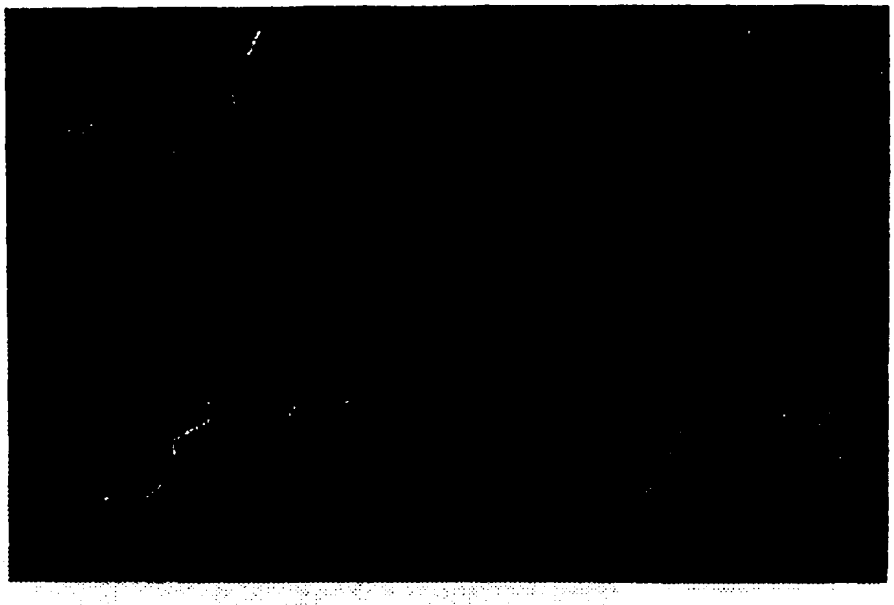


Fig. 10A

Fig. 10B

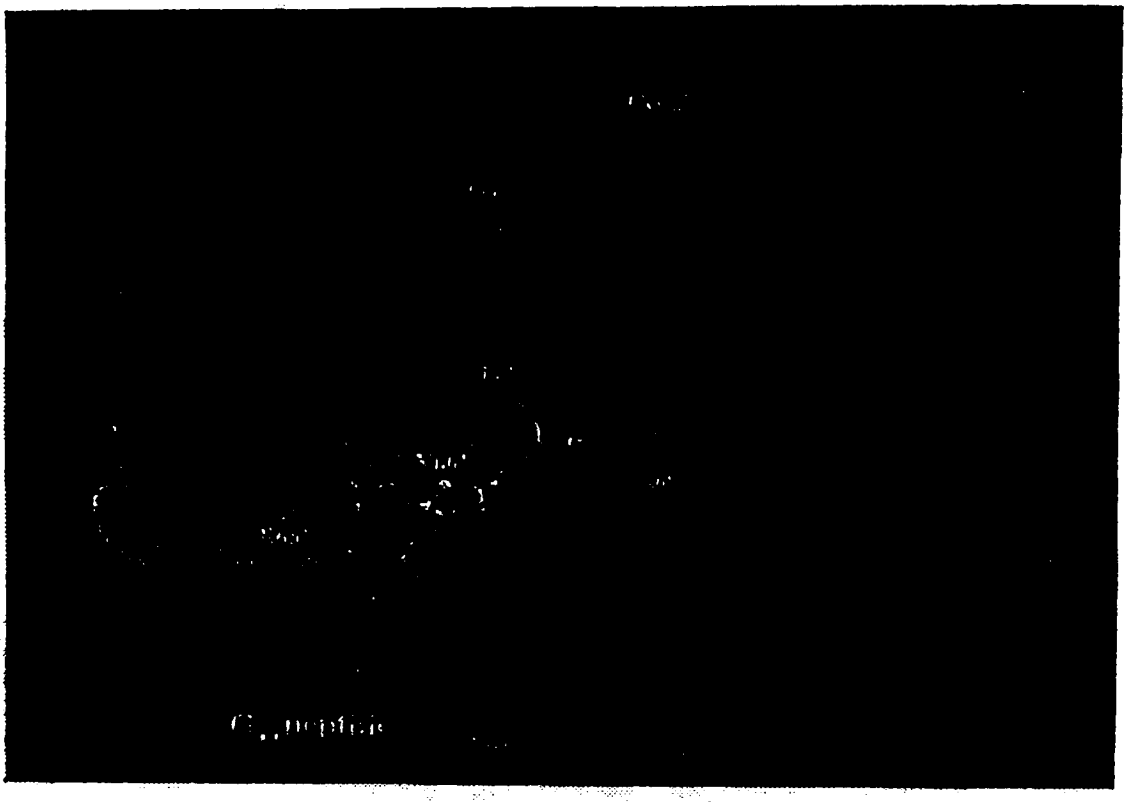


Fig. 11A

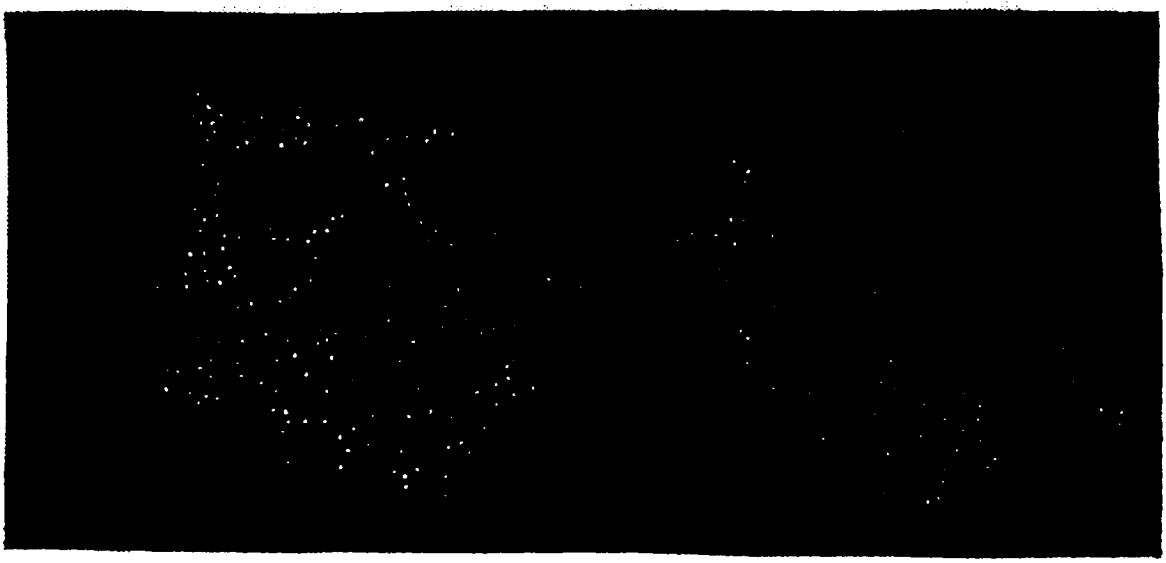


Fig. 11B

Fig. 11C

Fig. 11E

| protein | putative PP1-binding motif | residues |
|---|---|---|
| GAC1 | S P E **K** N V R **F** A I E | 66-76 |
| PIG2 | S S G **K** S V R **F** A A H | 50-60 |
| GIP2 | I R S **K** S V H **F** D Q A | 217-227 |
| YIL045W | Q R S **K** S V H **F** D R V | 193-203 |
| YIL045W | V F V **K** N I Y **F** S N A | 412-422 |
| REG1 | T K N **R** H I H **F** N D R | 461-471 |
| REG2 | P R E **R** H I K **F** N D N | 164-174 |
| SCD5 | F K S **K** K V R **F** S E H | 270-280 |
| GIP1 | L S E **K** F I P **F** N N L | 180-190 |
| GIP1 | K K K **R** C V N **F** R N K | 441-451 |
| SHP1 | K V T **R** E I T **F** W K E | 232-242 |

# *Fig. 12A*

| protein | Putative PP1-binding motif | residues |
|---|---|---|
| GAC1 | S P E K N V R F A I E | 66-76 |
| PIG2 | S S G K S V R F A A H | 50-60 |
| GIP2 | I R S K S V H F D Q A | 217-227 |
| YIL045W | Q R S K S V H F D R V | 193-203 |
| YIL045W | V F V K N I Y F S N A | 412-422 |
| REG1 | T K N R H I H F N D R | 461-471 |
| REG2 | P P E R H I K F N D N | 164-174 |
| SCD5 | F K S K K V R F S E H | 270-280 |
| GIP1 | W N L K F I P F N N L | 180-190 |
| GIP1 | K K K R C V N F R N K | 441-451 |

*Fig. 12B*

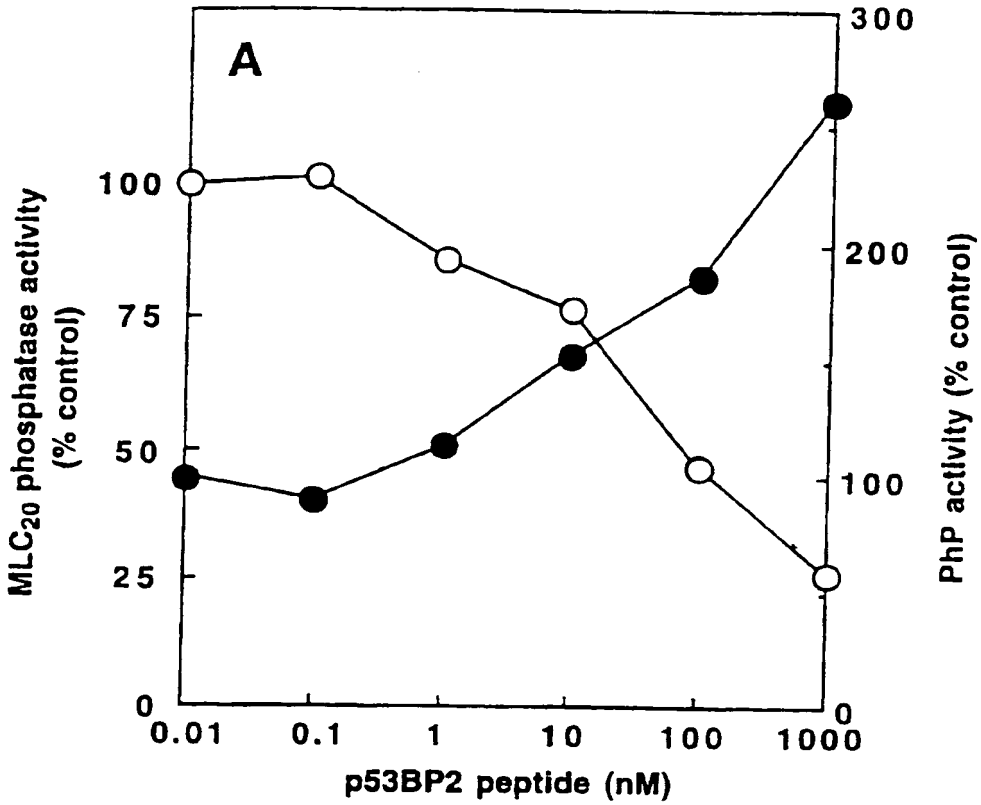

A
100
75
50
25
0
300
200
100
0
0.01
0.1
1
10
100
1000
MLC20 phosphatase activity (% control)
PhP activity (% control)
p53BP2 peptide (nM)

*Fig. 13A*

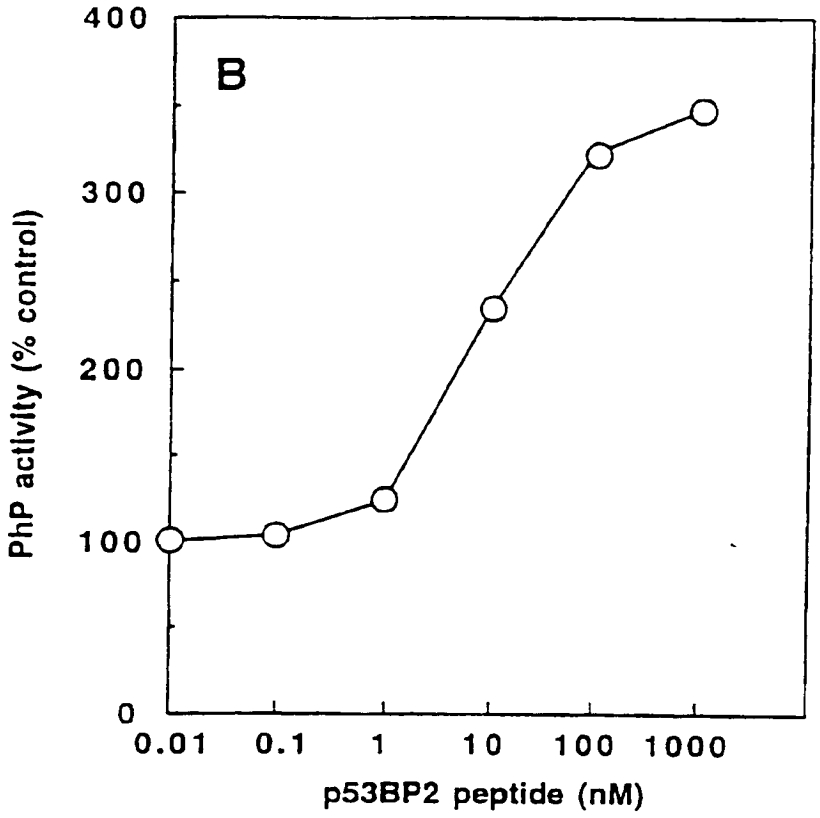

B
400
300
200
100
0
PhP activity (% control)
0.01
0.1
1
10
100
1000
p53BP2 peptide (nM)

*Fig. 13B*

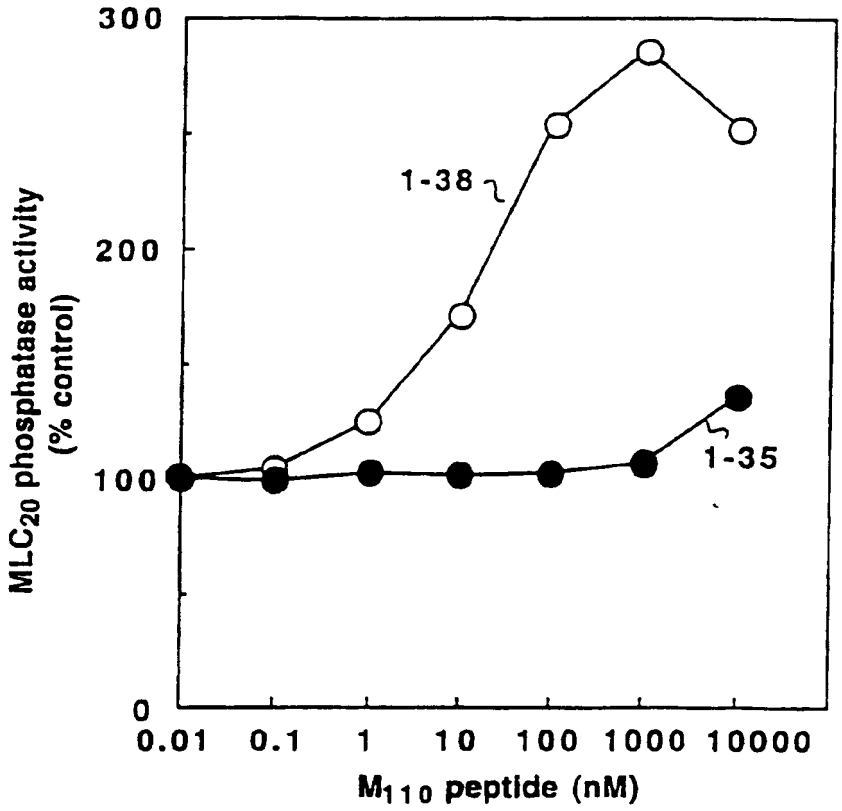

300
200
100
0
MLC20 phosphatase activity
(% control)
1-38
1-35
0.01
0.1
1
10
100
1000
10000
M110 peptide (nM)

*Fig. 14*

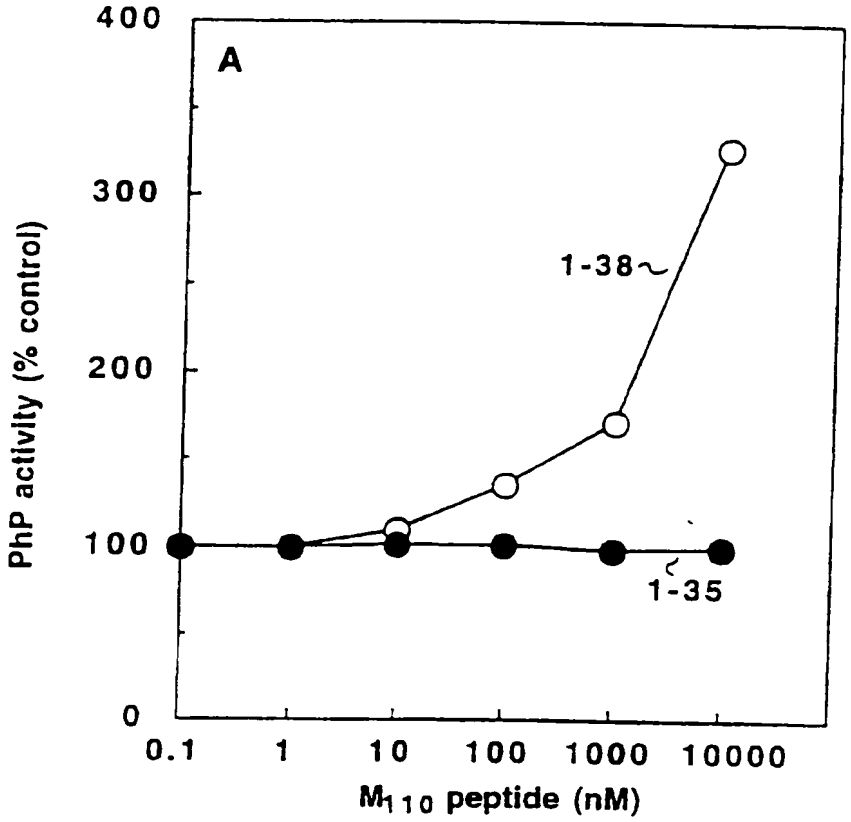

400
300
200
100
0
A
1-38
1-35
PhP activity (% control)
0.1
1
10
100
1000
10000
M110 peptide (nM)

*Fig. 15A*

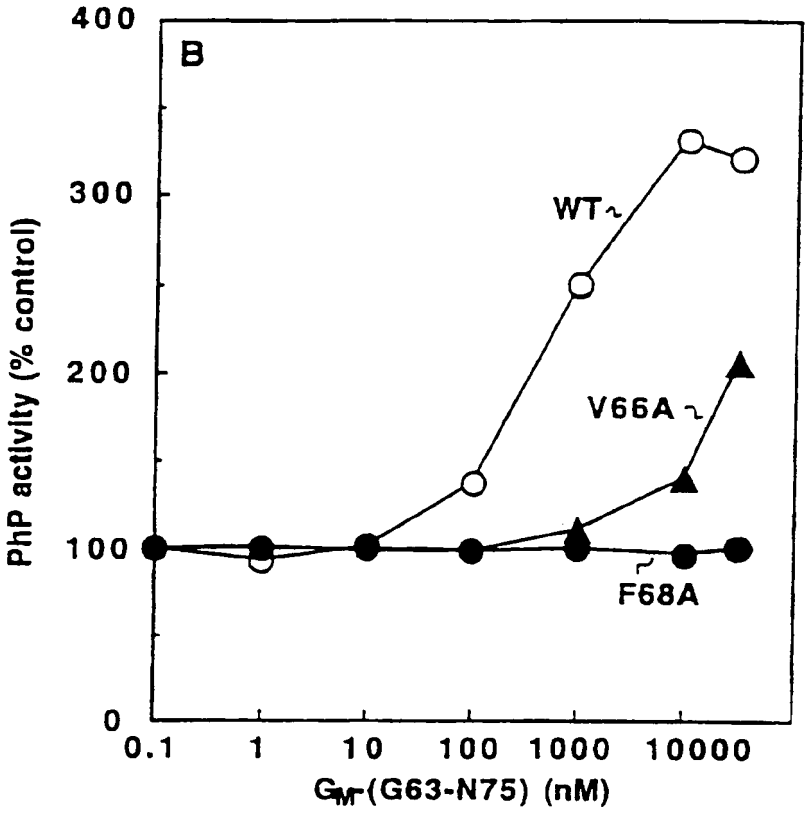

B
400
300
200
100
0
PhP activity (% control)
WT
V66A
F68A
0.1
1
10
100
1000
10000
$G_M$-(G63-N75) (nM)

*Fig. 15B*

*Fig. 16*

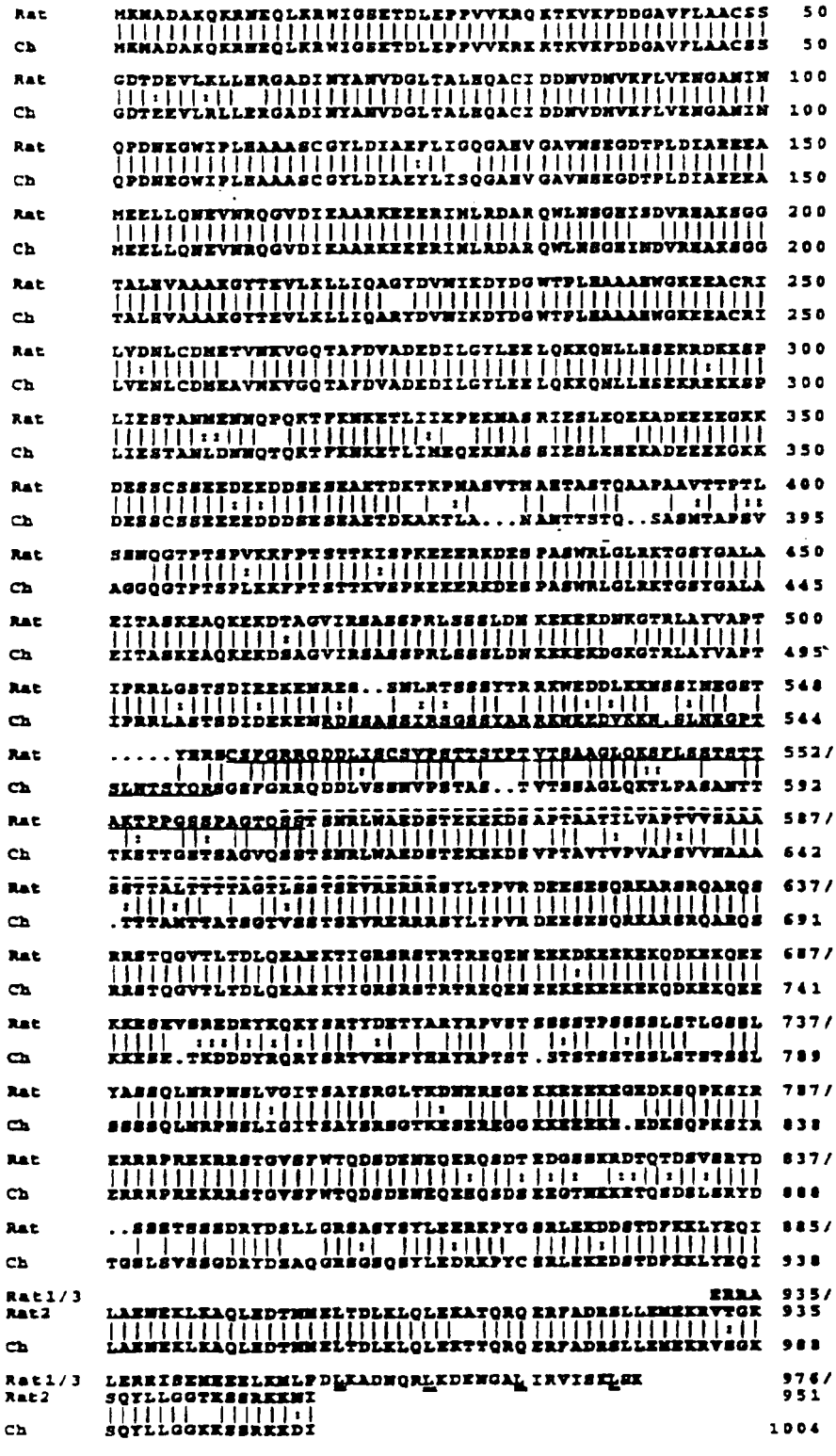


Fig. 17

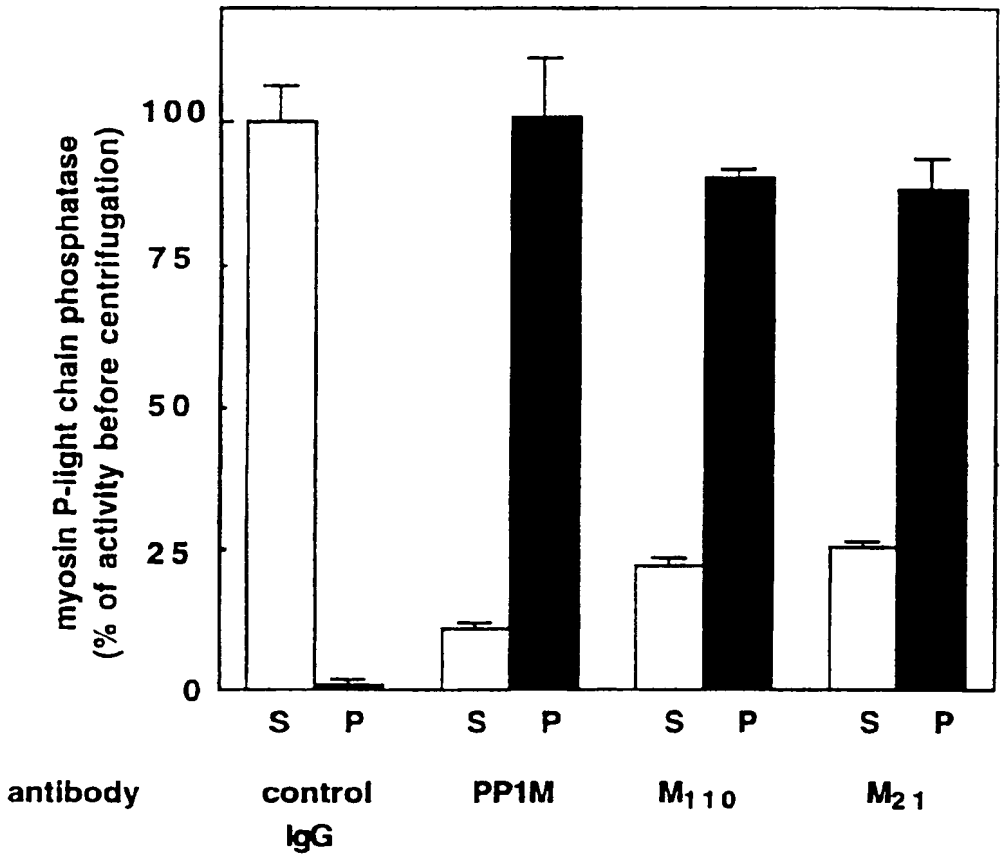

myosin P-light chain phosphatase
(% of activity before centrifugation)
100
75
50
25
0
S P S P S P S P
antibody
control IgG
PP1M
M110
M21

*Fig. 18A*

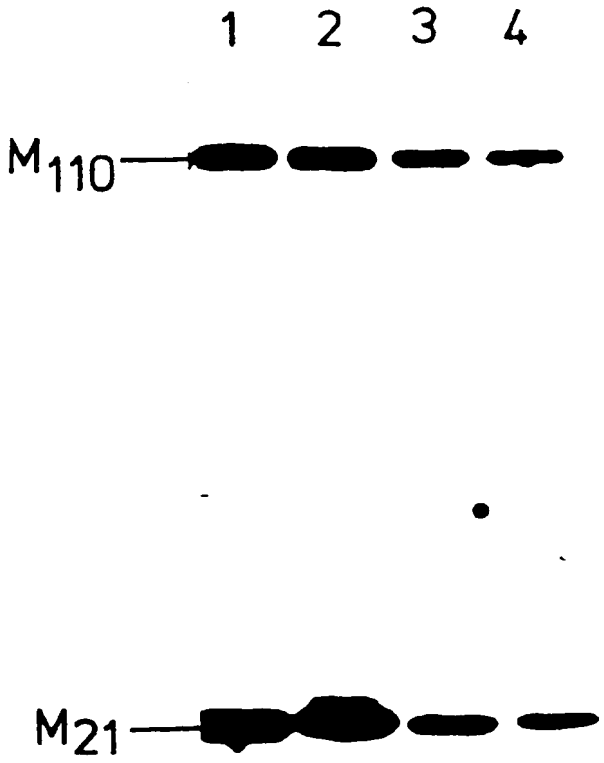



*Fig. 18B*

A

1 2 3 4 5 6 7 8

MBP
714-934
$M_{110}$-(1-477)

MBP

$M_{110}$-(1-309)

GST

B

1 2 3 4 5 6 7 8

C

1 2 3 4 5 6 7 8

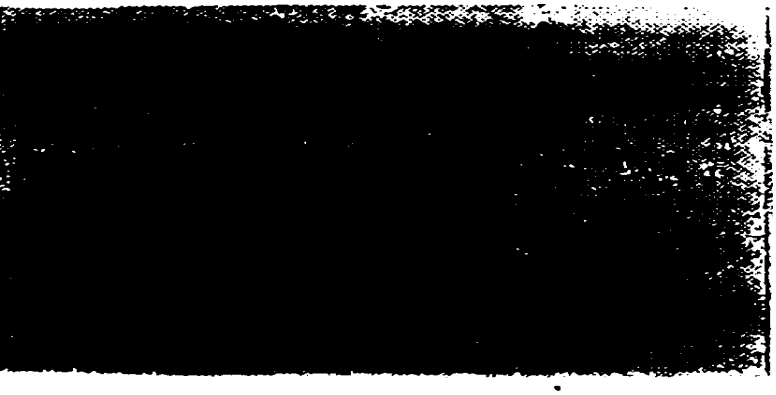


*Fig. 19*

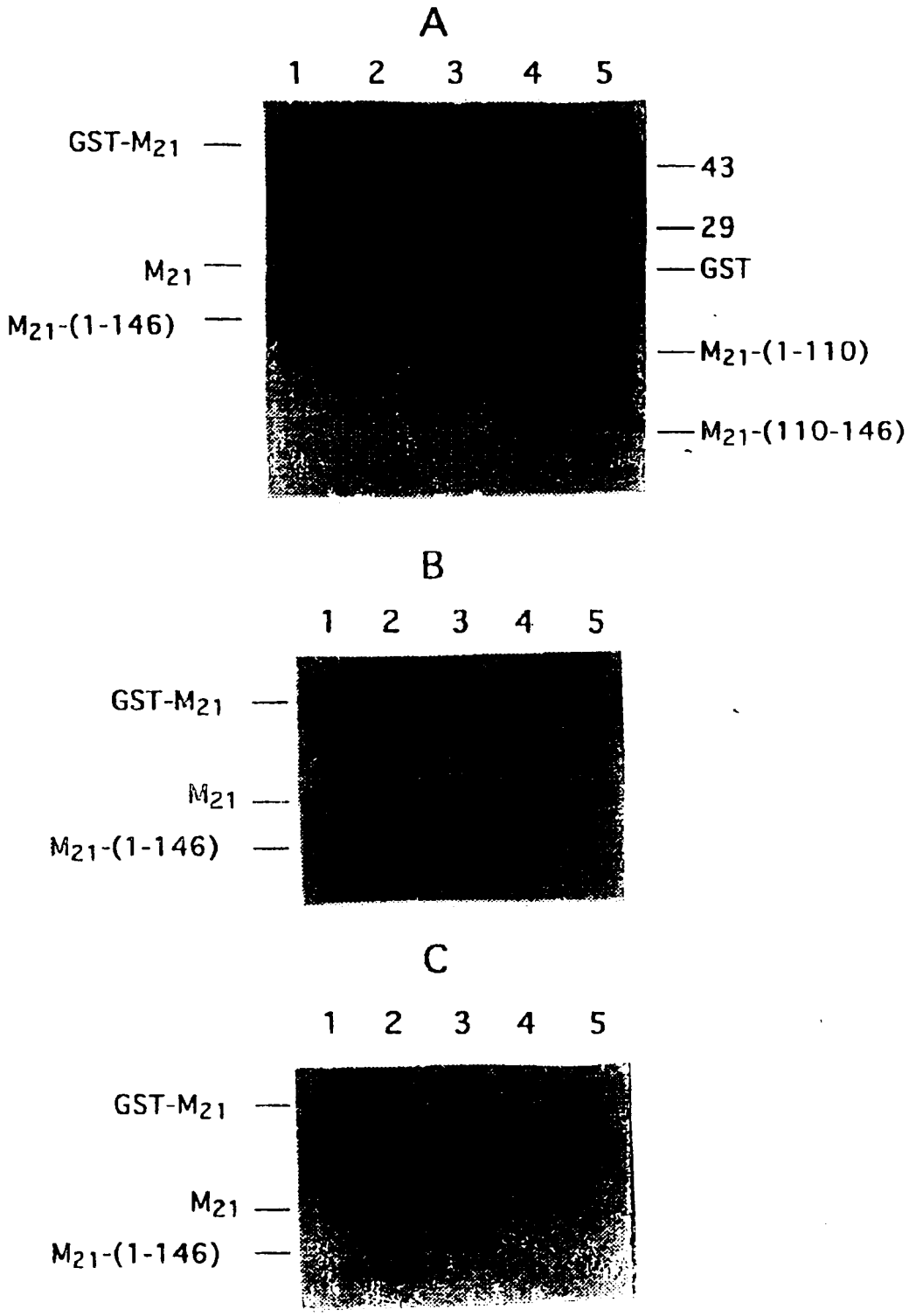

A
1 2 3 4 5
GST-M21
M21
M21-(1-146)
43
29
GST
M21-(1-110)
M21-(110-146)
B
1 2 3 4 5
GST-M21
M21
M21-(1-146)
C
1 2 3 4 5
GST-M21
M21
M21-(1-146)

*Fig. 20*

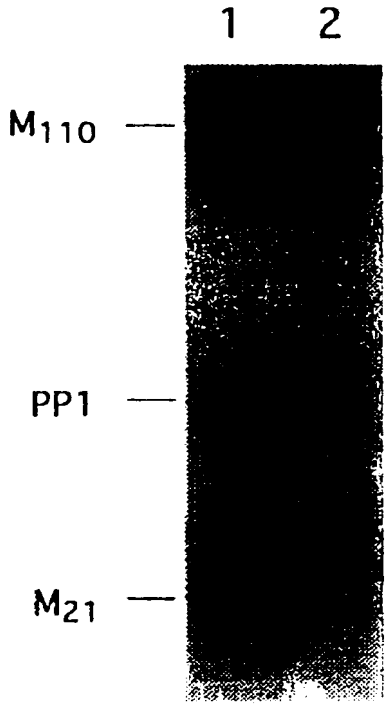



*Fig. 21*

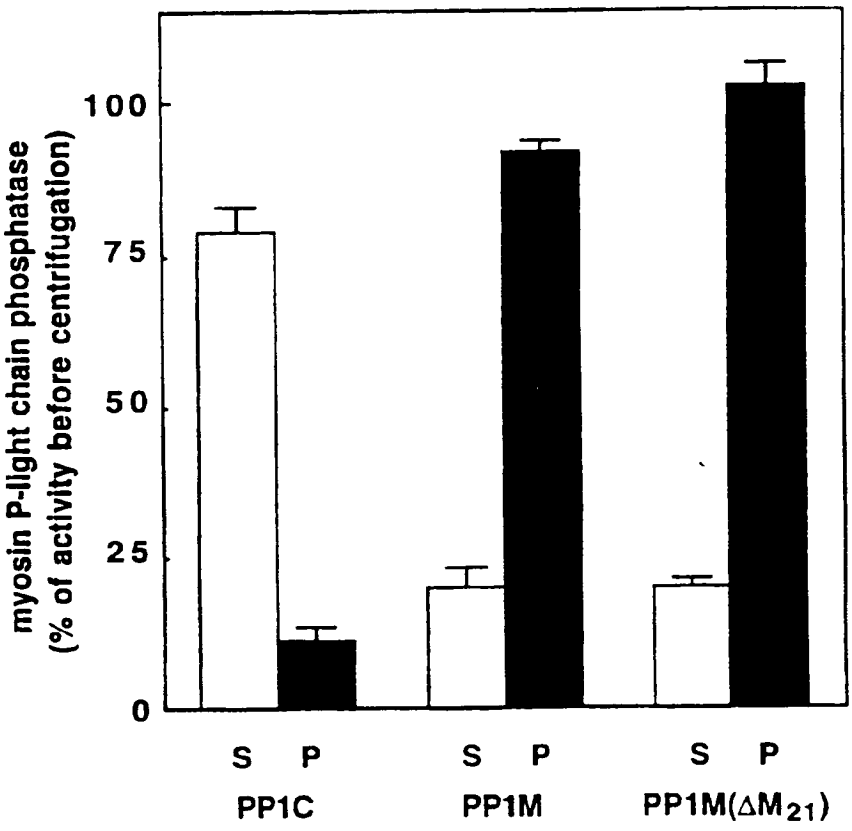
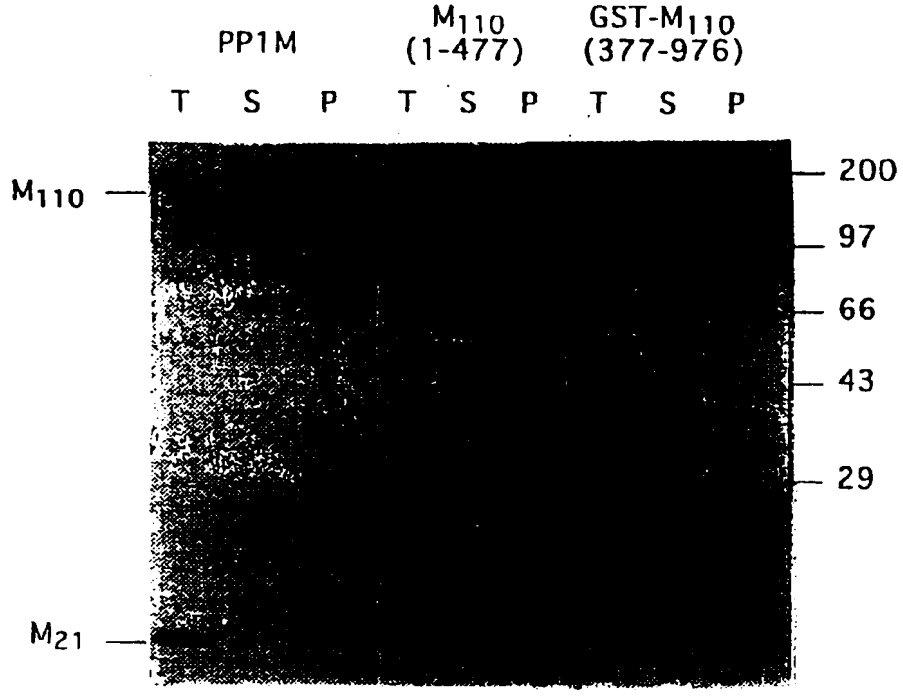

myosin P-light chain phosphatase
(% of activity before centrifugation)
100
75
50
25
0
S P
PP1C
S P
PP1M
S P
PP1M(ΔM21)

*Fig. 22*

A


PP1M
M110 (1-477)
GST-M110 (377-976)
T S P T S P T S P
M110
M21
200
97
66
43
29

B

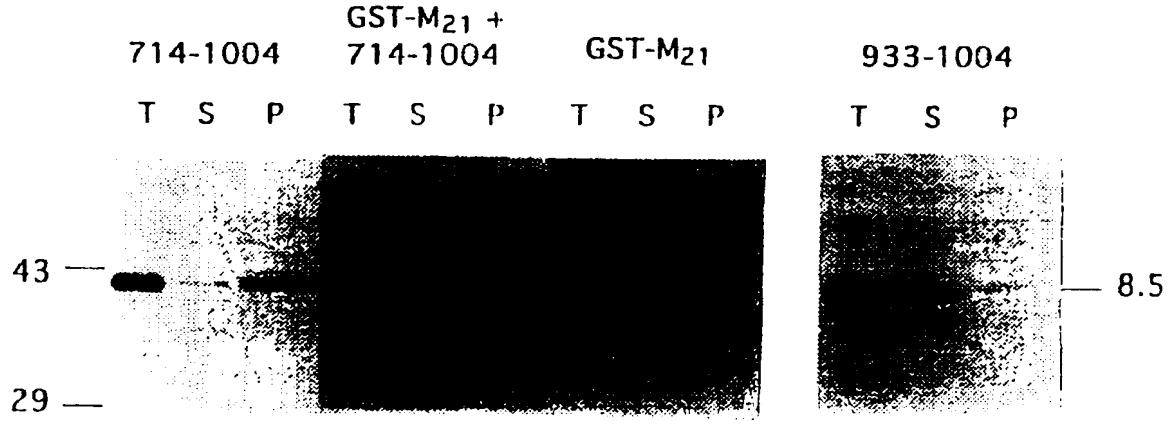

714-1004
GST-M21 + 714-1004
GST-M21
933-1004
T S P T S P T S P T S P
43
29
8.5

*Fig. 23*

A

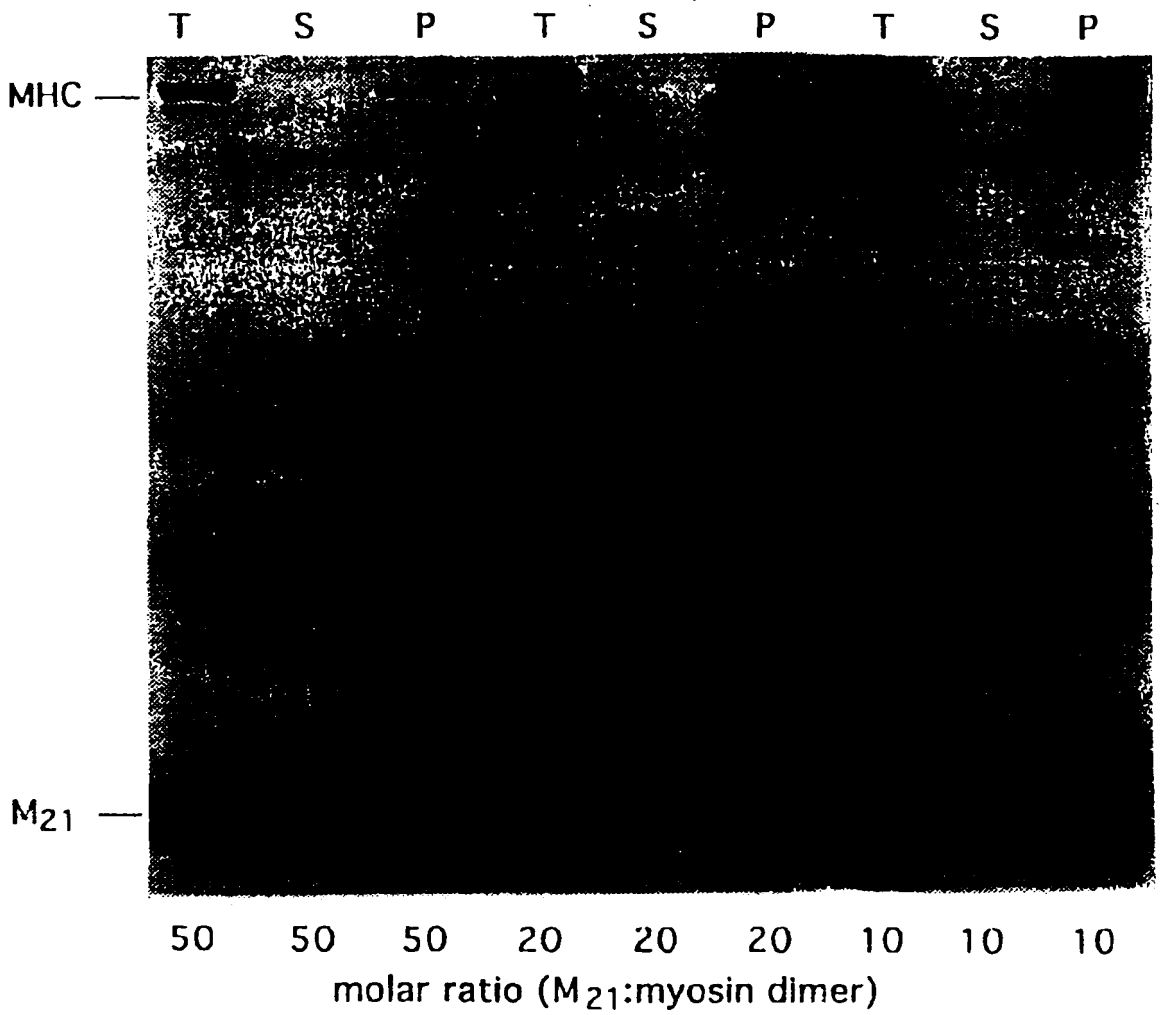

T S P T S P T S P
MHC
M21
50 50 50 20 20 20 10 10 10
molar ratio (M21:myosin dimer)

*Fig. 24A*

B

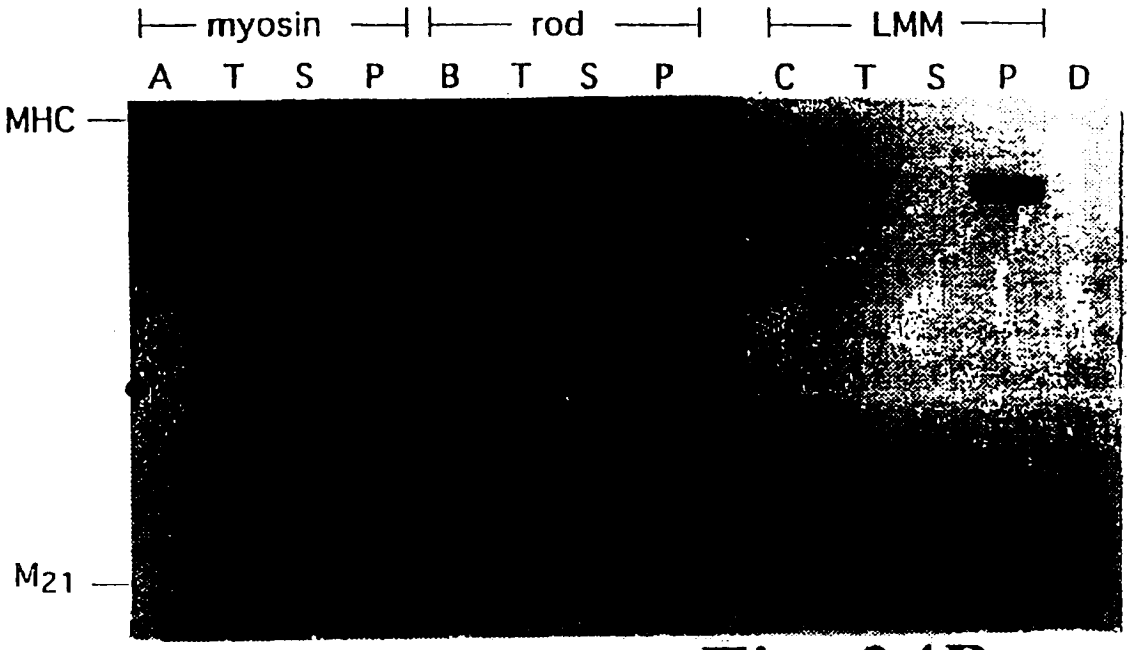



Fig. 24B

C

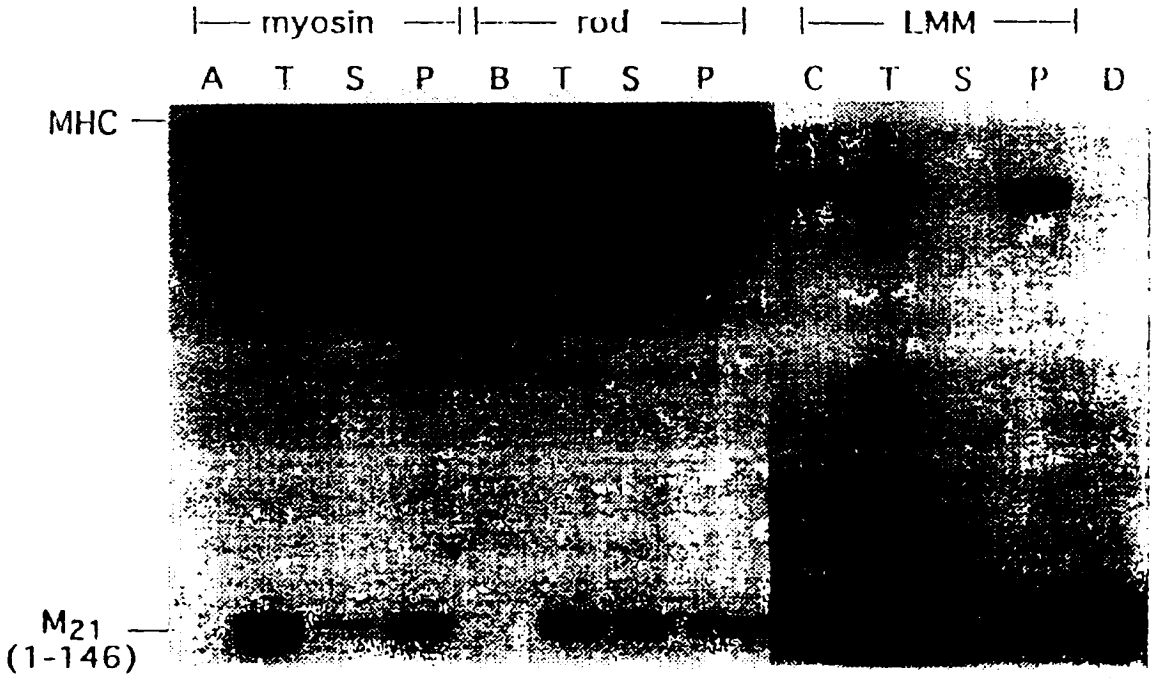



Fig. 24C

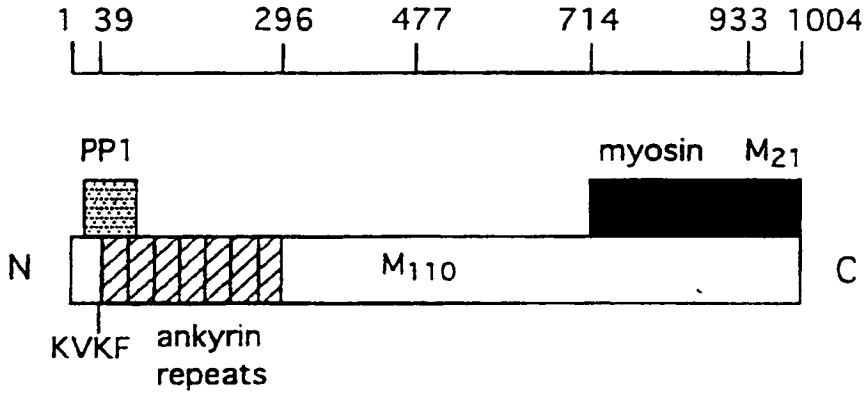

1 39 296 477 714 933 1004
PP1
myosin M21
N
M110
C
KVKF
ankyrin
repeats

*Fig. 25*

# INTERNATIONAL SEARCH REPORT

International Application No
GB 97/00898

A. CLASSIFICATION OF SUBJECT MATTER
IPC 6 G01N33/573 C12N9/12 C07K14/435

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)
IPC 6 G01N C12N C07K

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

C. DOCUMENTS CONSIDERED TO BE RELEVANT

| Category * | Citation of document, with indication, where appropriate, of the relevant passages | Relevant to claim No. |
|---|---|---|
| A | TRENDS IN BIOCHEMICAL SCIENCE, vol. 18, 1 May 1993, OXFORD UK, pages 172-177, XP002037474 M.J. HUBBARD ET AL.: "On target with a new mechanism for the regulation of protein phosphorylation" cited in the application see the whole document --- | 1-35 |
| A | JOURNAL OF MOLECULAR BIOLOGY, vol. 254, 1995, NEW YORK NY USA, pages 942-959, XP002037475 M.P. EGLOFF ET AL.: "Crystal structure of the catalytic subinit of human protein phosphatase 1 and its complex with tungstate." see the whole document --- -/-- | 1-35 |

[X] Further documents are listed in the continuation of box C. [ ] Patent family members are listed in annex.

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"O" document referring to an oral disclosure, use, exhibition or other means
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"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone
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"&" document member of the same patent family

| Date of the actual completion of the international search | Date of mailing of the international search report |
|---|---|
| 13 August 1997 | 21 -08- 1997 |

| Name and mailing address of the ISA | Authorized officer |
|---|---|
| European Patent Office, P.B. 5818 Patentlaan 2 NL - 2280 HV Rijswijk Tel. (+ 31-70) 340-2040, Tx. 31 651 epo nl, Fax (+ 31-70) 340-3016 | Van Bohemen, C |

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# INTERNATIONAL SEARCH REPORT

International Application No
PCT/[redacted] 97/00898

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

| Category * | Citation of document, with indication, where appropriate, of the relevant passages | Relevant to claim No. |
|---|---|---|
| A | CRITICAL REVIEWS IN BIOCHEMISTRY AND MOLECULAR BIOLOGY, vol. 27, no. 3, 1992, BOCA RATON FL USA, pages 227-281, XP002037649 M. BOLLEN ET AL.: "The structure and role and regulation of type 1 protein phosphatase." cited in the application see the whole document --- | 1-35 |
| T | EMBO JOURNAL, vol. 16, no. 8, 1997, HEIDELBERG FRG, pages 1876-1887, XP002037247 M.P. EGLOFF ET AL.: "Structural basis for the recognition of regulatory subunits by the catalytic subunit of protein phosphatase 1." see page 1876, column 2, line 10 - line 49 ----- | 1-35 |

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